STIC-Biotech/ChemLib

170160

From:

Myers, Carla

Sent:

Tuesday, November 01, 2005 8:38 AM

To:

STIC-Biotech/ChemLib

Subject:

sequence search for 10/788,779

Please search SEQ ID NO: 1-10 (these sequences are primers of 24 to 30 nucleotides) and limit the length of the search hits to 50 nucleotides.

Please provide a printout of the first 40 results.

The CRF has been entered http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=10788779

Thank you-

Carla Myers AU 1634 Remsen Bldg / Rm 2E79 Mailbox: REM 2C70 571-272-0747

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search
NA# ______ AA#:_____
S/L: ____ Oligomer:_____
Encode/Transl: _____
Structure #: _____ Text:____
Inventor: _____ Litigation: ____

Vendors and cost where applicable STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

Vol	untary Results Feedback Form												
>	I am an examiner in Workgroup: Example: 1610												
· >	Relevant prior art found, search results used as follows:												
	☐ 102 rejection												
	☐ 103 rejection												
	Cited as being of interest.												
	Helped examiner better understand the invention.												
	Helped examiner better understand the state of the art in their technology.												
	Types of relevant prior art found:												
	☐ Foreign Patent(s)												
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)												
>	Relevant prior art not found:												
	Results verified the lack of relevant prior art (helped determine patentability).												
	Results were not useful in determining patentability or understanding the invention.												
Con	nments:												

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg



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ATERISPAGE PERNY (ESPEN)

f .

A98580 Sequence 5 E38129 Method for AR437122 Sequence AR14248 Sequence BR048674 Sequence

Seguence Alpha-amy Seguence

Sequence Sequence

Sequence

Sequence

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

Database

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1 (bases 1 to 24)
Seidman, C., Seidman, J., Watkins, H. and Rosenzweig, A.
Method for detecting hypertrophic cardiomyophathy associated
mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 24; DB 6; Length 24; ilarity 100.0%; Pred. No. 1.4; Conservative 0; Mismatches 0; Indels
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hematopoietic cells.
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JP 2002543825-A/41.

synthetic construct

synthetic construct

other sequences; artificial sequences.

1 (bases 1 to 26)

Lu, P.S.

    .24
    /organism="unknown"
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CST438207
CQ009087
AX129908
CQ864330
AX476206
                                                               AX004095
AR123280
AR323280
AR3923694
AR095496
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AR173808
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AR065612
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AR448674
BD085791
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I12894.1 GI:910871
Unclassified.
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BD271387
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BD271387 Molecular
AX049220 Sequence
AX040825 Sequence
AX050823 Sequence
AX511114 Sequence
BV142795 PZ02991 Z
BV142797 PZ02991 Z
BV142799 PZ02991 Z
BV142799 PZ02991 Z
BV142799 PZ02991 Z
BV142801 PZ02991 Z
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AR079445 Sequence
AR168767 Sequence
AR217267 Sequence
AR264164 Sequence
AR404008 Sequence
AR406110 Sequence
                                                             November 18, 2005, 11:12:34; Search time 665.886 Seconds (without alignments) 1746.433 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                        4708233 segs, 24227607955 residues
                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                            - nucleic search, using sw model
                                                                                                   US-10-788-779-1
24
1 CAAGGATCGCTACGGCTCCTGGAT
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AX049820
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9b htg: *
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9:
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PAT 26-JUL-1995

linear

Sequence Thermosta

Sequence

AX004095
AR123280
AR395694
AX092759
AX062045
AR01823
AR01823
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Gaps

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Score

Result

PAT 17-JUL-2003

linear

us-10-788-779-1.rge

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PAT 27-SEP-2002
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                                                                                                                                                                                                                                                                                                67.5%; Score 16.2; DB 6; ilarity 85.7%; Pred. No. 9.8e+03; Conservative 0; Mismatches 3;
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85.7%; Pred. No. 9.8e+03;
iive 0; Mismatches 3;
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Patent: WO 0069898-A 329 23-NOV-2000;
Arbor Vita Corporation (US)
Location/Qualifiers
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Patent: WO 0069897-A 329 23-NOV-2000;
Arbor Vita Corporation (US)
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Sequence 329 from Patent WO0069897.
AX050823
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Sequence 362 from Patent W00231512.
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AX511114.1 GI:23392022
                 AX049825.1 GI:12226255
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60/170453 PR
60/182296 PR
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.larity 85.7%; Pred. No. 9.8e+03;
Conservative 0; Mismatches 3; Indels
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Location/Qualifiers
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Key
                                                                                                         US 60/134114,14-MAY-1999 US 60/134118,13-LOCT-1999 US 60/162498,13-DEC-1999 US 60/176195,14-FEB-2000 US 60/196528,11-APR-2000 US 60/196528,11-APR-2000 US 60/196267
Molecular interactions in hematopoietic cells
Patent: JP 2002543825-A 41 24-DEC-2002;
ARBOR VITA CORP
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Patent: WO 0669856-A 329 23 NOV-2000;
Arbor Vita Corporation (US)
Location/Qualifiers
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Sequence 329 from Patent WO0069896.
AX049220
                                           Artificial Sequence
JP 2002543825-A/41
24-DEC-2000
12-MAY-2000 JP 2000618312
14-MAY-1999 US 60/134114
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29-CCT-1999 US
11-APR-2000 US
11-APR-2000 US
11-APR-2000 US
PI PETER S IU
PC CIZNS/06,A6
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Gaps

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38 bp DNA linear STS 05-MAY-2004
P202991 Zea mays SBp. mays Mol7(1) Zea mays Mol7(1) Zea mays STS
genomic, sequence tagged site.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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57 51 47 58 63 70 77 77 72 72
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/db_xref="taxon:4577"
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/dev_stage="seedling"
/note="Corgan: leaf; genomic DNA from inbred line"
<1. ->="8"
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MCMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
Unpublished (2003)
                                                                                                                                      / Match 66.7%; Score 16; DB 11; Length 38; Local Similarity 79.2%; Pred. No. 1.2e+04; nes 19; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Eax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatggagaagttcctcaagcag
Primer B: gtacgtttattcgacaagcagc
STS size: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
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/db_xref="taxon:4577"
/clone lib="Zea mays Mol7(1)"
/dev_stage="seedling"
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Template: 50 ng
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dNTPs:
each 200 um
Tag Polymerase: Redrag (Sigma)
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69 60 54 57 57 52 55 61 58 57
64 68 66.
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/organism="Zea mays"
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Sequencing buffer
d-Rhodamine kit (ABI)
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                                                                                                                                            Query Match
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1 (bases 1 to 38)

MCMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.

MRZ-UCI Joint Syn Discovery

Unpublished (2003)
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44 44
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                                                                                                                                                                                                  Query Match 67.5%; Score 16.2; DB 6; Length 26; Best Local Similarity 85.7%; Pred. No. 9.8e+03; Matches 18; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
121 Steinhaus Hall, Irvine, CA 92697-2525, USA
121 Steinhaus Hall, Irvine, CA 92697-2525, USA
Fax: (949) 824-2581
Email: bgaut@uci.edu
                                                          1..26
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/db_xref="teaxon:32630"
/note="158KIF forward primer"
Patent: WO 0231512-A 362 18-APR-2002;
Arbor Vita Corporation (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer A: gagatggagaagttcctcaagcag
Primer B: gtacgttttattcgacaagcagcc
STS size: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protocol:
PCR amplification of genomic DNA
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Total Vol: 10 ul
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/mol_type="genomic DNA"
/cultivar="OH43"
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each 200 uM
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Sequencing buffer
d-Rhodamine kit (ABI)
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Primer:
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KEYWORDS
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TITLE
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                                       FEATURES
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69 67

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Gaps

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BV142798

BV142798

38 bp

DNA

linear

STS 05-MAY-2004

PZ02091 Zea mays STS

genomic, sequence tagged site.

BV142798.1 GI:47024999
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Zeamatophyta; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
I (basea: 1 to 38)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)
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/note="Organ: leaf; genomic DNA from inbred line"
<1...>38
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                                            Length 38;
                       Score 16; DB 11; Length 30 Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 Steinhaus Hall, Irvine, CA 92697-2525,
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatggagaagttcctcaagcag
Primer A: gagatggagaagttcctcaagcag
Finer B: gagatggagaagttcctcaagcag
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                                                                                     0; Mismatches
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Template: 50 ng
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/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="CML69"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)
                                            66.7%;
79.2%;
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                                        Query Match
Best Local Similarity 79.2<sup>3</sup>
Matches 19; Conservative
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Best Local Similarity
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BV142798
                                                                                                                                                                                                                                                                                                                                   ACCESSION
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P202991 Zea mays ssp. mays Mol7(2) Zea mays Mol7(2) Zea mays STS
genomic, sequence tagged site.
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1 (basea: 1 to 38)

McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.

MPZ-UCI Joint SNP Discovery
Unpublished (2003)
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23 23 35 35 42 33 56
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sequencing ready reaction with amplifag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.
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/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .>38
/note="Organ: leaf; genomic DNA from inbred line"
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                                                                                                    66.7%; Score 16; DB 11; Length 38; 79.2%; Pred. No. 1.2e+04; ive 0; Mismatches 5; Indels
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Dept. Eachogy and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Email: bgaut@uci.edu
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28 28 28 23
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Primer B: gtacgttttattcgacaagcagcc
STS size: 38
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50 51 39 51 43 23 19 29 29 35 32
53 55 48.
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/cultivar="Mo17(2)"
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Total Vol: 10 ul
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d-Rhodamine kit (ABI)
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                                                                                                    Query Match
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KEYWORDS
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BV142800 38 bp DNA linear STS 05-MAY-2004 PZ02991 Zea mays BSP. parviglumis USDA PI566686 Zea mays USDA PI566686 Zea mays subsp. parviglumis STS genomic, sequence tagged
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Zea mays subsp. parviglumis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplifag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.
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MCMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.

MPZ-UCI Joint SNP Discovery

Unpublished (2003)
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.larity 79.2%; Pred. No. 1.2e+04;
Conservative 0; Mismatches 5; Indels
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/organism="Zea mays subsp. parviglumis"
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/cultivar="teol1"
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Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatggagagttcctcaagcag
Primer B: gtacgtttattcgacaagcagc
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/dev_stage="seedling"
/dev_stage="seedling"
/loorgan: leaf; genomic DNA"
/loorgan: leaf; genomic DNA"
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Total Vol: 10 ul
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RedTag (Sigma)
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BV142800.1 GI:47025001
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Best Local Similarity
Matches 19; Conserv
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Zea mays subsp. parviglumis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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MCMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
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/organism="Zea mays_subsp. parviglumis"
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/clone_lib="zea mays JSGyLOS 130"
/dev.stage="seedling"
/note-3"organ: leaf; genomic DNA"
<1...>38
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0; Mismatches
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Fax: (949) 824-2181
Email: bgaut@uci.edu
Trimer A: gagatggggaagttcctcaagcag
Primer B: gtacgttttattcgacaagcagc
STS size: 38
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PCR amplification of genomic DNA
Tommlate: 50 ng
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/cultivar="teo1"
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RedTaq (Sigma)
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Best Local Similarity 79.2'
Matches 19; Conservative
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19; Conservative
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Murgita, R.A.
Recombinant human alpha-fetoprotein as an immunosuppressive agent
Patent: US 6288034-A 12 11-SEP-2001;
Location/Qualifiers
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Murgita, R.A.
Recombinant alpha-fetoprotein for treating and diagnosing cancers
Patent: US 6416734-A 13 09-UUL-2002;
Location/Qualifiers
                                                                                                                                                            1 (bases 1 to 33)
Murgita, R.A.
Recombinant human alph-fetoprotein as an immunosuppressive agent
Patent: 18 596528-A 12 12-0CT-1999;
Location/Qualifiers
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Sequence 12 from patent US 6288034.
AR168767
               33 bp | 1
Sequence 12 from patent US 5965528.
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AR217267
AR217267.1 GI:23316737
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Subraryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
MPZ-UGI Joint SNP Discovery
Unpublished (2003)
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                                              BV142801 38 bp DNA linear STS 05-MAY-2
PZ02991 Zea mays ssp. parviglumis Wilkes Site 6 Zea mays Wilkes
Site 6 Zea mays subsp. parviglumis STS genomic, sequence tagged
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/mol type="genomic DNA"
/cultivar="teol7"
/db xref="taxon:76912"
/clone lib="Zea mays Wilkes Site 6"
/dev stage="seedling"
/note="organ: leaf; genomic DNA"
<1. .>38
                                                                                                                                                                                                                                                                                                                                                                                                                      321 Steinhaus Hall, Irvine, CA 92697-2525, USA Tel: (949) 824-2564 Exa: (949) 824-2181 Email: bgaut@uci.edu
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U.C. Irvine
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Primer B: gtacgttttattcgacaagcag
STS size: 38
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
GNTPs: each 200 uM
Taq Polymerase: Redraq (Sigma)
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Redrag (Sigma)
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BV142801.1 GI:47025002
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              PAT 18-DEC-2003
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1 (Bases 1 to 32) Wurst, W.D. and Prochiantz, A.D. Murst, W.D. te identification of target genes for transcription
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/organism="synthetic construct"
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/note="Computer Generated Probe Sequence."
                                                                                                                                 1 (bases 1 to 33)
Murgita, R.A.
Recombinant alpha-fetoprotein for treating cancers
Patent: US 6630445-A 12 07-OCT-2003;
Location/Qualifiers
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Patent: WO 2016649-A 1340 28-FEB-2002,
Illumina, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1340 from Patent WO0216649.
         33 bp 1
Sequence 12 from patent US 6630445.
AR406110
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/organism="unknown"
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A98580.1 GI:6781632
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synthetic construct
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                                                                                                                                                                                                                                                                                                                                         Unknown.
Unknown.
Unclassified.
1 (bases 1 to 33)
1 (bases 1 to 33)
Murgita, R.A.
Expression and purification of cloned human alpha-fetoprotein
Patent: US 6331611-A 17 18-DEC-2001;
Location/Qualifiers
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Sequence 17 from patent US 6331611.
AR264164
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Sequence 12 from patent US 6627440.
AR404008.1 GI:40151939
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1 (bases 1 to 32)
Wurst,W. and Prochiantz,A.
Method for identification of target genes of transcription factors
Patent: US 6656735-A 5 02-DEC-2003;
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Borchert, T.V., Svendsen, A., Andersen, C., Nielsen, B., Nissen, T.L. and Kjaerulff, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 32)
Borchert, T. Vedel., Svendsen, A., Andersen, C., Nielsen, B., Nissen, T. Lauesgaard. and Kj.ae butted.rulff, Sslashedren.alpha.-amlase mutants
Patent: US 6204232-A 44 20-MAR-2001;
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Patent: US 6673589-A 44 06-JAN-2004;
Location/Qualifiers
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Sequence 44 from patent US 6204232.
AR143248
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Sequence 44 from patent US 6673589.
AR448674
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/mol_type="genomic DNA"
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Unclassified.
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1 (bases 1 to 32)

Labsidianup Lassified.

1 (bases 1 to 32)

Labsidianup Lab and Alan, P.

TITLE
Method for identifying target gene of transcription factor
JOURNAL Patent: JP 1999187876-A 5 13-JUL-1999;

GSF PORSCH ZENTRUM FURE UMWELT & GESUNDHEIT GMBH, CENTRE NATIONAL
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COMMENT OS Unidentified
DE LA RECHERCHE SCIENTIFIQUE
COMMENT OS Unidentified
PR 13-JUL-1999
PP 14-SEP-1999 JP 1998260205
PP 14-SEP-1999 DF 1998260205
PP 15-SEP-1999 DF 19740578.9
PP 16-SEP-1999 DE 19740578.9
PP 16-SEP-1999 DE 19740578.9
PP 18-SEP-1999 JP 1998260205
PP 18-SEP-1999 JP 1999260205
PP 18-SEP-1999 JP 199920205
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                     Patent: EP 0902092-A 5 17-MAR-1999;
GSF FORSCHUNGSZENTRUM UMWELT (DE); CENTRE NAT RECH SCIENT (FR)
Location/Qualifiers
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    .32
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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Sequence 5 from patent US 6656735.
AR437122 GI:40200206

    .32
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Best Local Similarity 81.0°
Matches 17; Conservative
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Best Local Similarity
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Unclassified.
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PAT 16-MAY-2001

RESULT 26 BD085791/c

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Length 36;
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Hayden, M.R., Brooks-Wiison, A.R. and Pimstone, S.N.
Process for identifying modulators of ABC1 activity
Patent: US 6617122-A 233 09-SEP-2003;
Location/Qualifiers
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                                                                                                                                                     Score 14; DB 6; Length 30;
Pred. No. 1.2e+05;
0; Mismatches 5; Indels
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Pred. No. 1.4e+05;
0; Mismatches 2;
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80.0%; Pred. No. 1.9e+05;
ive 0; Mismatches 4;
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Bartley, T.D. and Fox, G.M.
Antibodies to ligands for HEK4 receptors
Patent: US 6169167-A 11 02-JAN-2001;
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
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Sequence 233 from patent US 6617122.
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Sequence 11 from patent US 6169167.
AR123280.1 GI:14108246
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/organism="unknown"
/mol_type="genomic DNA"
                                                                             /note="Oligonucleotide"
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Best Local Similarity 77.3%;
Matches 17; Conservative 0
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Best Local Similarity 88.2
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Matches 16; Conservative
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Datent: JP 2001521739-A 36 13-NOV-2001;

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OS Unidentified

NO Unidentifiers

OS Unidentifiers

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PR 30-OCT-1997 DK 1240/97, 14-UUL-1998 DK PA 199800936 PI

TORBEN VEDEL BORCHERT, ALLAN SVENDEN, KARSTEN ANDERSEN, PI BIYANNE

LENFELDT NIELSEN TORBEN LAUGSGIRLD NISSEN, SOREN PI CARLIPH

PC C12N1S/09, C11D3/386, C12N1/21, C12N15/09, (C12N15/00, C12N1/21, C12N1:09),

PC (C12N1/21, C12R1:07), (C12N1/21, C12N1:09),

PC (C12N1/21, C12R1:07), (C12N1/21, C12N1:09),

PC (T2N1/21, C12R1:07), (C12N1:07), (C12N1:09),

PC (T2N1/21, C12R1:07), (C12N1:07), (C12N1:08),

PC (T2N1/21, C12R1:07), (C12N1:08),

PC (T2N1/21, C12R1:07), (C12N1:08),

PC (T2N1/21, C12R1:07), (C12N1:08),

PC (T2N1/21, C12R1:08),

PC (T2N1/21, C12R1:08)
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Borchert, T.V., Svendsen, A., Andersen, K., Nielsen, B.L., Nissen, T.L.
and Caellph, S.
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Patent: Wo 9923222-A 42 14-MAY-1999;
CAMBRIDGE ANTIBODY TECH (GB); OSBOURN JANE KATHARINE (GB)
Location/Qualifiers
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                                                                                                                                                                                                        linear
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Sequence 42 from Patent WO9923222.

    .32
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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                          CAAGGATCGCTACGGCTCCTGGAT 24
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                                                     31 CATTGATCGTAACGGGTCCTGGTT
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                                                                                                                                                                                                                             Alpha-amylase variant.
BD085791
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PAT 18-DEC-2003

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Unknown.
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AR177808
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                                                                                                              Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                     Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hdl cholesterol and triglyceride levels
Patent: WO 0115576-A 171 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Genes and polypeptides relating to human colon cancers
Patent: WO 03104275-A 68 18-DEC-2003;
Oncotherapy Science, Inc. (JPP); Japan as represented by the
president of the university of Tokyo (JP)
Location/Qualifiers
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// Organism="synthetic construct"
// Organism="synthetic DNA"
// Mol type="unassigned DNA"
// db_xref="taxon:32630"
// note="an artificially synthesized primer sequence"
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synthetic construct
other sequences; artificial sequences.
                           21 bp | 1
Sequence 171 from Patent W00115676.
                                                                                                                                                                                                                                                               1. .21
/organism="Homo sapiens"
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Sequence 68 from Patent WO03104275.
AX962045.1 GI:40881455
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Sequence 3 from patent US 6004780.
AR095496 AR095496.1 GI:10023423
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                                                                    AX092759.1 GI:13444816
                                                                                                 Homo sapiens (human)
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                         AX092759
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ORGANISM
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AR095496/c
                                                                                                               ORGANISM
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AUTHORS
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VERSION
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AX962045
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Phillips,G., Cunningham, B.A. and Crossin, K.L.
Phillips,G., Cunningham, B.A. and Crossin, K.L.
Phillips,G., Cunningham, B.A. and Crossin, K.L.
type III repeats and methods of use
Patent: US 6313265-A 8 06-NOV-2001;
Location/Qualifiers
                                                                                                                                                                                                                                   Gaps
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1 (bases 1 to 49)
Wayne,J. and Xu,S.-y.
Method for cloning and producing the Tsp45I restriction endonuclease in B. coli
Patent: US 5866422-A 17 02-FEB-1999;
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                                                                                                                                                                                                Length 40;
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80.0%; Pred. No. 1.8e+05;
tive 0; Mismatches 4;
                                                                                                                                                                                            56.7%; Score 13.6; DB 6; 80.0%; Pred. No. 1.8e+05;
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              1 (bases 1 to 40)
Soppet, D.R. and Li,H.
Growth factor HTTER36
Patent: US 6004780-A 3 21-DEC-1999;
Location/Qualifiers
                                                                                                                                                                                                                                0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
                                                                                                                                         DNA"
                                                                                                                                                                                                                                                                                                                                                                                           AR031823 49 bp
Sequence 17 from patent US 5866422.
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                                                                                                                        /organism="unknown"
/mol_type="unassigned
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Best Local Similarity
Watches 16; Conservat
Unclassified.
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Best Local Similarity
Matches 16; Conserv
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DEFINITION ACCESSION VERSION KEYWORDS

CQ875256/c

LOCUS

RESULT 35

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ORGANISM

SOURCE

REFERENCE AUTHORS

JOURNAL

FEATURES

ORIGIN

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PAT 08-JUL-2002
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                                                                                                                                                                                                                                                                                           Length 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Mathur, E.J., Lee, E. and Bylina, E.
Thermostable phosphatases
Patent: JP 2001510983-A 12 07-AUG-2001;
DIVERSA CORP
PN JP 2001510983-A/12
PD 07-AUG-2001
PF 19-UN-1997 JP 1998503409
PR 19-UN-1996 US 60/033752
PI ERIC J MATHUR, EDD LEE, EDWARD BYLINA
                                                                                                                                                                                                                                                                                          Score 13.4; DB 6;
Pred. No. 2.3e+05;
0; Mismatches 6;
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                                                                      Unthown.

M Unknown.
Unclassified.

E 1 (bases 1 to 30)

AS Grotendorst, G.R. and lida, N.
Leukocyte derived growth factor 2

AML Patent: US 6673893-A 11 06-JAN-2004;

Location/Qualifiers
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   Sequence 11 from patent US 6673893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Sequence 5 from Patent WO0246456.
AX457963.1 GI:21724858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 bp
                                                                                                                                                                                                        1. .30
/organism="unknown"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                  4 CGACGGTGGCGACGACTCCTGGA 26
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BD062912
BD062912.1 GI:22608515
JP 2001510983-A/12.
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                                   AR448962.1 GI:42677748
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Key
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ilarity 73.9%;
Conservative
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Best Local Similarity
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DEFINITION
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                                                                                    ORGANISM
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TITLE
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AX457963
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Patent: WO 2004075733-A 162 10-SEP-2004;
CHILDREN'S HOSPITAL MEDICAL CENTER (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32650"
/note="Synthetic oligonucleotide primer sequence"
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Grotendorst, G.R. and lida, N.
DNA encoding leukcoyte derived growth factor-2 (LDGF-2)
Patent: US 5849554-A 11 15-DEC-1998;
Location/Qualifiers
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Pred. No. 2.3e+05;
0; Mismatches 6; Indels
55.8%; Score 13.4; DB 6; Length 24; 73.9%; Pred. No. 2.3e+05; ive 0; Mismatches 6; Indels
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                                                                                                                                                                                     CQ875256 24 bp DNA Sequence 162 from Patent WO2004075733.
                                                                                                                                                                                                                                                                    synthetic construct
synthetic construct
other sequences; artificial sequences.
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AR065612
AR065612.1 GI:5995828
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/organism="unknown"
/mol_type="unassigned DNA"
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                                                                  2 AAGGATCGCTACGCTCCTGGAT 24
                                                                                         AAGGATCCCTACCACCCTTGGT 24
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               Best Local Similarity 73.9
Matches 17; Conservative
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Unclassified.
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 Query Match
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ORIGIN

Matches

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JOURNAL FEATURES

TITLE

RESULT 37 AR448962 LOCUS

DEFINITION ACCESSION VERSION

RESULT 36

AR065612

ORGANISM

KEYWORDS

REFERENCE AUTHORS

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CST438207 50 bp DNA linear MAM 04-NOV-2002 Chrysochloris stuhlmanni partial prmp gene for prion protein. AJ438207
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Submitted (06-MAR-2002) Poux C., Biochemistry (161), University of
Nijmegen, NCMLS, PO Box 9101, 6500 HB Nijmegen, NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prion protein; prmp gene.
Chrysochloris stuhlmanni
Chrysochloris stuhlmanni
Eukaryota; Metazoa; Chromiata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Chrysochloridae; Chrysochloris.
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                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                           Isothermal amplification of nucleic acids on a solid support Patent: WO 0246456-A 5 13-JUN-2002; Applied Research Systems ARS Holding N.V. (AN)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poux,C., Van Rheede,T., Madsen,O. and De Jong,W.W. Sequence gaps join mice and men: phylogenetic evidence from deletions in two proteins Mol. Biol. Evol. 19 (11), 2035-2037 (2002)
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/mol_type="genomic DNA"
/db_xref="taxon:185454"
1. .50
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/product="prion protein"
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/db_xref="G1:22799966"
/db_xref="UniProt/TrEMBL:QBMIG7"
/translation="MVKSGLGCWILLLEMAT"
                                                                                                                                                                                         1. .44
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/note="synthetic construct"
               synthetic construct
synthetic construct
other sequences; artificial sequences.
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Matches 17; Conservative
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaq91121 Beta-card	Aca63111 Human bet	Adr05297 Human bet	Adm68395 PCR prime	Aaf16851 KIAA0316	Aaf17495 KIAA0316	Aac99432 Primer #4	Abt06636 PDZ domai	Abq96682 KIAA 0316	Adj80120 RE-DSB ca	Ack06221 Human mic	Ack05595 Human mic	Aat35182 Human alp	Abz70298 Dihydropy	Aaq04591 Probe use	Abg01333 Oligonucl	Abg06613 Oligonucl	Abq06654 Oligonucl	Ack06282 Human mic	Aax22971 Canine En
SUMMARIES	ΙD	AAQ91121	ACA63111	ADR05297	ADM68395	AAF16851	AAF17495	AAC99432	ABT06636	ABQ96682	ADJ80120	ACK06221	ACK05595	AAT35182	ABZ70298	AAQ04591	ABQ01333	ABQ06613	ABQ06654	ACK06282	AAX22971
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AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hyperrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

Non-invasive method for diagnosis of hypertrophic cardio-myopathy useful for testing asymptomatic individual(s).

Example 1; Col 10; 22pp; English.

Aaa76301 Mycobacte	Acd54952 HBV DNAzy	Adm63061 Hepatitis	Aax59667 Mutagenic	Abg83921 Mouse pol	Abk50283 Human mot	Abx12001 Human sta	Aci28366 Human mic	Aad59416 PCR prime	Aax57219 Cysteine	Ado43696 PCR prime	Abx14381 PCR prime	Aaz35063 Feline CD	Aat34298 HEK4 bind	Aac69334 Human ABC	Aaf93000 Polymorph	Ack06220 Human mic	Aci04808 Human mic	Ack05594 Human mic	Aaz35681 IL-2/GM-C	Abs79090 Human apo	Ade71167 tPA-Nef P	Acd27669 HIV-1 hum	Adi00667 RT-PCR pr	Abz21018 Zinc fing
AAA76301	ACD54952	ADM63061	AAX59667	ABQ83921	ABK50283	ABX12001	AC128366	AAD59416	AAX57219	ADO43696	ABX14381	AAZ35063	AAT34298	AAC69334	AAF93000	ACK06220	ACI04808	ACK05594	AAZ35681	ABS79090	ADE71167	ACD27669	ADI00667	ABZ21018
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36	31	31	32	33	33	33	25	26	30	32	33	22	36	21	21	25	25	25	28	31	31	31	31	33
8.09	0.09	0.09	0.09	60.09	0.09	0.09	59.2	58.3	58.3	58.3	58.3	57.5	57.5	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7
14.6	14.4	14.4	14.4	14.4	14.4	14.4	14.2	14	14	14	14	13.8	13.8	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6
21	22	23	c 24	25	26	27	28	29	c 30	31	32	c 33	34	c 35	c 36	c 37	c 38	c 39	40	41	c 42	c 43	44	45

ALIGNMENTS

Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy; diagnosis; primer; mutation; detection; ss. Watkins H, Rosenzweig A; Beta-cardiac myosin heavy chain PCR primer A. (HARD) HARVARD COLLEGE. (BGHM) BRIGHAM & WOMENS HOSPITAL. (GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA. AAQ91121 standard; cDNA; 24 BP 92US-00989160. 92US-00989160. (first entry) Seidman C, WPI; 1995-245715/32. 19-FEB-1996 11-DEC-1992; 11-DEC-1992; US5429923-A. 04-JUL-1995. Seidman J, Synthetic. AAQ91121; RESULT 1

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asymptomatic individuals suspected of having the disease. The method has a broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B. Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease and phenylketonuria
                                                                                                                                                                                                                                                                                                                             Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC; familial hypertrophic cardiomyopathy; SHC; Gaucher's disease; sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia; buchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease; phenylketonuria; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
hemophilia, by detecting a mutation in an amplified product of a beta
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                                                                                               100.0%; Score 24; DB 2; Length 24; 100.0%; Pred. No. 0.17;
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                                                                       Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
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                                                                               Query Match
Best Local Similarity
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Local 24; Conservative
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SEIDMAN J.
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                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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(SEID/)
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(ROSE/)
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The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (sporadic or familial, SHC and FHC) comprises detecting a mutation associated with hypertrophic cardiomyopathy in an amplified product of a beta cardiac myosin heavy chain DNA. The mutations associated with SHC/FHC are detected in the myosin gene isolated from blood, by detecting mis-matched areas in RNA-DNA hybrid double strands (RNA from the normal gene, DNA from the suspect determine life expectancy in affected individuals e.g. using a Kaplan-Moier curve for the classified type of FHC causing point mutation. Also included are an RNA probe comprising ribonucleotides arranged in a sequence which is complementary to at least a portion of beta-cardiac myosin heavy-chain DNA and a set of DNA oligonucleotide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

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oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain DNA. The method is useful for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. This method is especially useful for diagnosing SHC and FHC, as well as for determining the estimated the life expectancy of a person with familial hypertrophic cardiomyopathy. In particular, the method is useful for determining an individual's genetic information, and diagnosing e.g. Gaucher's disease, haemophilia, buchenne's muscular dystrophy, sickle cell anaemia, Tay-sacks disease, phenylketonuria or cystic fibrosis. The present sequence is a PCR primer used to amplify a region of the beta cardiac myosin heavy chain cDNA containing an FHC-associated mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (familial or sporadic, FHC, SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy, comprising amplifying beta-cardiac myosin heavy-chain DNA forming an associated with hypertrophic cardiomyopathy in the amplified product, thus, facilitating the diagnosis of hypertrophic cardiomyopathy also included are a set of DNA oligonucleotide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting mutations associated with hypertrophic cardiomyopathy to diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac myosin heavy-chain DNA and detecting the mutation in the amplified product.
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                           1 CAAGGATCGCTACGGCTCCTGGAT 24
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95US-00469172.
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SEIDMAN J.
WATKINS H.
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exemplification of the invention.

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                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; zinc finger protein 57_21; diabetes; cancer; PCR; primer; ss.
                                                                                                                                                                                                                                                  chain having a disease-related point mutation.
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amplify beta-cardiac myosin heavy-chain DNA (the set of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function of an endothelial cell or haematopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a PDZ domain protein and a PL domain protein to result in inhibition of leukocyte activation. The present sequence is a PCR primer for a PDZ domain. PDZ domains of proteins are named after three prototypical proteins: PSD95, Drosophila large disc protein and Zonula Occludin 1 protein. PDZ domain proteins are involved in synapse formation by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New inhibitors of binding of a PDZ protein and PL protein for inhibiting T cell-mediated response by hematopoietic cells, or for treating diseases characterized by inflammatory and humoral immune responses, e.g.
                                                                                                                                                                                                                                                                                                                                                             PL domain protein; leukocyte activation; synapse formation; transmembrane neurotransmitter receptor; autoimmune disease; transplantation rejection; inflammation; allergy; inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis; asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease; ischaemia; vasulitis; Crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                               Endothelial cell; haematopoietic cell; PDZ domain protein; PCR primer;
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                                                                  Gaps
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                                  Length 33;
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Sequence 33 BP; 8 A; 9 C; 9 G; 7 T; 0 U; 0 Other;
                              DB 11;
                              Score 16.4; DB 11;
Pred. No. 6.7e+02;
0; Mismatches 1;
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14-MAX-1999; 99US-0134117P.
14-MAX-1999; 99US-0134118P.
29-OCT-1999; 99US-0166498P.
13-DBC-1999; 99US-0176453P.
14-JAN-2000; 2000US-0176453P.
14-FBB-2000; 2000US-0176453P.
11-APR-2000; 2000US-01256P.
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94.4%;
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11-APR-2000; 2000US-0196528P.
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                                                                                                 3 AGGATCGCTACGGCTCCT
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                                Query Match 68.3
Best Local Similarity 94.4
Matches 17; Conservative
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Modulating a biological function of an endothelial cell or hematopoietic
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21-OCT-1999;
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14-JAN-2000;
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                  interactions. The inhibitors identified by the present invention can be used to treat a disease mediated by haematopoietic cells, e.g. autoimmune disease, inflammation, allergy (e.g. drug allergies), inflammatory bowel diseases, unflammation, ileitis, psoriasis, respiratory allergic diseases, ulcerative colitis, ileitis, psoriasis, respiratory allergic rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes, rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes, infectious diseases (e.g. viral infection), ischaemia, vasulitis and transplantation rejection of a solid organ transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating a biological function of a hematopoietic cell for treating an allergic response, or diseases mediated by immune system cells, comprises introducing into the cell a PDZ-PL interaction enhancer or inhibitor.
  organising transmembrane neurotransmitter receptors through intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplantation rejection; inflammation; allergy; inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis; asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endothelial cell; haematopoietic cell; PDZ domain protein; PCR primer; PL domain protein; leukocyte activation; synapse formation; transmembrane neurotransmitter receptor; autoimmune disease;
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                                                                                                                                                                                                                                                                                                           67.5%; Score 16.2; DB 4; Length 26; 85.7%; Pred. No. 8.2e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                  Seguence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;
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99US-0162498P.
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Matches 18; Conservative
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The present invention relates to a method for modulating a biological function of an endothelial cell or haematopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a PDZ domain protein to result in inhibition of a PDZ domain protein to result in inhibition of a PDZ domains of proteins are named after three prototypical proteins. PBD5 Jonains are involved in synapse formation 1 proteins are involved in synapse formation by creating transmembrane neurotransmitter receptors through intracellular interactions. The inhibitors identified by the present invention can be used to treat a disease mediated by the present invention can be used to treat a disease mediated by the present invention can be used to treat a disease mediated by the present invention can be used to treat a disease mediated by the present invention can be used to treat a disease mediated by the present invention can be used to treat a disease mediated by the present invention can be used to treat a disease mediated by the present invention can be used a transplant diseases (e.g. viral infection), ischaemia, vasulitis and crohn's disease. The inhibitors can also be used to prevent transplant transplant
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                                                                                                                            function of an endothelial cell or hematopoietic cell. The method between a bpz protein and a PLO protein. The inhibits binding between a PDZ protein and a PLO protein. The inhibitor is used to treat a disease mediated by hematopoietic cells, e.g. autoimmune disease. It may also be used to prevent transplantation rejection of a solid organ allergy, inflammatory bowel diseases, ulcerative colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis, graft rejection, transplantation rejection, tatherosclerosis, cancers, infectious diseases, ischemia, vesulitis and Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to methods and reagents for determining the apparent affinity (Kd) of binding between a PDZ domain and a ligand. The invention also relates to methods and reagents for determining the Ki of an inhibitor of binding between a PDZ domain and a ligand, identifying an agent that enhances binding of a PDZ domain and a ligand, and determining the potency (K-enhancer) of binding between a PDZ domain and a ligand, by
cell, useful for treating autoimmune diseases and infectious diseases, by administering an antagonist that inhibits binding between a PDZ protein
                                                                                                                  invention relates to a new method for modulating a biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assays for determining the affinity of binding between a PDZ domain and a ligand, and determining the Ki of an inhibitor of the binding, comprises using a polypeptide comprising a PDZ domain and a non-PDZ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;
ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;
inflammatory; humoral immune response; inflammation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            67.5%; Score 16.2; DB 4; Length 26; 85.7%; Pred. No. 8.2e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;
                                                                            Disclosure, Page 28-43; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDZ domain PCR primer SEQ ID No 362.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 43; 164pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 85.7 nes 18; Conservative
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              PDZ domain and a non-PDZ domain on a surface. The modulator (preferably, an inhibitor) of interaction between PDZ and PL is useful for treating a disease characterised by leukocyte activation, e.g., an autoimmune disease that is characterised by inflammatory or humoral immune response, and for reducing inflammation in a subject. This sequence represents a PDZ domain protein related PCR primer of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method (M1) for modulating a biological function of an endothelial cell or haematopoietic cell. M1 comprises introducing into the cell, an agent that inhibite binding of a PDZ (PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein) protein and a PDZ ligard (PL) protein in the cell, and so modulates the
determining the ligand bound with an immobilised polypeptide comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hematopoletic cell e.g., a T-cell or B-cell comprises introducing into the cell, an agent that inhibits binding of a PDZ protein and a PDZ ligand protein in the cell.
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                                                                                                                                                                                             Length 26;
                                                                                                                                                                                           Score 16.2; DB 6; Length 2
Pred. No. 8.2e+02;
0; Mismatches 3; Indels
                                                                                                                                                      Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIAA 0316 PDZ domain forward PCR primer 158KiF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 48-49; 207pp; English.
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                                                                                                                                                                                                                                                                            2 AAGGATCGCTACGGCTCCTGG
                                                                                                                                                                                                                                                                                                               2 AAGGATCCCTCCGGCTCCTCG
                                                                                                                                                                                           67.5%;
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24-NOV-2000; 2000US-0072515.
24-NOV-2000; 2000US-00722069.
28-NOV-2000; 2000US-00724553.
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                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ96682 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-2002 (first entry)
                                                                                                                                                                                                                                    18; Conservative
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                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                             Query Match
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biological function. Also described is a method (M2) for determining whether a test compound is an inhibitor of binding between a PDZ protein and a PL protein. M1 is used for modulating a biological function of an endothelial cell or haematopoletic cell e.g., T-cell or B-cell, by an inflammatory or humoral immune response, or an autoimmune disease. An inflammatory or humoral immune response, or an autoimmune disease. An activation, where the disease is characterised by leukocyte activation, where the disease is characterised by an inflammatory or humoral immune response, e.g., an autoimmune disease. The compounds e.g., burnoral immune response, e.g., an autoimmune disease. The compounds e.g., inflammatory and humoral immune responses e.g., inflammatory and humoral immune responses e.g., inflammatory and humoral immune responses e.g., inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis, inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis, diseases such as asthma, allergic rhinitis, transplantation rejection (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver, autologous, bone marrow, xenotransplantation), atherosclerosis, cancers, angiogenesis-dependent disorders, infectious diseases and ischaemia.

ABQ96620 to ABQ96732 and ABB63153 ro ABB63518 represent sequences used in the exemplification of the present invention \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

67.5%; Score 16.2; DB 6; Length 26; 85.7%; Pred. No. 8.2e+02; ive 0; Mismatches 3; Indels 2 AAGGATCGCTACGGCTCCTGG 22 Query Match
Beet Local Similarity b..
Local Similarity b..
Then 18; Conservative à 요

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Gaps

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2 AAGGATCCTCCGGCTCCTCG 22

ADJ80120 standard; DNA; 24 BP. RESULT 10 ADJ80120

(first entry) 06-MAY-2004 ADJ80120;

RE-DSB cassette internal primer, SEQ ID No 79.

in vivo; site-directed mutagenesis; mutation; integrative recombinant oligonucleotide; IRO; CORE-cassette; primer; ss; counterselectable reporter.

Unidentified

WO2003012036-A2

13-FEB-2003

26-JUL-2002; 2002WO-US023634

27-JUL-2001; 2001US-0308426P

(USSH) US DEPT HEALTH & HUMAN SERVICES.

ĽĶ; Lewis Storici F, Resnick MA,

WPI; 2003-289875/28

In vivo mutagenesis enabling site-specific mutations, deletions and insertions with integrative oligonuclectides, useful as diagnostic tools where biological consequences are assessed in the creation of strains or

Disclosure; SEQ ID NO 79; 96pp; English.

The invention relates to a novel method for in vivo site-directed mutagenesis which involves introducing a mutation into a target double-stranded nucleic acid sequence having a first and second strand in a cell. The method comprises introducing a double-stranded nucleic acid cassette into a target nucleic acid sequence at an insertion point,

transforming the cell with a first oligonuclectide, and selecting for employs using integrative recombinant oligonuclectides (IRDS). The cassette is an Reporter (RE)-cassette and contains a first portion homologous to a nucleic acid sequence on a first side of the insertion homologous to a second nucleic acid sequence on a second side of the insertion point, and a nucleic acid sequence on a second side of the insertion point, and a nucleic acid sequence encoding a reporter located between the first portion and the second portion. The first oligonucleotide comprises a nucleic acid sequence concern the chosen strand) of the target nucleic acid sequence of the insertion on the first side of the insertion point, and a nucleic acid sequence the chosen strand of the target nucleic acid sequence of position on the second side of the insertion point, and sequence at a position on the second side of the insertion point, and comprising at least one nucleotide that differs from the chosen strand of the target nucleic acid sequence cencoding the reporter gene indicates integration of the oligonucleotide sequence comprising at least one nucleotide that differs from the carget conding the reporter gene indicates integration of the oligonucleotide sequence comprising at least one nucleotide that differs from the carget conding the cassetter at a different position within a gene, such that consequences assessed. The methods and compositions are useful as consequences assessed. They can also be used in targeted changes in the consequences assessed. They can also be used in targeted changes in the variant used in the consequence of various organisms, modification of large human genes and larger variant used in the number of various organisms, modification of large human genes and larger variances of site-directed mutagenesis. This polymucleotide represents a variance of various organisms, publication of large human genes and larger variances as the consequence on a larger consequence. ö Gaps ö 63.3%; Score 15.2; DB 10; Length 24; 85.0%; Pred. No. 2.4e+03; Indels Sequence 24 BP; 2 A; 9 C; 11 G; 2 T; 0 U; 0 Other; primer used in the method of the invention.

0; Mismatches Query Match
Best Local Similarity 85.0'

3 AGGATCGCTACGGCTCCTGG 22

8

Aggarcaccacacarccaga 22 셤

ACK06221 standard; DNA; 25 14-OCT-2003 (first entry)

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison. US2003104410-A1 Homo sapiens.

Human microarray DNA oligonucleotide SEQ ID NO 106202.

(AFFY-) AFFYMETRIX INC.

15-MAR-2002; 2002US-00098263. 16-MAR-2001; 2001US-0276759P

05-JUN-2003.

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 106202; 9pp; English.

The invention in the coorse a marcoatray comparison of the invention in the invention in the coorse a marcoatray comparison of the perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by phybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. Each of the probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms. Or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid for the signation to identify or detect the sequence or specific comparisons of any gene, in mapping the 5' terminion of many gene, in mapping the 5' terminion of many gene, in situations of supplied the sequence or specific conditional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence or sequence invention discloses a microarray comprising a plurality of nucleic 8899999999999999999999888

Sequence 25 BP; 7 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

ö Gaps ; 0 63.3%; Score 15.2; DB 9; Length 25; 85.0%; Pred. No. 2.46+03; ive 0; Mismatches 3; Indels Query Match
Best Local Similarity 85.0

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ACK05595/c RESULT 12

ACK05595 standard; DNA; 25 BP.

ACK05595;

(first entry) 14-OCT-2003 Human microarray DNA oligonucleotide SEQ ID NO 105576.

ss; probe; expressed sequence tag; microarray; gene expression; tic variation; biallelic marker; polymorphism; human; cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC.

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 105576; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its

perfect match, perfect mismatch, antisense match or antisense mismatch.
Also disclosed is a method of gene expression analysis. The array is used
in monitoring gene expression levels by hybridisation to a DNA library,
in analysis of genetic variation or in hybridisation of tag-labelled
compounds. The nucleic acid probes are specifically designed for analysis
of at least one target sequence. The method of analysis comprises
compounds are attached to a solid support. The analysis comprises monitoring
compounds are attached to a solid support. The analysis comprises monitoring
gene expression levels, identifying biallelic markers or polymorphisms,
cor family members of a gene and a cross species comparison. Each of the
mucleic acids further comprises a tag sequence. The array of nucleic acid
probes is useful in in situ hybridisation, in Southern, Northern or dotcorrect and subclones containing sequence or specific
mutations of any gene, in mapping the 5' termini of mRNA molecules by
primer extensions or in screening CDNA or genomic libraries or subclones
for additional subclones containing segments of DNA that have been
conclained and previously sequenced. The sequence presented is one of the
nucleic acid probes incorporated in the microarray. Note: The sequence
data for this patent can also be obtained in electronic format directly
from USPTO at sequence.html

Seguence 25 BP; 7 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Gaps .; 0 63.3%; Score 15.2; DB 9; Length 25; 85.0%; Pred. No. 2.4e+03; Indels Mismatches ..0 Ouery Match
Best Local Similarity 85.07

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RESULT 13

AAT35182 standard; DNA; 33 BP **AAT35182**

AAT35182;

27-NOV-1996 (first entry)

Human alpha-foetoprotein DNA primer DomII3.

Alpha-foetoprotein; AFP; cell proliferation; bone marrow; autoimmune disease; breast cancer; prostate cancer; neoplasm; tumour; myelotoxicity; therapy; cell culture medium; primer; PCR;

Synthetic.

polymerase chain reaction; ss.

WO9622787-A1

01-AUG-1996

966000SD-0M96 24-JAN-1996; 95US-00377309. 95US-00377311. 95US-00377316. 95US-00377317. 95US-00505012. 24-JAN-1995; 24-JAN-1995; 24-JAN-1995; 24-JAN-1995

(MURG/) MURGITA R A.

21-JUL-1995;

Murgita RA;

WPI; 1996-362459/36.

New isolated recombinant human alpha-fetoprotein - used for treating autoimmune diseases or neoplasms, for inhibiting myelotoxicity or promoting bone marrow cell proliferation.

Example; Page 40; 133pp; English

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Bovine metallo-thionein regulatory region fragment - providing inducible expression of polypeptide in presence of heavy metal.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene being screened is bovine metallothionein regulatory gene it can used as an operator linked to the coding region of an heterologous sequence, and is induced in the presence of heavy metals esp. Cd and
                                                                   Probe used to screen cDNA library of bovine heavy metal responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 62.5%; Score 15; DB 2; Length 36; Best Local Similarity 78.3%; Pred. No. 3.1e+03; Matches 18; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36 BP; 6 A; 8 C; 16 G; 6 T; 0 U; 0 Other;
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                                                                                                                ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAAGGATCGCTACGGCTCCTGGA 23
                                                                                                              Metallothionein; bMT-II; operator;
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29-AUG-2000; 2000US-0228854P.
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                                         (first entry)
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                                                                                                                                                                                                                                                                                                              Williams ME, Murphy MF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                                                                           WPI; 1990-157607/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200216649-A2.
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                                         27-SEP-1990
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                                                                                                                                                                                                  23-MAY-1990
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              AAQ04591;
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       PCR primers (AAT35179-85) were used to amplify cDNA coding for fragments of human mature recombinant alpha-foetoprotein (AFP). Plasmid pI18, which contains the coding region of AFP (see also AAT3513), was used as template. Primer DomII3 (AAT35182) was used with primer DomII5 (AAT35181) to amplify AFP domain II (AAR99224) cDNA, and with primer DomI25 (AAT35179) to amplify domain I+II (AAR99222) cDNA. The recombinant AFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a PCR
                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to dihydropyrroline-5-carboxylic acid reductase 8.91 (see ABP59181). The protein can be used for treating diseases such as cancer and HIV infection. The present sequence is a primer, which was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                         Dihydropyrroline-5-carboxylic acid reductase 8.91; enzyme; cancer; HIV infection; anti-HIV; cytostatic; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide-dihydropyrroline-5-carboxylic acid reductase 8.91 and polynucleotide for coding it.
                                                                                                                                                                                                                                                                                                                                                                                               Dihydropyrroline-5-carboxylic acid reductase 8.91 PCR primer #4.
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                                                                                                                                                      Length 33;
                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                          Sequence 33 BP; 10 A; 6 C; 6 G; 11 T; 0 U; 0 Other;
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                                                                                                                                                 62.5%; Score 15; DB 2; I ilarity 78.3%; Pred. No. 3.1e+03; Conservative 0; Mismatches 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 17 (Disclosure); 32pp; Chinese.
                                                                                                                                                                               0; Mismatches
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                                                                                              fragments have therapeutic appln
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AAQ04591/c
ID AAQ04591 standard; DNA; 36 BP.
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Best Local Similarity
Local 18; Conserve
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Best Local Similarity
Matches 18; Conserv
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Length 24; Indels

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25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid above method is useful for detecting a target nucleic acid, which (I) The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an oligonucleotide array (I) comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 60.8%; Score 14.6; DB 6; Length 24; Local Similarity 81.0%; Pred. No. 4.7e+03; nes 17; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                           Sequence 24 BP; 1 A; 7 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24 BP; 7 A; 9 C; 7 G; 1 T; 0 U; 0 Other;
                                                                       Score 14.6; DB 6;
Pred. No. 4.7e+03;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide array; adapter sequence; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide adapter/capture probe 6645
                                                                                                                                                                       4 GGATCGCTACGCCTCCTGGAT 24
                                                                                                                                                                                                                  2 derrederacedederri 22
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                                                                       60.8%;
81.0%;
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29-AUG-2000; 2000US-0228854P.
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ID ABQ06654 standard; DNA; 24
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                                                                                                                         Conservative
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                                                                                        Local Similarity
nes 17; Conserv
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                                                                                                                                                                                 The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
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                                           Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide array; adapter sequence; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGTTCGCTACGGCGGCTGGTT 22
                                                                                                                                         Claim 1; Page 75; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GGATCGCTACGGCTCCTGGAT
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29-AUG-2000; 2000US-0228854P.
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WPI; 2002-292068/33
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Best Local Similarity
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This invention describes the identification of transcription factor responsive elements and/or target genes and/or cofactors of transcription factors. The method comprises: (a) introducing a gene trap vector into a eukaryotic cell in culture, where the vector contains a reporter gene, a polyadenylation sequence and a selectable marker gene; (b) selecting cells containing the vector; (c) contacting the cells with a transcription factor; (d) identifying and culturing cells that exhibit a change in reporter gene activity; and (e) identifying the target genes and/or cofactors of the transcription factors and/or the transcription factor responsive elements. The gene trap technique has been used to show that the Engrailed homeodomain (EnHD) has target sequences within an internal promoter/enhance of the bulllous pemphigoid antigen (BPAG1) gene locus of embryonic stem cells. This sequence represents a PCR primer used
                                                                        Transcription factor responsive element, cofactor, embryonic stem cell; gene trap vector, engrailed homeodomain; EnHD; BPAG1; target gene; En-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identification of transcription factor targets - using gene trap vector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.8%; Score 14.6; DB 2; Length 32;
81.0%; Pred. No. 4.8e+03;
Live 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32 BP; 3 A; 10 C; 9 G; 10 T; 0 U; 0 Other;
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(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                   gene trap vector; engrailed homeodomain; En
bullous pemphigoid antigen; PCR primer; ds.
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les 17; Conservative
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                        Canine EnHD PCR primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wurst W, Prochiantz A;
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                                                                                                                                                                                                       Canis familiaris.
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Matches
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BXBXBXBXBXGXGXG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening the 5' termini of mRNA molecules by primer extensions or in screening segments of BNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acids to at least two or more nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                         EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.8%; Score 14.6; DB 9; Length 25; 81.0%; Pred. No. 4.7e+03; live 0; Mismatches 4; Indels
                                                                        Human microarray DNA oligonucleotide SEQ ID NO 106263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 106263; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AAGGATCGCTACGGCTCCTGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || |||| ||| ||||| ||||| ||| AACGATCTCTAAGGCTCCAAGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX22971 standard; DNA; 32 BP
                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-2001; 2001US-0276759P
                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.8
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                               cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                US2003104410-A1
                                                                                                                                                                                                                                  Homo sapiens.
                  14-OCT-2003
                                                                                                                                                                                                                                                                                                                                   05-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mittmann MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1999
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Gaps

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AAX22971;

HXXXH

RESULT 20 AAX22971

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Lee

Pavco P,

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and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, inczymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene carcinoma. The present sequence represents one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences disclosed in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
                                                                                                                                                                                                                                                                                                       Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage; hepatitis B virus infection; hepatitis; hepatocellular carcinoma; cirrhosis; liver failure; lamivudine; interferon; genetic drift; virucide; hepatotropic; antiinflammatory; oytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Score 14.4; DB 8; Length 31; 75.0%; Pred. No. 5.9e+03; Live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus (HBV) enzymatic nucleic acid #2653.
                                                                                                                                                        Mcswiggen J, Morrissey D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31 BP; 8 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CAAGGATCGCTACGGCTCCTGGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 caaddcradcracaacaacradar 29
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 190; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1992; 92US-00882712.
07-FEB-1994; 94US-00193627.
08-NOV-1999; 99US-00456430.
20-MAR-2000; 2000US-00531025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-2003; 2003US-00342902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM63061 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 75.0 tes 18; Conservative
                                                                                                                                                     Macejak D,
Roberts E;
                                                                                                                                                                                                                                                   WPI; 2003-229207/22.
                             LEE P.
DRAPER K.
ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2004054156-A1.
PAVCO P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-2004
                                                                                                                                                     Blatt L, N
Draper K,
                                                                                                                                                                                                                                                                                                                                                                              infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM63061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                          (DRAP/)
(ROBE/)
(PAVC/)
                                (LEEP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 23
ADM63061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fatches
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HANDER AND STANFORM TO THE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a PCR primer for the Mycobacterium tuberculosis MPT 63 gene. Once amplified, the gene can be used in DNA vaccines to elicit an immune response in humans, thus enabling immunisation against the bacterium. This gives protection from tuberculosis (TB) either by DNA vaccine alone or by combining the vaccine with the present BCG version to give an enhanced immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecule, Hepatitis C virus, HCV; Hepatitis B virus, HBV; RNA stability, RNA expression, RNA synthesis, antisense, enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule, aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid immunization utilizing antigens from Mycobacterium tuberculosis to protect against tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.8%; Score 14.6; DB 3; Length 36; 81.0%; Pred. No. 4.8e+03; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 BP; 9 A; 14 C; 6 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 31; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GGATCGCTACGCTCCTGGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
                                                                                                                                                                               (POWD-) POWDERJECT VACCINES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virucide; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGATCCCTACGGCTCCCAAAT
                         09-FEB-2000; 2000WO-US003374.
                                                                                    99US-0119515P.
99US-0161699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2001; 2001US-00817879.
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2001US-0296876P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-2001; 2001US-0335059P, 05-DEC-2001; 2001US-0337055P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002; 2002WO-US009187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACD54952 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HBV DNAzyme sequence #691.
                                                                                                                                                                                                                                            Fuller DL;
                                                                                                                                                                                                                                                                                                          WPI; 2000-524486/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLATT L.
MACEJAK D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200281494-A1
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                                                                                    09-FEB-1999;
                                                                                                                 26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-2003
                                                                                                                                                                                                                                            Macklin MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACD54952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RIBO-)
(BLAT/)
(MACE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MCSW/)
(MORR/)
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RESULT 22 ACD54952

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The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185, R11, Q172, F145, N195, H107, K108, G109, D166, W167, D168, G169, S170, R11, G172, K269, K269, W270, D211, L272, G273, A274, L275, K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The used in the production of sweeteness and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present PCR primer was used to construct the variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene enhancer 84-57.31; embryotic development deformity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes mouse polycomb gene enhancer 84-57.31 (1). Also described is a process for preparing (1) using DNA recombination techniques. (1) can be used for treating several diseases e.g. embryotic development deformity and tumours. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide encoding it, useful for treating several diseases e.g. embryotic development deformity and tumors.
      Nissen TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse polycomb gene enhancer 84-57.31 PCR primer 4 SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%; Score 14.4; DB 2; Length 32; 75.0%; Pred. No. 5.9e+03; ive 0; Mismatches 6; Indels
      Nielsen BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32 BP; 12 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3xample 5; Page 18 (Disclosure); 34pp; Chinese.
                                                                                                                 New Termamyl-like alpha-amylase variants.
      Andersen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAAGGATCGCTACGGCTCCTGGAT 24
                                                                                                                                                               Example 5; Page 48; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carrearceraceercereerr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2000; 2000CN-00125168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ83921 standard; DNA; 33
      Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-529776/57.
                                                                     WPI; 1999-326987/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; polycomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention
      Sorchert TV,
                           Kjaerulff S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CN1342699-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mao Y, Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ83921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ83921
      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an enzymatic nucleic acid molecule that specifically cleaves RNA derived from hepatitis B virus (HBV) and comprishing one or more binding arms, without requiring the presence of a 2'-OH group within the molecule for activity. The nucleic acids are useful for treating hepatitis b virus infection, hepatitis, hepaticis or combination with other therapies such as lamivudine and interferons. The nucleic acids are useful as diagnostic tools to examine genetic drift and mutations within diseased cells, for detecting the presence of HBV RNA in a cell, for the study of RNA and for down-regulating gene expression of target genes in bacterial, fungal, viral, plant or mammalian cells. This sequence represents an enzymatic nucleic acid molecule which cleaves HBV RNA in the invention. Note: The sequence data for this patent is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Termamy1-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction;
                                                                                                                                                                                                                                                                                       Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes specifically cleaving RNA derived from hepatitis B virus and comprising one or more binding arms, useful for treating hepatitis and cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutagenic primer DA23 used to amplify termamy1-like alpha-amylase DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 60.0%; Score 14.4; DB 12; Length 31; Best Local Similarity 75.0%; Pred. No. 5.9e+03; Matches 18; Conservative 0; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31 BP; 8 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                        Morrissey D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        available in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 5195; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sweetener; ethanol; starch; textile desiz
saccharification process; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGGCTAGCTACAACGACTGGAT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAAGGATCGCTACGGCTCCTGGAT 24
                                                                                                                                                                                                      Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
09-AUG-2000; 2000US-00636385.
24-OCT-2000; 2000US-00696347.
08-JUN-2001; 2001US-00877478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97DK-00001240.
98DK-00000936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-DK000471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX59667 standard; DNA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVO-NORDISK AS.
                                                                                                              BLATT L.
MCSWIGGEN J A.
MORRISSEY D.
                                                                                                                                                                                                 Draper K, Blatt L,
                                                                                                                                                                                                                                               WPI; 2004-247781/23
                                                                                         DRAPER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9923211-A1
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14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                          (MORR/)
                                                                                                              (BLAT/)
(MCSW/)
                                                                                         (DRAP/)
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AAX59667/c
ID AAX59
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Gaps

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represents a PCR primer for (1), which is used in an example from the

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US2003104410-A1
                                                                                                                                                                                                                                                                                             Mao Y, Xie Y;
                                                                             10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                 CN1363564-A.
                                                                                                                                                                                                       14-AUG-2002.
                                                                                                                         Human; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC128366;
                                                       ABX12001;
                                                                                                                                                                                                                                                                          (BODE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
            RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACI28366
                       ABX12001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel polypeptide-human motor protein analogous protein 10.12, the polymucleotide encoding this polypeptide and a method for producing this polypeptide by using recombinant DNA technology. The invention also discloses the method for curing several diseases, such as protein metabolism disturbance related disease, membrane protein in dysfunction related disease and call withering dysfunction related disease and call withering an antagonist for resisting this polypeptide and its therapeutic action, and the application of the polymucleotide encoding this novel human motor protein analogous protein 10.12. The present sequence is a PCR primer used to clone the cDNA encoding human motor protein analogous protein
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A novel polypeptide-human motor protein analogous protein 10.12 and polynucleotide for coding this polypeptide.
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0
                                                   ch 60.0%; Score 14.4; DB 6; Length 33; 1 Similarity 75.0%; Pred. No. 5.9e+03; 18; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0%; Score 14.4; DB 6; Length 33; ilarity 75.0%; Pred. No. 5.9e+03; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                   Human motor protein analogous protein 10.12 PCR primer #2.
                                                                                                                                                                                                                                                                        Motor protein analogous protein 10.12;
protein metabolism distrutbance related disease; Human;
membrane protein dysfunction related disease; ss;
cell withering dysfunction related disease; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33 BP; 10 A; 10 C; 6 G; 7 T; 0 U; 0 Other;
                               Sequence 33 BP; 6 A; 13 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 22 (Disclosure); 38pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
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                                                                                                              CATGGATCCCTACGTCACCTCCAT
                                                                                                1 CAAGGATCGCTACGGCTCCTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2000; 2000CN-00116665
                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-2000; 2000CN-00116665
                                                                                                                                                                              ABK50283 standard; DNA; 33
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-305418/35.
                                                  Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
           present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xie Y;
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                           15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                           02-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                     CN1329083-A.
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                                                                                                                                                                                                     ABK50283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mao Y,
                                                                                                                                                                    ABK50283
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The invention discloses a human starchy precursor bindin 10.78 polypeptide. Also disclosed are the polynuclectide for coding it, the process for preparing the polypeptide by DNA recombination, the application of the polypeptide in treating diseases (e.g. cancer, HIV infection), the antagonist of the polypeptide and its medical action, and the application of the polynucleotide. The sequence presented is the PCR primer, #2, which was used to amplify human starchy precursor bindin 10.78 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide-human starchy precursor bindin 10.78 and polynucleotide for coding it.
                                                                                                                                                                                                                                                                     ss; starchy precursor bindin 10.78; cancer; HIV; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                        Human starchy precursor bindin 10.78 specific PCR primer, #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.0%; Score 14.4; DB 8; Length 33; 75.0%; Pred. No. 5.9e+03; Live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human microarray DNA oligonucleotide SEQ ID NO 28357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33 BP; 7 A; 13 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 18 (disclosure); 32pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CO LTD SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CAAGGATCGCTACGGCTCCTGGAT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JAN-2001; 2001CN-00105033
ABX12001 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACI28366 standard; DNA; 25
                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BODE GENE DEV
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Best Local Similarity
                                                                                                                                                                                                                                                                                                         antagonist; primer
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Synthetic.
                                                                                                                                                                                                                                                subunits.
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                                                                                                                                                                                                                                                                                  The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence in the method of analysis comprises in hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence. The array of nucleic acid subscions or in strumbing the 5' termin of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of pNA that have been incleic acid probes incorporated in the microarray. Note: The sequence of the form titer or an also be obtained in electronic format directly from the microarray. Note: The sequence of the form o
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0
                                                                                                                                                                                            in situ hybridization, in
to identify or detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; transgenic rodent; transgenic; voltage-gated potassium channel;
Kvbetal.1; knock-in subunit; psychiatric; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer fosR used in PCR analysis as internal positive control.
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0
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Pred. No. 7.2e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 8 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from USPTO at segdata.uspto.goc/seguence.html
                                                                                                                                                                                          New array of nucleic acid probes, useful for Southern, Northern or dot-blot hybridization sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 28357; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 GATCGCTACGGCTCCTGGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCTCTAAGGCTCCAGGA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.2%;
84.2%;
                              15-MAR-2002; 2002US-00098263
                                                              16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anxiolytic; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD59416 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.2
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                              (AFFY-) AFFYMETRIX INC
                                                                                                                                                            WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS2003024001-A1
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05-JUN-2003.
                                                                                                                              Mittmann MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD59416;
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                                                                                                                                                                                                                                                                                                                                                                                                                        A-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a transgenic rodent comprising an endogenous gene cluster encoding a metated voltage-gated potassium channel Kvbeta1.1 subunit is a knock-in subunit of an A-type potassium channel. Kvbeta1.1 subunit is a knock-in subunit which is unable to confer N-type inactivation of the channel but retains the ability to co-associate with Kv1 family of alpha-subunits. The invention is useful as a model for psychiatric and neurological disorders to identify anxiolytic compounds and pro-cognitive functions. The invention is useful as a model for evaluating the efficacy of test compounds that modulate Kvbeta1.1 activity. The invention also is useful as a positive anxiolytic control. The present sequence is a PCR primer used in PCR analysis as internal positive control
                                                                                                                                                                                                                                                                                                                                                                                                                Novel transgenic rodent comprising knock-in Kv beta 1.1 subunit of A-t
potassium channel, which is unable to confer N-type inactivation of
channel but retains ability to co-associate with Kv1 family of alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                               Comery TA, Askew R, Brandt M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.3%; Score 14; DB 10; Length 26; 77.3%; Pred. No. 9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26 BP; 4 A; 5 C; 11 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cysteine noose library primer CL1.MUT.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 caaggarggcrrgggcrcaggg 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 16; 40pp; English
                                                                                                                                                                                                                                               Marquis KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAAGGATCGCTACGGCTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97GB-00023062.
16-JUL-2002; 2002US-00196890.
                                                                    27-JUL-2001; 2001US-0308485P.
09-NOV-2001; 2001US-0331140P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-GB003255.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 77.3 nes 17; Conservative
                                                                                                                                                                                                                                            Kwak SP, Rhodes K,
Rosenzweig-Lipson S;
                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-456314/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-313343/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY08379
                                                                                                                                                                           (AMHP ) WYETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9923222-A1
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Homo sapiens
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                                                                                                                                                                                                                                  ABX14381
    8 X C C C
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                                                     This invention describes the construction of libraries of antibody variable domains containing modified complementarity determining regions (CDRs) carrying a cysteine nose and which have cytokine agonist and antagonist mechanisms of action. The method of the invention can be used to obtain peptide ligand mimetics capable of binding a target antigen. The binding members may also be used to provide agonists or antagonists of targets such as cytokines. In particular specific binding members for MTP-1 alpha receptors are useful for treatment of HTV infection and for in vitro investigation of mechanisms of HTV infection. A selection of peptide ligand mimetics from CDR3 cysteine noose libraries provide a means to select a different and potentially more effective population of peptide ligands than direct display of similar cysteine noose ligands on the surface of bacteriophage. The products of the invention have anti-HTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a method for enhancing cellular proliferation. The method comprises introducing into a cell a compound that alters the expression or activity of a Histone Nuclear Factor P (HiNF-P) polypeptide to enhance proliferation of the cell. The method of the invention is useful for the diagnosis, prevention and treatment of diseases or conditions associated with aberrant expression or activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulating cellular proliferation using a Histone Nuclear Factor P (HiNF-P) or Nuclear Protein or Ataxia-Telangiectasia locus (NPAT) polypeptide, useful for diagnosing or treating cancer, immune disorders and/or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cellular proliferation; histone nuclear factor P; HiNR-P; bone disorder; cancer; immune disorder; cardiovascular disorder; viral infection; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                  58.3%; Score 14; DB 2; Length 30; llarity 77.3%; Pred. No. 9.1e+03; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                5; Indels
Cysteine noose antibody libraries and their production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stein JL, Mitra P;
                                                                                                                                                                                                                                                                         Sequence 30 BP; 5 A; 13 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer used to isolate cDNA encoding HiNF-P.
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 72; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                              1 CAAGGATCGCTACGGCTCCTGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Wijnen AJ, Xie R,
                               Example 6; Page 42; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       caaggacgcracgcrrgcgc 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO43696 standard; DNA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYMA-) UNIV MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stein GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO43696;
                                                                                                                                                                                                                                                                                                    Query Match
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ADO43696
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the HiNF-P polypeptide, such as bone disorders, cancer, immune disorders, cardiovascular disorders and viral infections. PCR primers ADO43696-ADO43697 were used to isolate cDNA encoding HiNF-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide-human zinc finger protein 11.88 and encoding polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the isolation of human zinc finger protein 11.88, and the polymucleotide sequence encoding it. Also described is the process for preparing the protein by DNA recombination and the application of the polypeptide and polymucleotide in treating various diseases such as cancer and human immunodeficiency virus (HIV) infection. The present sequence represents a PCR primer used to clone cDNA encoding human zinc finger protein 11.88
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                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer #2 for cDNA encoding human zinc finger protein 11.88.
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0
                                                                                                                                                                         Length 32;
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                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; zinc finger protein 11.88; cancer; HIV infection;
human immunodeficiency virus infection; primer; ss.
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                                                                                                                Sequence 32 BP; 5 A; 11 C; 9 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                         Score 14; DB 12;
Pred. No. 9.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 17 (disclosure); 32pp; Chinese
                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                      2 chaddarcarcacarcicarda 23
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                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                               1 CAAGGATCGCTACGGCTCCTGG
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                                                                                                                                                                      Query Match 58.3%;
Best Local Similarity 77.3%;
Matches 17; Conservative
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AAZ35063/c
ID AAZ35063 standard; DNA; 22
XX
AC AAZ35063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABX14381 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-2003 (first entry)
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PCR primers 819-31 (AAT34297) and 819-28 (AAT34298) were used to amplify a portion of HEK4 binding protein cDNA (see also AAT34292) coding for amino acids 1-179 of the protein (see also AAW0035). The PCR fragment was cloned into vector PCFM1656 and truncated HEK4 binding protein was expressed in Escherichia coli FM5 (ATCC 53911) transformants. The protein was used as an antigen in rabbits. The antisera recognised HEK4 binding
                                                                                                                                                                                                                                                                         Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to modulate growth and differentiation of, e.g. liver and kidney cells, and to treat cancer and nervous system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ABC1 cholesterol transporter; chromosome 9q31; ATP-binding casette; HDL deficiency discorder; high density lipoprotein; Tangier disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerebrovascular disease; peripheral vascular disease;
Alzheimer's disease; Nemann-Pick disease; Huntington's disease;
X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
prognosis; prophylaxis; drug screening; transgenic animal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.5%; Score 13.8; DB 2; Length 36; 88.2%; Pred. No. 1.1e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ABC1 gene intron 9 polymorphic site, SEQ ID NO:233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36 BP; 9 A; 9 C; 10 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was used as an antigen in rabbits. The antise
protein in CHO cells in Western blot analysis
                                                                                                                                                                                                                                                                                                                                                             Example 5; Page 31; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0124702P.
99US-0138048P.
99US-0139600P.
99US-0151977P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AAGGATCGCTACGGCTC 18
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XENON BIORESEARCH INC
                                                                96WO-US001079
                                                                                                           95US-00379802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                           Fox GM;
                                                                                                                                                                                                                                    WPI; 1996-362633/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 15; Conserv
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                                                                                                                                                  (AMGE-) AMGEN
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08-JUN-1999;
17-JUN-1999;
01-SEP-1999;
                                                                  16-JAN-1996;
                                                                                                           27-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                         01-AUG-1996
                                                                                                                                                                                         Bartley TD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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AAC69334/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This oligonuclectide represents primer 8/97.31 that was used in the PCR amplification of the feline CD70 (B7-2) (see AAZ34838) cDNA. The amplified gene was used in the construction of homology vector 1015.18.8A (LP1-CD86/IRES-CD80), which was used to create recombinant raccompox viruses (RPV) expressing feline CD80 and CD86. The invention relates to a recombinant virus, e.g. RPV, that contains at least one foreign nucleic acid, inserted into a nonessential genomic region, that encodes feline CD80, CD80, CD86 or CTLA-4 protein (see AAY32283-87), or their immunogenic fragments, and is expressed when the recombinant virus is introduced into a sultable host. The recombinant virus may further comprise a foreign nucleic acid encoding an immunogen derived from a feline pathogen. It is used to modulate an immunogen in a feline, particularly as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HBK4 binding protein; HBK4 receptor; BPH-like receptor; protein tyrosine kinase; ligand; growth; differentiation; cancer; nervous system disorder; therapy; polymerase chain reaction; PCR; primer;
                                                                                  feline; cat; recombinant virus; vaccine; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel recombinant virus useful as immunomodulators, particularly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.5%; Score 13.8; DB 3; Length 22; 88.2%; Pred. No. 1.1e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 BP; 4 A; 5 C; 10 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                          (SCHE ) SCHERING-PLOUGH LTD.
(SCHE ) SCHERING-PLOUGH VETERINARY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEK4 binding protein PCR primer 819-28.
                                      Feline CD86 gene PCR primer 8/97.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 122; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CGCTACGGCTCCTGGAT 24
                                                                                                                                                                                                                                                                                            99WO-US009504
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(first entry)
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                                                                             CD86; B7-2; feline; cat;
therapy; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Cochran MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-062155/05
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hes 15; Conserv
                                                                                                                                                                                                          WO9957295-A1
                                                                                                                                                                                                                                                                                            30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ,
  28-FEB-2000
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                                                                                                                                                                    Felis catus.
                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccines
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US2003104410-A1
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                                                                                                                                                Hayden MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACK06220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                       (UYBR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 37
ACK06220/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the human ABC1 cholesterol transporter protein a member of the APP-binding cassette (ABC transporter) superfamily of a member of the APP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly croteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene are associated involved in cholesterol efflux from the cell. The gene are associated involved in cholesterol efflux from the cell. The gene are associated involved in cholesterol efflux from the cell. The gene are associated involved in cholesterol efflux from the cell. The gene are associated another the from the cell. The gene are associated involved in the blod correlate with a high risk of cardiovascular frangier disease (TD) and familial HDL deficiency (FHA). These diseases of Genese, particularly corromary attention provides genetic offers and conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and cranspensic cells and non-human animals comprising human ABC1 mucleic cardiovascular disease. Comprising the administration of an expression cardiovascular disease compounds which minic ABC1 extrement or prevention also cardiovascular disease compounds which minic ABC1 extrement of cardiovascular disease compounds which minic ABC1 extrement of disease associated corresponds which minic ABC1 gene to create the cardiovascular disease, especially coronary artery disease, coronary restencings or peripheral vascular disease. They may also be used in the treatment of disease associated cardiovascular disease, coronary restencings or peripheral vascular disease. Huntington's disease, X-linked adrenoleukodystrophy and cardiovascular disease. All the animonal procession Not CABLOUGS and ASC1 gene en the exact sequences of Genember ABC1 genember and proved to resten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                        New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.7%; Score 13.6; DB 3; Length 21; 80.0%; Pred. No. 1.4e+04; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic sequence for ABC1 polymorphic site #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CAAGGATCGCTACGGCTCCT 20
                                                                                                                   Example; Fig 11; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 CAATGAGGGCTTTGGCTCCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF93000 standard; DNA; 21 BP
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 Hayden MR, Wilson AR,
                             WPI; 2000-587528/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR- or RXR-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New array of nucleic acid probes, useful for in situ hybridization, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
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                                                                                                                                                                                                                                                                                                                                 Clee SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                 Brooks-Wilson AR, Pimstone SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4; 317pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAAGGATCGCTACGGCTCCT 20
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                                                                                                                                                                                                                      BRITISH COLUMBIA
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                                                                 01-SEP-1999; 99US-0151977P.
15-MAR-2000; 2000US-00526193.
23-JUN-2000; 2000US-0213958P.
01-SEP-2000; 2000WO-IB001492
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                                                                                                                                                                                                                                                     (XENO-) XENON GENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcriptional activity.
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tes 16; Conservative
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific companiestion to identify of detect the sequence or specific companiestion of any gene, in mapping the 5' termini of mRNA molecules by primer extensions of any gene, in mapping the 5' termini of mRNA molecules by companies and previously sequenced. The sequence presented is one of the isolated and previously sequenced. The sequence presented is one of the cucleic acid probes incorporated in the microarray. Note: The sequence containing sequence presented is one of the containing the sequence presented is one of the cucleic acid probes incorporated in the microarray. Note: The sequence containing sequence presented is one of the form USPTO at sequence. The sequence than land and sequence or probes incorporated in the microarray. Note: The sequence or probes the sequence or probes incorporated in the microarray.
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Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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tic variation; biallelic marker; polymorphism; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                    Claim 1; SEQ ID NO 106201; 9pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GATCGCTACGCTCCTGGAT 24
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AC104808/C
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The inventor in disturbes a microarray computating a purality or interior acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression nevels. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. Each of the nucleic acid gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotones but hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' terminin of maNA molecules by primer extensions or in screening SONA or genomic libraries or subclones for additional subclones containing segments of DNA that have been considered and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence date from USPPO at sequence than
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                                                              comprising a plurality of nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.7%; Score 13.6; DB 9; Length 25; 80.0%; Pred. No. 1.4e+04; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human microarray DNA oligonucleotide SEQ ID NO 105575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 105575; 9pp; English.
                   Claim 1; SEQ ID NO 4799; 9pp; English.
                                                           The invention discloses a microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AAGGATCGCTACGGCTCCTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AAGGAAGGCAACGGGTCCTG 4
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Best Local Similarity 80.00,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AFFY-) AFFYMETRIX INC.
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acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html invention discloses a microarray comprising a plurality of nucleic Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;

Score 13.6; DB 9; Length 25; Pred. No. 1.4e+04; 0; Mismatches 4; Indels 24 5 GATCGCTACGGCTCCTGGAT 56.7%; Best Local Similarity 80.0 Matches 16; Conservative Query Match g ò

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AAZ35681 standard; DNA; 28 BP. RESULT 40 AAZ35681

(first entry) 26-JAN-2000 AAZ35681;

IL-2/GM-CSF fusion protein construction oligonucleotide P4.

11-2; interleukin 2; granulocyte macrophage colony stimulating factor; GM-CSF; fusion protein; ss.

Homo sapiens Synthetic

CN1225368-A. 11-AUG-1999. 99CN-00113461 05-FEB-1999;

99CN-00113461 05-FEB-1999; (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.

Gao J; Huang S, Wang X,

WPI; 1999-581110/50.

Interleukin -2/granulocyte-macrophage colony stimulating factor fusion protein.

Claim 5; Page 1; 17pp; Chinese.

The present invention describes an interleukin-2/granulocyte-macrophage colony stimulating factor fusion protein (IL-2/GM-CSF fusion protein).

The fusion protein is produced by genetic engineering technology by subcloning against IL-2 and end reform and a GM-CSF connection IL-2/GM-CSF expression plasmid is constructed. The fusion protein can be used to convert Escherichia coli obtaining high effect expression. The fused protein possesses IL-2 and GM-CSF dual activity. The present sequence represent an oligonucleotide used in the construction of the IL-2/GM-CSF fusion protein 8888888888

Sequence 28 BP; 3 A; 9 C; 8 G; 8 T; 0 U; 0 Other;

Gaps . 0 56.7%; Score 13.6; DB 2; Length 28; 80.0%; Pred. No. 1.4e+04; ive 0; Mismatches 4; Indels 0 Local Similarior nes 16; Conservative Query Match datches

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23 2 GGATCCTTATCGCTCCTGGA 21 4 GGATCGCTACGGCTCCTGGA g ઠ

Search completed: November 18, 2005, 11:52:17 Job time : 169.262 secs

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1 CAAGGATCGCTACGGCTCCTGGAT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34239544 segs, 19032134700 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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1 CAAGGATCGCTACGGCTCCTGGAT 24
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                OM nucleic
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                                                                                                                                                                            Run on:
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Gaps

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Score 17.6; DB 1; Length 50; Pred. No. 2e+03; 0; Mismatches 4; Indels

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gplAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU103061 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone COLF1890, mRNA sequence.
                                                                                                                                                                                                                                                                                                                   Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library,
/note="Twetter: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0079 row: D column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                Contact: Robert B, Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0079D21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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AU103061.1 GI:13552582
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                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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84112, US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone libe_mil9 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units: For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DHIOB cells were transformed and then screened on LB plates with ampicillin."
                                                                       CG716757 41 bp DNA linear GSS 20-OCT-2003 1119046B12.1EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                              Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Malbot V
Department of Biological Sciences
Stanford University
Stanford University
Tel: 650 723 2227
Fax: 650 723 8221
Email: Walbot@stanford.edu
Email: Walbot@stanford.edu
Reverse complemented post-ligation site of ends cut by single endonuclease.
Plate: 1119046 row: 7
                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Zea mays"
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Location/Qualifiers
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/dev_stage="adult"
/lab_host="DH108"
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                                                                                                                            survey sequence.
CG716757
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                RESULT 2
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Gaps

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50 bp mRNA linear EST 28-JAN-2004 AU103064 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC00745, mRNA sequence.
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Yi. Yoshitomo-Uakagawa,Ki. Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2),
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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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/clone_lib="Sugano Homo sapiens cDNA library"
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/clone_lib="Sugano Homo sapiens cDNA library"
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81.0%; Pred. No. 4.9e+04;
iive 0; Mismatches 4; Indels
                                                                     Length 50;
                                                                     DB 1; L
3.2e+04;
                                                                  Score 15; DB 1
Pred. No. 3.2e4
0; Mismatches
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/db_xref="taxon:9606"
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                                                                  62.5%;
ilarity 78.3%;
Conservative
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17; Conservative
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nes 18; Conserv
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                                                                                                                                                                                                                   Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Beatl: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Yr., Yoshitomo-Nakagawa,Kr., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
Iength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitcon-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2),
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L basea 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

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                                    Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.5%; Score 15; DB 1; Length 50; 78.3%; Pred. No. 3.2e+04; ive 0; Mismatches 5; Indels
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .50
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.5°
Best Local Similarity 78.3°
Matches 18, Conservative
                         (bases 1 to 50)
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                      Query Match
Best Local Similarity 84.2*
Matches 16; Conservative
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Fax: 801 585 7177
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AZ476398
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                       Department of Vicology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 bp mRNA linear EST 28-JAN-2004 AU107042 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAT06952, mRNA sequence.
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L bases 1 to 50.

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

ENEORED. 2 (5), 388-393 (2001)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/clone="KAT06852"
/clone="KAT06852"
/clone=lib="Sugano Homo sapiens CDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.8%; Score 14.6; DB 1; Length 50; 81.0%; Pred. No. 4.9e+04; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db xref="taxon:9606"
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                                                                                                                                                                         Contact: Yutaka Suzuki
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Best Local Similarity 81.09
....hes 17; Conservative
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  AUTHORS
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Laboratory Mouse DNA Resources (thttp://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil#132114 gbl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                           AZ476398 14-0CT-2000 1M0295B16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0295B16 F, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 44)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Plasmid inserts
Plasmid inserts
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/clome_llb="Mouse_l0kb_plasmid_UUGCNM lbrary"
/note="Wector: PWD4zny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                         Gaps
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       Length 50
                                                                      Indels
Score 14.2; DB 1;
Pred. No. 7.4e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0295 row: B column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UGC1M0295B16"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                               5 GATCGCTACGGCTCCTGGA 23
                                                                                                                                                                                                              34 GATAACTAAGGCTCCTGGA 16
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ima:u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI317060

uk72a02.yl Schiller mouse AtT20 Mus musculus cDNA clone
IMAGE:1974506 5' similar to SW:HEMN SYNY3 P73245 PROBABLE
OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
ampping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Sugano Homo sapiens cDNA library"
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Seg primer: -40RP from Gibco
High quality seguence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.6; DB 1;
Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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/clone="HRC00126"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Contact: Yutaka Suzuki
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Best Local 9
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AI317060
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JOURNAL
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KEYWORDS
SOURCE
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                                 TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Grience, University of Tokyo
Institute of Medical Grience, University of Tokyo
Institute of Medical
Institute
In
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                                                                                                                                                                                                                                                                                                                                                 EST 28-JAN-2004
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                                                                                                                                                                                                                                                                                                                   AU102662 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS07035, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S., Okubo, K., mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
                                                                                    Gaps
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Pred. No. 9.1e+04;
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                                                                                    0; Mismatches
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/organism="Homo sapiens"
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                           58.3%;
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                                                                                 17; Conservative
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                        Query Match
Best Local Similarity
Matches 17; Conserv
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AU102662/c
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AU103063
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Gaps ; 0

4; Indels

EST 17-DEC-1998

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us-10-788-779-1.rst

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BQ589685 44 bp mRNA linear EST 06-DEC-2002 E012680-024-020-L13-SP6 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-020-L13 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

1 (baess 1 to 44)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
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/lab_host="EMDH10B"
/clone lib="MPIZ-ADIS-024-storage root"
/clone="Vector: pGWVSPORT6; Site_1: Sal1; Site_2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            orientation:
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                              Score 13; DB 9; Length 39;
Pred. No. 2.6e+05;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 44 Std Brror: 0.00
Plate: 20 row: L column: 13
Seq primer: SP6; CAPAGAATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GABI:190477"
/db_xref="taxon:161934"
/clone="024-020-L13"
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                                                                 54.2%;
76.2%;
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                                                           Query Match
Best Local Similarity 76.2°
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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VERSION
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BQ589685
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La Submitted (13-007-2013) Balzergue S., UWRGV, INRA/CNRS, 2 rue

Submitted (13-007-2013) Balzergue S., UWRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (18) resulting from

the PCR were directly sequence from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplane' (http://www.genoplante.com and

http://genoplane-info.infobiogen.fr).
/cell line="pituitary cell line"
/lab host="SOLR"
/clone=lib="SOLR"
/clone=lib="Sochiller mouse At720"
/clone=lib="Sochiller mouse At720"
/note="Organ: pituitary; Vector: pBluescript SK-
/note="Organ: pituitary; Vector: pBluescript SK-
(Stratagene); Site_1: EcoRI; Site_2: XhoI; Double-stranded cDNA was prepared From cell line Atr-20 using primer
5'-GAGAGAGAGAGAAACTAGTCTGAGT(18) -3. An EcoRI adaptor was used on the 5' end of the cDNA as follows:
5'-AATTCGCCACGAG-3'. The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. This library was constructed by Dr. Martin Schiller (Johns Hopkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana T-DNA flanking sequence, left border, clone 446607, genomic survey sequence.
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T-DNA integration into the Arabidopsis genome depends on sequences
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/cultiva=="wassillewakija"
/db_xref="taxon:3702"
/clone="40607"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/note="T-DNA flanking sequence
left border"
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                    50 bp mRNA linear EST 28-JAN-2004
AU103069 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HUV00521, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
ENERO Rep. 2 (5), 388-393 (2001)
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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale
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/clone_lib="Sugano Homo sapiens cDNA library"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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EMBO Rep. 2 (5), 388-393 (2001)
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Location/Qualifiers
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Department of Virology
                                                                                                                                                        Homo sapiens (human)
Homo sapiens
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Best Local Similarity 76.2'
Matches 16; Conservative
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2426f01.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:293689 5' similar to gb:X56807_cds2 DESMOCOLLIN 3A/3B PRECURSOR (HUMAN);, mRNA sequence.
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2),
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/note="Organ: Liver and Spleen; Vector: pf7T3D (Pharmacia)
with a modified polylinker: Site_l: Pac I: Site_2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
[5. AACTGGAAGAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double-stranded cDNA was ligated to Eco RI adaptors
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ASO303624"
/clone_lib="Sugano Homo sapiens cDNA library"
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/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.2%; Score 13; DB 1; Length 50; larity 76.2%; Pred. No. 2.6e+05; Conservative 0; Mismatches 5; Indels
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/mol_type="mRNA"
/db_xref="dDB:3801536"
/db_xref="taxon:9606"
/clone="IMAGE:293689"
                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                             1997).
Location/Qualifiers
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                                                                                                                                                                                             149-156 (1997)
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Matches 16; Conserv
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/clone="XL080g02"
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Matches 14; Conserv
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(Pharmacia), digested with Pac I and cloned into the Pac I and Eco H is sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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PRI0149d_H10 - PRI0149d.B21 (35) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
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/clone lib="mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (Dases 1 to 35)
Srinivasan, J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer R)
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Max-Planck-Institute for Developmental Biology
Speannant. 37-39, Tuebingen D-72076, Germany
Fal: 00497071601371
Fax: 00497071601498
Email: ralf. sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
Seq primer: 777
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                                                                                                            Query Match . 53.3%; Score 12.8; DB 7; Length 31; Best Local Similarity 87.5%; Pred. No. 3.2e+05; Matches 14; Conservative 0; Mismatches 2; Indels
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'strain="California"
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AU107276.1 GI:13556797
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Pristionchus pacificus
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Matches 17; Conserva
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1-length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 50)
                                                                                                                Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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The information of this clone is available through the following
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1 (bases 1 to 34)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
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/mol_type="mRNA"
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/clone="QAS08965"
/clone_lib="Sugano Homo sapiens CDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 53.3%; Score 12.8; DB 1; Length 50; I Similarity 87.5%; Pred. No. 3.2e+05; 14; Conservative 0; Mismatches 2; Indels
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BJ064678
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Pax: 81-559-81-6855
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Contact: Tadasu Shin-i
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/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://xenopus.nibb.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                           Contact: Yutaka Suzuki
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23 CAAGAATCGCTTCCGTTCC 41
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Best Local Similarity 78.9
Matches 15, Conservative
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/tissue_type="loaf"
/dev stage="adult"
/dev stage="adult"
/dev stage="adult"
/lab_bost="blails"
/clone lib="3591 - RescueMu Grid P"
/note="Corgan: leaf; Vector: RescueMu (engineered from pBluesCript backbone); Site 1: BamHi Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units: For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid P was grown at Molokai in 2002. DNA was
extracted from leaf strips, double digested using BamHi
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3591 15 1 D10.1EL y 1 3591 - RescueMu Grid P Zea mays genomic, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot {\bf V}
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    (bases 1 to 42)

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Tel: 650 723 227
Fax: 650 725 8227
Fax: 650 725 8227
Fax: 650 726 8227
Fax: 650 725 8227
Fax: 650 728 827
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                       /dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
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/cultivar="mixed background W23/A188/B73/K55"
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                                                                                                                                                                                        Length 34;
                                                                                                                                                                                     52.5%; Score 12.6; DB 4; Length 3 68.2%; Pred. No. 4e+05; ive 0; Mismatches 7; Indels
/tissue_type="whole embryo"
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Matches 15, Conservative
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1 CAAGGATCGCTACGGCTCC 19

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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: Shirokanedai, Minatcku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
Ilength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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AU103065 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC01582, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Suzuki, Y. Tara, H., Teunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Bakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
FIND Rep. 2 (5), 388-393 (2001)
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Pred. No. 4e+05;
0; Mismatches
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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AU105726.1 GI:13555247
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78.9%;
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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Sitel: EcoRI
R. Site2: NotI S' Seq Primer M13F Normalised library constructed
from pooled early embryos, from 8- cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS,
                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 38) Anderson, S.I., Finlayson, H.A. and Archibald, A.L. Development of cDNA and BST resources for studying reproduction and Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group) DNA, clone:T11738T, 3' flanking sequence of Tos17 insertion in rice strain ND9022, genomic
                                                                               EST 28-JUN-2004 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 09-AUG-2003
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/clone="c0005191_B05"
/tissue type=="mmknyo"
/clone_lib="KN277"
/note="vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2:
Not1; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Target Site Specificity of the Tos17 Retrotransposon Shows a Preference for Insertion within Genes and against Insertion in Retrotransposon-Rich Regions of the Genome Plant Cell 15 (8), 1771-1780 (2003)
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AJ655775
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Genomics and Bioinformatics
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AG213917
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                           Sus scrofa
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                             RESULT 25
AJ655775/c
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AG213917/c
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Smail: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitcomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a S'-end-enriched CDNA library. Gene 200 (1-2),
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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                                                                                                                                                                                                                                                                                                                  /clone="HS105236"
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.6; DB 1; Length 50;
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/db_xref="taxon:9606"
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78.9%;
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifica at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1159805 49 bp mRNA linear EST 28-OCT-199 qc73c05.x1 Soares placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA clone IMAGE:1715240 3' similar to TR:Q15726 Q15726 MALIGNANT MELANOWA METASTASIS-SUPPRESSOR. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarthini; Hominidae; Homo. I (bases 1 to 49) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse lokb plasmid UNGCN library."
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the INAGE Consortium (infe@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 545 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.4; DB 8;
Pred. No. 4.9e+05;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1715240"
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92.9%;
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Unpublished (1997)
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S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

I onpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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2M0092F16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0092F16 R, genomic survey sequence.
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                      12897251
2 (bases 1 to 46)
Miyao, A., Kato, M. and Hirochika, H.
Direct Submission
Submitted (16-APR-2002) Akio Miyao, National Institute of
Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai, Tbarkab, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp, URL:http://tos.niag.affrc.go.jp/, Tel:81-298-38-7020,
                                                                                                                                                                                                                                                                                                                                                               /cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="T11738T"
/clone lib="PCR product directly amplified from rice genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="The 3' end of retrotransposon Tos17 was found
immediately upstream of this sequence."
                                                                                                                                                                                                                                                                                         /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="ND9022"
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Pred. No. 4.9e+05;
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0092F16"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunndgenetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0092 row: F column: 16
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Best Local Similarity
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AZ820416/c
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Gaps

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50 bp mRNA linear EST 28-JAN-2004 AU104805 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS10961, mRNA sequence.
                                                                                                                                              /db xref="taxon:3702"
/clone="SALK 044281.17.00.n"
/clone="SALK 044281.17.00.n"
/clone="Dib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g08240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.8%; Score 12.2; DB 8; 82.4%; Pred. No. 6.1e+05; iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecoType="Col-0"
                                                                                                                         Arabidopsis thaliana (thale cress)
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                                    BH907825 BH907825.1 GI:22720758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 82.4%;
14; Conservative
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Unpublished (2001)
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            survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CF277394 45 bp mRNA linear EST 14-AUG-2003 14ETL--02-014.bl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-014,
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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 45)
1 (hases 1 to 45)
2 (handle)
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3 (handle)
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4 (handle)
5 (handle)
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6 (handle)
7 (handle)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongG!, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                       Gaps
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with oligoribonucleotides and then used as templates
RT-PCR."
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/lab_host="B.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
|mol_type="mRNA"
|cultivar="Nackdong"
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                                                                                                                                                                                                              Score 12.4; DB 1; Length 49;
Pred. No. 5e+05;
0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
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clone="14ETL--02-014"
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                                                                                                                                                                                                              th Similarity 72.7%; 16; Conservative C
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Gaps

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Indels

Length 48;

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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Bell: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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                                                     AU107142 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone ZRV6C680, mRNA sequence.
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Pan troglodytes DNA, clone: RP43-073N21.T7, genomic survey
                                                                                                                                                                                                                         Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Otta,T., 150gal,T., Tankar,T., Morishita,S., Okubo,K.,

Sakaki,Y., Nakamura,Y., Suyama, A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Park, H., Rim, Y., Kim, S., Han, Y., Woo, T., Park, K., Bun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/dlone="gRV6C680"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.8%; Score 12.2; DB 1;
82.4%; Pred. No. 6.1e+05;
ive 0; Mismatches 3;
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/organism="Homo sapiens"
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                                                                                                                                                          AU107142.1 GI:13556663
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                                                                                                                                                                                                         Homo sapiens (human)
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Best Local &
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                           RESULT 33
AU107142/c
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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1 (Dases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/organism="Homo sapiens"
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/mol_type="mRNA"
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/clone="CAS10961"
/clone_lib="Sugano Homo sapiens cDNA library"
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_traxon:9606"
/clone="HRC08216"
/clone="HRC08216"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 50.8%; Score 12.2; DB 1; Length 50; l Similarity 82.4%; Pred. No. 6.1e+05; 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                               Score 12.2; DB 1;
Pred. No. 6.1e+05;
0; Mismatches 3;
                                                                                                                                                                 1997).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AGGATCGCTACGGCTCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AGGATCGCTACGGCTCC 19
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                                                                                                                                                          (49-156 (1997)
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Best Local Similarity
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Best Local Similarity
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AU104807
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Gaps

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Length 50; 3; Indels

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (Dases 1 to 38)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
(E-mail:redatone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ492391 38 bp DNA linear GSS 05-0CT-2000 1M0326D04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0326D04 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0%; Score 12; DB 9; Length 30; Best Local Similarity 75.0%; Pred. No. 7.5e+05; Matches 15; Conservative 0; Mismatches 5; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                        organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 0326 row: D column: 04
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="RP43-073N21.T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0326D04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 38.
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Mus musculus
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: EcoRI
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AZ492391.1 GI:10665066
                                                                                                                                                                                                                                                    : ECORI
                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
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                                                                                                                                                     Sequencing: T7
                                                                                                                                                                                                  Vector
R.Site 1
R.Site 2
                                                                                                                          PRIMERS
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gil 47721141gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot \boldsymbol{\mathrm{V}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stanford University

Sp. California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Reverse complemented post-ligation sequence from source sequence.

Plate: 1008097 row: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cloud lib="1008 - RescueMu Grid I"
/cloud="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
/clone_lib="Mouse 10kb plasmid UUGCIM library"
//note=="Westcr: PWD42Inv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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/organism="Zea mays"
/onlityaz="genomic DNA"
/cultivaz="mixed background W23/A188/B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%; Score 12; DB 8; Length 38; 75.0%; Pred. No. 7.5e+05; Mirmatches 5; Indels
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Location/Qualifiers
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AGGATCGCTACGGCTCCTGG 22
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Best Local Similarity 75.03
Matches 15; Conservative
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50 bp mRNA linear EST 28-JAN-2004 AU103066 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC03739, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitokomo.Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.

1 (Dases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Bata,H., Ota,T., 1 sogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S. Okubo,K., Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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EMBO Rep. 2 (5), 388-393 (2001)
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75.0%; Pred. No. 7.6e+05;
tive 0; Mismatches 5;
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                                   21 GACCGGTCAGGCTCCTGGTT
          5 GATCGCTACGGCTCCTGGAT
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Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmdb.iastate.edu and follow the links for 'RescueMu', Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 49) Marra, M.; Hillier, L., Allen, M.; Bowles, M.; Dietrich, N.; Dubuque, T.; Geisel, S.; Kucaba, T.; Lacy, M.; Le, M.; Martin, J.; Morris, M.; Schellenberg, K.; Steptoe, M.; Tan, F.; Underwood, K.; Moore, B.; Wylle, T.; Lennon, G.; Soares, B.; Wilson, R.; and
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/dev_stage="10.5dpc embryos"
/lab_host="DH10B"
/clone_lib="Life Tech mouse embryo 10 5dpc 10665016"
/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1:
Sal1; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. _10.5dpc embryos. pCMV-SPORT2 vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA087268 49 bp mRNA linear EST 23-OCT-19 mol2g10.rl Life Tech mouse embryo 10 5dpc 10665016 Mus musculus CDNA clone IMAGE:553410 5' similar to TR:G285961 G285961 MRNA ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University, School of MedicineP
14444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                              Gaps
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Location/Qualifiers
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Pred. No. 7.5e+05;
); Mismatches 5; Indels
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/clone="IMAGE:553410"
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Gaps

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us-10-788-779-1.rst

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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzuki, Mirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
Inength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Institute of Medical Science, University of Tokyo
A-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzukiki,Y., Ysbhitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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1. (bases I to SO)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA stark sites

Endo Rep. 2 (5), 388-393 (2001)
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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3 AGCAGCGCTCCGGGCCCTGG 22
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Search completed: November 18, 2005, 21:12:34 Job time: 1150.98 secs

Sequence 11, Appl Sequence 11, Appl Sequence 1126, Ap Sequence 126395, Sequence 72, Appl Sequence 91, Appl

Sequence

Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 27766, A

Sequence 41969,

Appl Appl Appl Appl Appl Appl

62126, A 1, Appli 4, Appli 26, Appl

Sequence (Sequence 1 Sequence

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Database :

Result

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Query Match 100.0%; Score 24; DB 1; Length 24; Best Local Similarity 100.0%; Pred. No. 0.029; Matches 24; Conservative 0; Mismatches 0; Indels
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APPLICANT: SEIDMAN, JOHN
APPLICANT: WATKINS, HUGH
APPLICANT: WATKINS, HUGH
APPLICANT: WATKINS, HUGH
APPLICANT: MATKINS, HUGH
APPLICANT: MATKINS, HUGH
APPLICANT: MATKINS, HUGH
APPLICANT: MATKINS
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
US-08-465-095-11

US-08-179-656A-11

PCT-0594-0030-126

US-09-396-1916-1126

US-09-396-196G-126395

US-09-347-878-72

US-09-134-078-38

US-09-134-078-38

US-09-134-078-38

US-09-396-196G-2766

US-09-396-196G-2166

US-09-396-196G-2126

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APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GML-111
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 227-7400
TELEFRAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: NUCleic acid
STRANDENESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/07989160; Patent No. 5429923; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: BOSTON
STATE: Massachusetts
COUNTRY: U.S.A.
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US-07-989-160-1
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4290, Ap
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842.154 Million cell updates/sec
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                                                                                                                       November 18, 2005, 00:26:13 ; Search time 46.6312 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
  GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-396-196G-60856
US-08-37-309-12
US-09-186-949A-13
US-09-186-949A-13
US-09-186-949A-13
US-09-186-949A-13
US-09-186-949A-13
US-09-187-978-12
US-09-940-308A-12
US-09-940-308A-12
US-09-940-308A-12
US-09-940-308A-12
US-09-940-308A-12
US-09-940-308A-12
US-09-940-308A-12
US-09-940-308A-12
US-09-940-308A-12
US-09-182-361A-5
US-09-183-412-44
US-09-183-412-44
US-09-183-412-44
US-09-196-196G-70013
US-09-396-196G-70013
US-09-948-129-11
US-09-948-129-11
US-09-948-129-11
US-09-948-129-11
US-09-948-129-11
US-09-396-196G-108959
US-08-3936-196G-108959
US-08-827-336-3
                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-960-756-17
                                                                                                                                                                                                                                                                                                                                                             1202784 segs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                 nucleic search, using sw model
                                                                                                                                                                                                           US-10-788-779-1
24
1 CAAGGATCGCTACGGCTCCTGGAT
                                                                                                                                                                                                                                                                                               IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Match Length
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Maximum DB seq length: 50
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Gaps

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14.6 14.6 14.7 14.2 14.2

113.6 113.6 113.6 113.6 113.6 113.6

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5 AAGGATCCTTAGCTCTCCTGGAT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                   Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                       LENGTH: 33
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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TELEX: 20
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Sequence 12, Application US/08377309A

Patent No. 585528

GENERAL INFORMATION:
TITLE OF INVENTION: AN IMMINOSUPPRESSIVE AGENT
FILE REFERENCE: 06727/005001
CURRENT APPLICATION UNMBER: US/08/377,309A

CURRENT FILING DATE: 1995-01-24
NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-166-723-12
Sequence 12, Application US/09186723
Sequence 12, Application US/09186723
Sequence 12, Application US/09186723
SENERAL NO. 6288034
SENERAL INVERMATION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT
FILE REFERENCE: 06727/0055002
CURRENT APPLICATION NUMBER: US/09/186,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 33;
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                                                                                                                                                                          APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 00/100,678
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Pred. No. 1.7e+02;
0; Mismatches 3;
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Pred. No. 6.7e+02;
0; Mismatches 5
                                                                                                             Sequence 60856, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
1 CAAGGATCGCTACGGCTCCTGGAT 24
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Best Local Similarity 78.3
Matches 18; Conservative
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-08-377-309-12
                                                                                        US-09-396-196G-60856
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| Sequence 17, Application US/08505012
| Patent No. 6315101
| Patent No. 6315101
| Patent No. 6315101
| Title OF INVENTION: EXPRESSION AND PURIFICATION OF CLONED
| TITLE OF INVENTION: EXPRESSION ALPHA-FETOPROTEIN
| NUMBER OF SEQUENCES: 24
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Fish & Richardson P.C.
| STREET: 225 Franklin Street, Suite 3100
| CITY: Boston
| STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.5%; Score 15; DB 3; Length 33; Best Local Similarity 78.3%; Pred. No. 6.7e+02; Matches 18; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                           62.5%; Score 15; DB 3; Length 33; 78.3%; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/505,012
FILING DATE: 21-011-1995
CLASSIFICATION NUMBER: US/08/377,317
FILING DATE: 24-014-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06727/007001
TELECOMMUNICATION INFORMATION:
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: 08/377,309
EARLIER FILING DATE: 1995-01-24
NUMBER FEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Gaps

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; TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS A
TITLE OF INVENTION: CELL PROLIFERATIVE AGENT
; FILE REPERENCE: 06727/06002
; CURRENT APPLICATION NUMBER: US/09/187,978A
; CURRENT PILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: 08/377,316
; EARLIER APPLICATION NUMBER: 08/377,316
; EARLIER PILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Murgita, Robert A.
TITLE OF INVENTION: Recombinant Alpha-Fetoprotein for TITLE OF INVENTION: Treating and Diagnosing Cancers FILE REFERENCE: 66727/004003
CURRENT APPLICATION WHOER: US/10/115,701A
CURRENT FILING DATE: 2002-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15; DB 4; I
Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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PRIOR APPLICATION NUMBER: 08/758,757
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 08/758,757
PRIOR PILING DATE: 1998-04-09
PRIOR PILING DATE: 1998-12-03
PRIOR PILING DATE: 1996-12-03
PRIOR PILING DATE: 1996-12-03
PRIOR PILING DATE: 1995-01-24
PRIOR PILING DATE: 1995-01-24
SROFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 12
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.5%;
Best Local Similarity 78.3%;
Matches 18; Conservative 0
                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-187-978-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-115-701A-12
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                                                           Sequence 13, Application US/09186949A

Fatent No. 6416734

GENERAL INFORMATION:
FAPLICANT: Murgita, Robert A.

TITLE OF INVENTION: Treating and Diagnosing Cancers
TITLE OF INVENTION: Treating and Diagnosing Cancers
FILE REFERENCE: 06727/004002

CURRENT APPLICATION NUMBER: US/09/186,949A

CURRENT FILING DATE: 1998-11-05

PRIOR APPLICATION NUMBER: US 08/758,757

PRIOR APPLICATION NUMBER: US 08/758,757

PRIOR APPLICATION NUMBER: US 08/377,311

PRIOR FILING DATE: 1995-01-24

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMION:
APPLICANT: Murgita, Robert A.
TITLE OF INVENTION: RECOMBINARY ALPHA-FETOPROTEIN FOR TITLE OF INVENTION: TERATING AND DIAGNOSIS
FILE REFERENCE: 06727/004001
CURRENT APPLICATION NUMBER: US/08/758,757
CURRENT APPLICATION NUMBER: 08/377,311
EARLIER APPLICATION NUMBER: 08/377,311
EARLIER APPLICATION NUMBER: 08/377,311
EARLIER PILING DATE: 1995-01-24
SABLIER PILING DATE: 1996-12-03
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Based on Homo sapiens US-09-186-949A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AAGGATCGCTACGGCTCCTGGAT 24
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APPLICANT: MIRGITA, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 12, Application US/08758757; Patent No. 6534479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 78.3
Matches 18; Conservative
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US-08-758-757-12
                           RESULT 6
US-09-186-949A-13
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US-08-758-757-12
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LENGTH: 33
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TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
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Best Local Similarity 78.3%;
Matches 18; Conservative
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                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US96-00996-17
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APPLICANT: Murgita, Robert A.
TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
TITLE OF INVENTION: an Immunosuppressive Agent
TITLE OF INVENTION: an Immunosuppressive Agent
FILE REFERENCE: 06727/00503
CURRENT APPLICATION NUMBER: US/09/940,308A
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 09/186,723
PRIOR APPLICATION NUMBER: US 09/186,723
PRIOR APPLICATION NUMBER: US 09/186,7309
PRIOR PILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application PC/TUS9600996
GENERAL INFORMATION:
APPLICANT: Murgita. Robert A.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF CLONED
TITLE OF INVENTION: HUMAN ALPHA-FETOPROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 62.5%; Score 15; DB 4; Length 33; Best Local Similarity 78.3%; Pred. No. 6.7e+02; Matches 18; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                            Length 33;
                                                                                                                                                                                                                                                                                                                                       5; Indels
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPEM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                     62.5%; Score 15; DB 4; I
78.3%; Pred. No. 6.7e+02;
iive 0; Mismatches 5;
PRIOR APPLICATION NUMBER: US 09/186,723
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: US 08/377,309
PRIOR FILING DATE: 1995-01-24
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                  2 AAGGATCGCTACGGCTCCTGGAT 24
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Best Local Similarity 78.3
Matches 18; Conservative
                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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PCT-US96-00996-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MA
                                                                                                                                                                                                                                          US-09-940-308A-12
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PRILING DATE: PCT/USD6/00996

CLASSITCATION: WINESE: PCT/USD6/00996

PRIOR APPLICATION DATE: 43-JAN-1996

CLASSITCATION: A2-JAN-1995

CLASSITCATION: A1-JAN-1995

CLASSITC
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Gaps

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Query Match 60.0%; Score 14.4; DB 4; Length 32; Best Local Similarity 75.0%; Pred. No. 1.3e+03; Matches 18; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                1 CAAGGATCGCTACGGCTCCTGGAT 24
                                                                                                                                                                                                                                                                                                                             31 CATTGATCGTAACGGGTCCTGGTT 8
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LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                   ; OTHER INFORMATION: Primer US-09-769-864-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
COCGANISM: mus musculus
US-09-396-196G-70013
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US-09-396-196G-70013
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ORGANISM:
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                                               Query Match 60.8%; Score 14.6; DB 4; Length 32; Best Local Similarity 81.0%; Pred. No. 1e+03; Matches 17; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Darne
APPLICANT: Nielsen, Darne
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REPERSENE: 3586-200-03
CURRENT APPLICATION NUMBER: US/09/183,412
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-07
EARLIER FILING DATE: 1997-11-30
EARLIER FILING DATE: 1997-10-30
EARLIER FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SSE ENGTH: 32
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APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Mielsen, Bjarne
APPLICANT: Mielsen, Bjarne
APPLICANT: Missen, Torben L.
APPLICANT: Kjacrulff, Soren
ITTLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5368.200-03
FURRENT APPLICATION NUMBER: US/09/769,864
CURRENT APPLICATION NUMBER: 09/183,412
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR PILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAAGGATCGCTACGGCTCCTGGAT 24
                                                                                                                                                                                                                                                                                                                     Sequence 44, Application US/09183412
Patent No. 6204232
GENERAL INFORMATION:
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                                                                                                                                                                                                  4 GGATCCCTACGCCTTCTTGAT 24
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Patent No. 6673589
                                                                                                                                                  4 GGATCGCTACGGCTCCTGGAT
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Borchert, Torben V. APPLICANT: Svendsen, Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Primer US-09-183-412-44
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US-09-769-864-44/c
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US-09-152-361A-5
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Matches
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US-09-396-196G-70024

Sequence 70024. Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Mitchael 
Sequence 70013, Application US/09396196G
Patent No. 681724.
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICANTON NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
ILENGTH: 25
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Best Local Similarity
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                                                         57.5%; Score 13.8; DB 3; Length 36; 88.2%; Pred. No. 2.6e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.5%; Score 13.8; DB 3; Length 36; 88.2%; Pred. No. 2.6e+03;
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Sequence 11, Application US/09048079

Sequence 11, Application US/09048079

Patent No. 616916

APPLICANT: Bartley, Timothy D.

APPLICANT: Bartley, Timothy D.

TITLE OF INVENTION: Ligands for EPH-Like Receptor

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGHORISS:

STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09048129
Patent No. 6063903
GENERAL INFORMATION:
APPLICANT: Bartley, Timothy D.
APPLICANT: Pox, Gary M.
TITLE OF INVENTION: Ligands for EPH-Like Receptor NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLILICATION NUMBER: US/09/048,129
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/379,802
FILING DATE:
                                                                                                                                                  18
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 88.2'
Matches 15; Conservative
                                                              Query Match 57.5
Best Local Similarity 88.2
Matches 15; Conservative
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STRANDEDNESS: single
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MOLECULE TYPE:
        ; MOLECULE TY.
US-08-379-802-11
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3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bartley, Timothy D.
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Ligands for EPH-Like Receptor
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STREET: USA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,802
                                                                                                              RESULT 18
US-09-36-196G-4290/c
iS-09-36-196G-4290/c
iSequence 4290, Application US/09396196G
iPatent No. 6821724
iGENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
ITILE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 4290
LUNGTH: 25
LENGTH: 25
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CAAGGATCGCTACGGCTCCTGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 CTAGGATCTCTGCGGAGCCTGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08379802
Patent No. 6057124
                                          5 GATCGCTACGGCTCCTGGA 23
                                                                               4 GATCGCGACTGCTCCGGGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-396-196G-4290
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Matches
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Thousand Oaks

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3e+03;
---- 4; Indels
                                                     Sequence 108958, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: AFFYMETIX, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRALESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymerix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 108959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.6; DB 4;
Pred. No. 3e+03;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DANIEL
GROWTH FACTOR HTTER36
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; Sequence 108959, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08827336; Patent No. 6004780; GENERAL INFORMATION: APPLICANT: SOPPET, DANIEL TITLE OF INVENTION: GROWTH FACTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GGATCGCTACGCCTCCTGGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GAÁTCGCTÁCGGTCCCAGGA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAATCGCTACGGTCCCAGGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0%;
Matches 16; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: mus musculus
US-09-396-196G-108959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: mus musculus
US-09-396-196G-108958
                                            US-09-396-196G-108958
                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 108958
LENGTH: 25
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US-08-827-336-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.5%; Score 13.8; DB 3; Length 36;
88.2%; Pred. No. 2.6e+03;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Hayden, Michael R.
APPLICANT: Brooks Wilson, Angela R.
APPLICANT: Brooks Wilson, Angela R.
APPLICANT: Encoks Wilson, Angela R.
APPLICANT: Pinstone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
TITLE OF INVENTION: CHOLESTEROL LEVELS
TILE REFERENCE: 50110/002005
CURRENT APPLICATION NUMBER: 05/124,702
PRIOR FILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-01
SRIOR FILING DATE: 1999-06-01
SRIOR FILING DATE: 1999-09-01
SROTHER OF SEQ ID NOS: 287
SEQ ID NO 233
LENGTH: 21
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                                  ZIP: 91320-1789

ZIP: P1320-1789

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PROPENTIAL OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                        FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/379,802
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-325
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
LENGTH: 35 base pairs
TYPE: nucleic acid
: "TYPE: nucleic acid
: "TYPE: aligned."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-526-193A-233/c
; Sequence 233, Application US/09526193A
; Patent No. 6617122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAAGGATCGCTACGGCTCCT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AAGGATCGCTACGGCTC 18
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Best Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-526-193A-233
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: CDNA
US-09-048-079-11
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Best Local Similarity
Matches 15; Conserva
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Gaps

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Sequence 17, Application US/08960756

Patent No. 5866422

GENERAL INFORMATION:
APPLICANT: WAYNE, JAY
APPLICANT: XJ SHUANG-YONG
ITILE OF INVENTION: METHOD FOR CLONING AND
ITILE OF INVENTION: PRODUCING THE TSP45I RESTRICTION ENDONUCLEASE IN B. COLI
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: New England Biolabs, Inc.
STREET: 32 Tozer Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.7%; Score 13.6; DB 2; Length 49; Best Local Similarity 80.0%; Pred. No. 3.3e+03; Matches 16; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                         Query Match

56.7%; Score 13.6; DB 3;

Best Local Similarity 80.0%; Pred. No. 3.2e+03;

Matches 16; Conservative 0; Mismatches 4;
                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,756
                          TELEPHONE: 301-309-8504
TELEPAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       1 CAAGGATCGCTACGGCTCCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAAGGATCGCTACGGCTCCT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE, POCKET NUMBER: NE
TELECOMMUNICATION INFORMATION: 978-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS.
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 32 Tozo
CITY: Beverly
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 27
US-08-960-756-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 01915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 21-Jul-1999
CLASSIFICATION: CURNOWN>
                                                                                                                                                        ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: JE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: US/08/827,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION US/09357905
; Sequence 3. Application US/09357905
; Patent No. 6413933
; GENERAL INFORMATION: GENERAL INFORMATION: GROWTH FACTOR HTTER36
; TITLE OF INVENTION: GROWTH FACTOR HTTER36
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS: ADDRESSE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
                                             ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BROOKES, ANDY, A. REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PF230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/827,336 FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDY, A.
REGISTRATION NUMBER: 36,373
REFREENCE/DOCKET NUMBER: PF23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CAAGGATCGCTACGGCTCCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 caggaraccracaarccr 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301-309-8512
NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 26
US-09-357-905-3/c
                                                                                                                                         COUNTRY:
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Gaps

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,656A
FILING DATE: 07-JAN-1994
CLASSIFICATION DATA:
APPLICATION ONTO
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 08/001,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/472,377
FILING DATE: 01-FEB-1990
ATTORNEY/AGENT INFORMATION:
                       COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAAGGATCGCTACGGCTCCTGGA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ 1D NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
: USA
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
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CITY: Boston
                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Mass
COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 30
US-08-179-656A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-465-095-11
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                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Phillips, Greg
APPLICANT: Cuningham, Bruce A.
APPLICANT: Crossin, Kathryn L.
TITLE OF INVENTION: OCNTAINING FIBROWTH-PROMOTING POLYPEPTIDES
TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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                                                                                                                                                                                                                                                                                                                                                                  18: The Scripps Research Institute
10550 No. 6313265th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08465095
Patent No. 5849534
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Iida, Naoka
TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DUS/NS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
FILING DATE: 24-ULL-1995
FILING DATE: 24-ULL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: TSRI 488.0
TELEPANINICATION INFORMATION:
TELEPANINICATION INFORMATION:
TELEPHONE: (619) 554-6312
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AAGGATCCCTACCACCCTTGGT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
WBDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                  Sequence 8, Application US/08506296B
Patent No. 6313265
45 CCAGGGTAGCTACGGCTCAT 26
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Best Local Similarity 73.9°
Matches 17, Conservative
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                           CITY: La Jolla
STATE: California
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE:
US-08-506-296B-8
                                                                                                             US-08-506-296B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-465-095-11
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08179656A
Patent No. 6673893
GENERAL INFORMATION:
APPLICANT: Ida, Maoka
TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,656
FILING DATE: 07-JAN-1994
APPLICATION NUMBER: 08/001,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/472,377
FILING DATE: 01-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERRICE/DOCKET NUMBER: GZI-003C2
TELECOMMUNICATION INFORMATION:
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4 CGACGGTGGCGACGACTCCTGGA 26
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: mus musculus
US-09-396-196G-126395
                                                                                                                                                                                                           RESULT 32
US-09-696-791-1126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.8%; Score 13.4; DB 4; Length 30; Best Local Similarity 73.9%; Pred. No. 3.9e+03; Matches 17; Conservative 0; Mismatches 6; Indels
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55.8%; Score 13.4; DB 5; Length 30;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECULAR SECULA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00300
FILING DATE: 07-JAN-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/001,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/472,377
FILING DATE: 01-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GZI-003CZ
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 11:
SEQUENCE GRARACTERISTICS:
FORMATION FOR SEQ ID NO: 11:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GZI-003C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH 30 base pairs
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 caacgargacgacgacrccraga 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAAGGATCGCTACGGCTCCTGGA 23
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA US-08-179-656A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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General 1126, Application US/09696791

Fatent No. 6770633

GENERAL INFORMATION:

APPLICANT: Robbins, Joan M.

APPLICANT: Tritz, Atchard

TITLE OF INVENTION: SKIN AND EYE DISEASES

FILE REFERENCE: 480124.407

CURRENT APPLICATION NUMBER: US/09/696,791

CURRENT APPLICATION NUMBER: US/09/696,791

SOFTWARE OF SEQ ID NOS: 4523

SOFTWARE PATENTIN VEY: 2.0

SOFTWARE: PATENTIN VEY: 2.0

SOFTWARE: PATENTIN VEY: 2.0

SOFTWARE: PATENTIN VEY: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.2; DB 4; Length 25; Pred. No. 4.7e+03; 0; Mismatches 3; Indels
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US-09-396-126395

Sequence 126395, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Mitchael Mittmann
APPLICANT: David Lockhart
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Mack
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SEQ ID NO 126395

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Cdk-we-hu ribozyme binding site US-09-696-791-1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 72, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
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Sequence 15, Application US/08211882
Sequence 15, Application US/08211882
GENERAL INFORMATION:
APPLICANT: Manoharan et al.
TITLE OF INVENTION: Derivatized Oligonucleotides Having
TITLE OF INVENTION: Improved Uptake And Other Properties
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz and No. 6153737ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 31;
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                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
FILING DATE: 06-DEC-1996
ATTORNEY,AGENT INFORMATION:
                                                                                                                              ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600 CITY: San Diego
                                APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: GLYCOSIDASE ENZYMES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09010/024002
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: HAILE, LIBA A.
REGISTRATION NUMBER: 38,347
REPERENCE/DOCKET NUMBER: 09C
TELECOMMUNICATION:
TELEPHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AGGATCGCTACGCTCCT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Genomic DNA US-09-134-078-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 31 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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                                                                                                                                                                                                   STATE:
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APPLICANT: Yuan, Chong-Shen
FILER REFERENCE: 1093 7-1652
CURRENT APPLICATION NUMBER: US/09/546,013
CURRENT APPLICATION NUMBER: 09/347,878
EARLIER APPLICATION NUMBER: 09/457,205
EARLIER FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
OTHER INFORMATION: of Human SAH hydrolase (mutant R431A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
OTHER INFORMATION: of Human SAH hydrolase (mutant R431A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REPERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SSOFTWARE: Patentin Ver. 2.0
LENGTH: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.0%; Score 13.2; DB 3; Length 27; 83.3%; Pred. No. 4.8e+03; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mutation
LOCATION: (13)..(15)
OTHER INFORMATION: Codon change from CGC to GCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (13)..(15)
; OTHER INFORMATION: Codon change from CGC to GCC
US-09-546-013-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 91, Application US/09546013
Patent No. 6610504
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US-09-134-078-38
; Sequence 38, Application US/09134078
; Patent No. 6368844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GGATCGCTACGGCTCCTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GGATCACTACGCCTACTG 20
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                                                                                                                                                                                                                     TYPE: DNA .
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 15, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: mutation
LOCATION: (13)..(19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 35
US-09-546-013-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-347-878-72
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LENGTH: 27
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INVENTION: Derivatized Oligonucleotides Having Improved Uptake and Other Pro
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US-09-396-196G-22766/C

Sequence 22766, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22766
LENGTH: 25
TITNEE DNA
TYPER DNA
TYPER DNA
TYPER DNA
TYPER DNA
TYPER DNA
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Best Local Similarity 76.2%; Pred. No. 5.9e+03;
Matches 16; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vuery match
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 13; Conservative 0; Mismatches
                FILE REFERENCE: ISIS-5024
CURRENT APPLICATION NUMBER: US/10/073,718
CURRENT APPLICATION NUMBER: US/10/073,718
CURRENT APPLICATION NUMBER: US/3859
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 1994-04-22
PRIOR FILING DATE: 1994-04-22
PRIOR FILING DATE: 1994-04-22
PRIOR FILING DATE: 1994-04-22
PRIOR FILING DATE: 1994-04-24
PRIOR FILING DATE: 1994-04-24
PRIOR FILING DATE: 1991-01-024
PRIOR FILING DATE: 1991-01-11
PRIOR FILING DATE: 1990-08-13
PRIOR FILING DATE: 1990-08-13
PRIOR FILING DATE: 1990-01-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VERSION 3.1
SEDICHARE: DATE: 1990-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: November 18, 2005, 11:21:57 Job time: 47.6312 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: No. 6831166el Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAAGGATCGCTACGGCTCCTG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 TCGCTACGGCTCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Mus musculus
US-09-396-196G-22766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-073-718-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.2%; Score 13; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 5.7e+03; Matches 13; Conservative 0; Mismatches 0; Indels
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54.2%; Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels
           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/182,374
FILING DATE: 24-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH LUCCI
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 1SIS-0649
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 15, Application US/10073718; Patent No. 6831166; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Manoharan, Muthiah
APPLICANT: Cook, Phillip Dan
APPLICANT: Bennett, Clarence Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
22-APR-1994
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                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-211-882-15
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Sequence 105576, Sequence 106202

Sequence 106202, Sequence 572806, Sequence 44525, A Sequence 44525, A Sequence 783296, Sequence 783296, Sequence 12, Appl

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Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM nucleic

Run on:

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Sequence 1, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDWAN, CHRISTINE
; APPLICANT: SEIDWAN, JOHN
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
6 US-11-131-042-362

6 US-11-036-317-219546

6 US-10-048-263B-105576

6 US-10-048-263B-105576

6 US-10-098-263B-105576

6 US-10-098-263B-105576

4 US-10-719-956-348306

4 US-10-719-956-3483296

6 US-11-036-317-743296

6 US-11-036-317-743296

6 US-11-036-317-72142

7 US-09-940-308-12

8 US-10-940-308-12

8 US-10-940-308-12

9 US-10-940-308-12

105-09-940-308-12

105-09-940-308-12

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105-09-940-308-12

105-09-956-388-1

105-09-956-2308-2

105-09-956-2308-2

105-09-956-2308-2

105-10-39-26-4886-26

105-10-119-956-2308-2

105-11-036-317-334044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD STREET, SUITE CITY: BOSTON STATE: MASSACHUSELTS COUNTRY: U.S.A.
     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109
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US-08-469-172-1
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Sequence 60856, A
Sequence 375, App
Sequence 362, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Appli
                                                                                                           November 18, 2005, 06:36:48; Search time 322.586 Seconds (without alignments) 615.265 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(ggn2_6/ptodata1/pubpna/US07_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US06_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US06_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US07_NEW_PUB.seq:*

(ggn2_6/ptodata1/pubpna/US08_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US08_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US08_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US09_PUBCOMB.seq:*

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(ggn2_6/ptodata1/pubpna/US09_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US09_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US09_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US09_NEW_PUB.seq:*

(ggn2_6/ptodata1/pubpna/US09_NEW_PUB.seq:*

(ggn2_6/ptodata1/pubpna/US09_NEW_PUB.seq:*

(ggn2_6/ptodata1/pubpna/US10B_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US0B_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US0B_PUBCOMB.seq:*

(ggn2_6/ptodata1/pubpna/US0B_PUBCOMB.seq:*

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               5.1.6
Compugen Ltd.
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0 US-10-788-779-1

2 US-10-809-189-60856

2 US-10-938-249-375

6 US-11-131-054-362
                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                     9794790 seqs, 4134909567 residues
               GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                  1 CAAGGATCGCTACGGCTCCTGGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             - nucleic search, using sw model
                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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24
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Match 1
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24 24 16.2 16.2 16.2

4 2 E 4 5

Score

Result No.

Sequence 12, Appl Sequence 12, Appl Sequence 1340, Ap Sequence 13653, Sequence 13165, Sequence 238457, Sequence 29838, Sequence 29838, Sequence 29838, Sequence 177036, Sequence 177036, Sequence 195, Ap Sequence 44, Appl Sequence 44, Appl Sequence 28357, Sequence 28357, Sequence 70024, Sequence 20024, Sequence 20024, A Sequence 20024, S Sequence 20029, Sequence 20029, Sequence 20012, Sequence 20022, Sequ

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Gaps
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APPLICANT: Lu, Peter S.
APPLICANT: Lu, Peter S.
APPLICANT: Schweizer, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Acheor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Hematopoietic
TITLE OF INVENTION: Molecular Interactions in Hematopoietic
TITLE OF INVENTION: Cells
TITLE OF INVENTION: Cells
TITLE OF INVENTION: Cells
CURRENT APPLICATION NUMBER: US/10/938,249
CURRENT FILING DATE: 2004-09-10
PRIOR PILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/134,114
PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.5%; Score 16.2; DB 22; Length 25; 85.7%; Pred. No. 1.3e+03; ive 0; Mismatches 3; Indels (
                                                                                                                                ; Score 24; DB 20; Length 24;
; Pred. No. 0.31;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR PELICATION NUMBER: 60/100,678
PRIOR PELICATION NUMBER: 60/100,678
PRIOR PELICATION NUMBER: 60/100,678
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NO 60856
LENGTH: 25
                                  MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                US-10-809-189-60856; Sequence 60856, Application US/10809189; Publication No. US20050048531A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     1 CAAGGATCGCTACGGCTCCTGGAT 24
                                                                                                                                                                                                                                             1 CAAGGATCGCTACGGCTCCTGGAT 24
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Publication No. US20050037969A1
GENERAL INFORMATION:
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                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 24; Conservative 0
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US-10-809-189-60856
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Matches 18; Conserv
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                                                                                     US-10-788-779-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SEIDMAN, CHRISTINE
SEIDMAN, JOHN
WATKINS, HUGH
ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
DISBASE-ASSOCIATED MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/788,779
FILING DATE: 27-Feb-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/469,172
FILING DATE: «Unknown»
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33, 505
REFERENCE/DOCKET NUMBER: GML-111
TELECOMMUNICATION:
TELEPHONE: (617) 227-7400
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTAATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GML-111
TELECOMMUNICATION INFORMATION:
TELEPONE: (617) 227-740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAAGGATCGCTACGGCTCCTGGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CAAGGATCGCTACGGCTCCTGGAT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 24 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-788-779-1
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Gaps

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Length 26;

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Sequence 219546, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Jan
APPLICANT: Blume, John
TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse; FILE REFERENCE: 3654.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: INFORMATION:
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Schweizer, Johannes
APPLICANT: Arbor Vita Corporation
ITILE OF INVENTION: Wolecular Interactions in Hematopoietic
ITILE OF INVENTION: Cells
FILE REPERENCE: 020054-001100US
CURRENT APPLICATION NUMBER: US/11/131,042
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: US 60/134,114
PRIOR APPLICATION NUMBER: US 60/134,117
PRIOR APPLICATION NUMBER: US 60/134,117
PRIOR APPLICATION NUMBER: US 60/134,117
PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR FILING DATE: 1999-10-29
PRIOR PILING DATE: 1999-10-29
PRIOR PLING DATE: 1999-10-29
PRIOR PLING DATE: 1999-10-29
PRIOR PLING DATE: 1999-10-29
PRIOR PLING DATE: 2000-01-14
                                             67.5%; Score 16.2; DB 26; Length 85.7%; Pred. No. 1.3e+03; Live 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 362, Application US/11131042; Publication No. US20050221388A1; GENERAL INFORMATION:
                                                                                                                                                                                    2 AAGGATCGCTACGGCTCCTGG 22
                                                                                                                                                                                                                                                  AAGGATCCCTCCGCTCCTCG 22
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ORGANISM: Artificial Sequence
                                                                                                                  18; Conservative
                                      Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-036-317-219546
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LENGTH: 26
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PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60/170,453

PRIOR FILING DATE: 1999-12-13

PRIOR FILING DATE: 2000-01-14

PRIOR PELIOR APPLICATION NUMBER: US 60/182,296

PRIOR APPLICATION NUMBER: US 60/192,296

PRIOR PRILING DATE: 2000-04-11

PRIOR APPLICATION NUMBER: US 60/196,267

PRIOR APPLICATION NUMBER: US 60/196,267

PRIOR APPLICATION NUMBER: US 60/196,267

NUMBER OF SEQ ID NOS: 543

NUMBER OF SEQ ID NOS: 543

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 26
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CURRENT APPLICATION NUMBER: US/11/131,054
CURRENT APPLICATION NUMBER: US/11/131,054
FRICA APPLICATION NUMBER: US/09/688,017
PRIOR PELING DATE: 2000-10-13
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR PELICATION NUMBER: US 60/134,117
PRIOR PELICATION NUMBER: US 60/134,118
PRIOR PELING DATE: 1999-05-14
PRIOR PELING DATE: 1999-05-14
PRIOR PELING DATE: 1999-06-14
PRIOR PELING DATE: 1999-10-21
PRIOR PELING DATE: 1999-10-21
PRIOR PELING DATE: 1999-10-21
PRIOR PELING DATE: 1999-10-23
PRIOR PELING DATE: 1999-10-23
PRIOR PELING DATE: 1999-10-24
PRIOR PELING DATE: 1999-10-24
PRIOR PELING DATE: 1999-10-24
PRIOR PELING DATE: 1999-10-24
PRIOR PELING DATE: 2000-01-14
PRIOR PELING DATE: 2000-01-14
PRIOR PELING DATE: 2000-02-11
PRIOR PELING DATE: 2000-02-11
PRIOR PELING DATE: 2000-02-11
PRIOR PELING DATE: 2000-02-11
PRIOR PELING DATE: 2000-00-11
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Publication No. US20050214869A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Schweizer, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Colls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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85.7%; Pred. No. 1.3e+03;
ive 0; Mismatches 3;
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COTHER INFORMATION: forward primer 158KIF
US-10-938-249-375
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; OTHER INFORMATION: 158KIF forward primer
US-11-131-054-362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AAGGATCGCTACGGCTCCTGG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7%
Matches 18; Conservative
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TYPE: DNA
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Sequence 79, Application US/10484989

Sequence 79, Application US/10484989

Sequence 79, Application US/10484989

Sequence 70, Application No. USZ0040171154A1

GENERAL INFORMATION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS

APPLICANT: HUMAN SERVICES

APPLICANT: HUMAN SERVICES

APPLICANT: Resnick, Michael A.

APPLICANT: Lewis, Lysle Kevin

TITLE OF INVENTION: OLIGONUCLEOTIDES

FILE REFERENCE: 4239-6760

TITLE OF INVENTION: OLIGONUCLEOTIDES

FILE REFERENCE: 2004-01-23

CURRENT APPLICATION NUMBER: US 60/308,426

PRIOR APPLICATION NUMBER: PCT/US02/23634

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2002-07-26

NUMBER OF SEQ ID NOS: 83

SEQ ID NO ?9

SEQ ID NO ?9

SEQ ID NO ?9
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                                                                                                                                                                                                                                                                  ; DB 26; Length 25;
2e+03;
             CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 219546
LENGTH: 25
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10556, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REPERENCE: 31181
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
FRIOR FILING DATE: 2003-01-08
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic oligonucleotide US-10-484-989-79
                                                                                                                                                                                                                                                                Score 15.8; I
Pred. No. 2e+C
0; Mismatches
CURRENT APPLICATION NUMBER: US/11/036,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AGGATCGCTACGGCTCCTGG 22
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                                                                                                                                                                                                                                                                                                                                                                                                   1 caaggaccecracageree 19
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ORGANISM: Artificial sequence
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-219546
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Yue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT APPLICATION NUMBER: 06/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 572806
                                                                                                                                                                                                                                                                                                                                                      Sequence 106202, Application US/10098263B
; Sequence 106202, Application US/10098263B
; Publication No. US2030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; TITLE OF INVENTION: 9.003-01-08
; CURRENT FILING DATE: 2003-01-08
; CURRENT FILING DATE: 2001-03-16
; RIOR FILING DATE: 2001-03-16
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106202
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SRQ ID NO 105576 LENGTH: 25 TYPE: DNA TYPE: DNA
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Pred. No. 3.9e+03;
0; Mismatches 3;
                                                                                                                                        63.3%; Score 15.2; DB 16;
85.0%; Pred. No. 3.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.3%; Score 15.2; DB 16; Best Local Similarity 85.0%; Pred. No. 3.9e+03; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                              0; Mismatches
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85.0%;
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Best Local Similarity 85.04
Matches 17; Conservative
                                                                                                                                                 Query Match 63.33
Best Local Similarity 85.0°
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapien
US-10-098-263B-106202
                                                                                        ; ORGANISM: Homo sapien
US-10-098-263B-105576
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SEQ ID NO 44526
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; Publication No. US20040146910A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; TILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44526, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 63.3%; Score 15.2; DB 24; Length 25; Local Similarity 85.0%; Pred. No. 3.9e+03; nes 17; Conservative 0; Mismatches 3; Indels
                                                                                                                       APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 35-71
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT PILLING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR PILLING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
ENGTH: 25
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Pred. No. 4.8e+03;
0; Mismatches 5; Indels
                                                         Sequence 368379, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
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Best Local Similarity 78.3%;
Matches 18; Conservative (
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US-10-719-956-368379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-44525
         RESULT 12
US-10-719-956-368379
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US-10-719-956-44526
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Best Local S:
Matches 17
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; Sequence 869432, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TILE REFERENCE: 3654.1
; CURRENT PILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR PILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 869432
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Micrarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 783296
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                                                                                     DB 24; Length 25; 4.8e+03;
                                                                                                                              5; Indels
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Pred. No. 4.8e+03;
O; Mismatches 5;
                                                                     62.5%; Sco. 78.3%; Pred. No. -... 78.3%; O; Mismatches
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                                                                                                                                                                                                             1 AAGGACCGCTACTTCTCCAAGAT 23
                                                                                                                                                                        2 AAGGATCGCTACGGCTCCTGGAT 24
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78.3%;
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-44526
                                                                                Query Match
Best Local Similarity 78.34
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 78.3
Matches 18; Conservative
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CORGANISM: Mus musculus
US-11-036-317-783296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-869432
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Best Local Similarity
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
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; Sequence 12, Application US/10838476
; Publication No. US20050026815A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; TITLE OF INVENTION: an Immunosuppressive Agent
; TITLE OF INVENTION: an Immunosuppressive Agent
; FILE REFERENCE: 06727/005004
; CURRENT APPLICATION NUMBER: US/10/838,476
; CURRENT PILING DATE: 2004-05-04
; PRIOR FILING DATE: 2001-08-27
; PRIOR FILING DATE: 1998-11-05
; PRIOR FILING DATE: 1998-11-05
; RIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 33;
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TITLE OF INVENTION: Treating and Diagnosing Cancers FILE REFERENCE: 06727/004003
GURRENT APPLICATION NUMBER: US/10/115,701A
CURRENT FILING DATE: 2002-04-04
FRIOR APPLICATION NUMBER: 08/758,757
FRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 08/758,757
FRIOR FILING DATE: 1998-04-09
FRIOR FILING DATE: 1998-04-09
FRIOR FILING DATE: 1996-12-03
FRIOR FILING DATE: 1996-12-03
FRIOR FILING DATE: 1995-01-24
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASISED for Windows Version 4.0
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78.3%; Pred. No. 4.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.5%; Score 15; DB 14; Best Local Similarity 78.3%; Pred. No. 4.7e+03; Matches 18; Conservative 0; Mismatches 5
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Publication No. US20050214823A1
GENERAL INFORMATION:
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, ORGANISM: Homo sapiens
US-10-838-476-12
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
US-10-115-701A-12
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Best Local Similarity
Matches 18; Conserv
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TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
TITLE OF INVENTION: an Immunosuppressive Agent
TITLE OF INVENTION: an Immunosuppressive Agent
FILE REFERENCE: 06727/005003
CURRENT APPLICATION NUMBER: US/09/940,308
CURRENT PILING DATE: 2001-08-2786,723
PRIOR APPLICATION NUMBER: US 08/126,723
PRIOR APPLICATION NUMBER: US 08/377,309
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 16
SOFTWARE FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 33
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                                                                                                                                                                               TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as TITLE OF INVENTION: an Immunosuppressive Agent FILE REFERENCE: 06727/005003 CURRENT APPLICATION NUMBER: US/09/940,308 CURRENT FILING DATE: 2001-08-27 PRIOR APPLICATION NUMBER: US 09/186,723 PRIOR PILING DATE: 1998-11-05 PRIOR APPLICATION NUMBER: US 08/377,309 PRIOR FILING DATE: 1995-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.5%; Score 15; DB 12; Length 33
Best Local Similarity 78.3%; Pred. No. 4.7e+03;
Matches 18; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 33
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; Publication No. US20020155996A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09940308 Publication No. US20040092437A1 GENERAL INFORMATION:
                                                                                                            ; Sequence 12, Application US/09940308
; Publication No. US20020193297A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-940-308-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-940-308-12
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Best Local Similarity
Matches 18; Conserv
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TYPE: DNA

RESULT 19

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TYPE: DNA

Length 25;

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Ouery Match
Best Local Similarity 81.09
Matches 17, Conservative
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APPLICANT: Mitthman, Michael; TITLE OF INVENTION: Human Microarray; FILE REFERENCE: 3118.1
CURRENT FILING DATE: 2003-01-08; PRIOR APPLICATION NUMBER: 06/276,759; PRIOR FILING DATE: 2001-03-16; NUMBER OF SEQ ID NOS: 131066; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 106263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.8%; Score 14.6; DB 10; Length 24; Best Local Similarity 81.0%; Pred. No. 7.4e+03; Matches 17; Conservative 0; Mismatches 4; Indels
                      PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SSOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 166635
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1340, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-68605-1
; CURRENT FILING DATE: 2001-08-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR APPLICATION NUMBER: US 60/228,854
; RIOR APPLICATION NUMBER: US 60/228,854
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; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-1340
                                                                                                                                                                                                                                                                                                    61.7%; Score 14.8; DB 26;
88.9%; Pred. No. 5.9e+03;
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2005-01-13
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.97
...hes 16; Conservative
                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-166635
CURRENT FILING DATE:
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; ORGANISM: Homo sa
US-10-098-263B-106263
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US-09-940-185-1340
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US-11-036-117-72142

i Sequence 72142. Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
    APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TITLE OF INVENTION: Wethod of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

TENGTH. 20142
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01.3
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 421165
LENGTH: 25
                                                      Gaps
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                                                   4; Indels
60.8%; Score 14.6; DB 16;
81.0%; Pred. No. 7.3e+03;
tive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.8%; Score 14.6; DB 26;
81.0%; Pred. No. 7.3e+03;
ive 0; Mismatches 4;
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Pred. No. 7.3e+03;
0; Mismatches 4;
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US-11-036-317-936457
; Sequence 936457, Application US/11036317
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                                                                                                                                             5 AACGATCTCTAAGGCTCCAGG 25
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81.0%;
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Best Local Similarity 81.0°
Matches 17; Conservative
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Matches 17; Conservative
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CORGANISM: Mus musculus
US-11-036-317-421165
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; ORGANISM: Mus musculus
US-10-719-900-298476
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Matches
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Publication No. US20050214823A1

Publication No. US20050214823A1

APPLICANT: Williams, Alan

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPERENCE: 3654-11.

CURRENT APPLICATION NUMBER: US/11/036,317

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SEQ ID NO 93457

LENGTH: 25
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US-10-719-900-298476

US-10-719-900-298476

Sequence 298476, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REPERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ 1D NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 298476

LENGTH: 25

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 298398, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
; APPLICANT: Kue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR RILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SEQ ID NO 298398
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                       60.8%; Score 14.6; DB 26; Length 25; ilarity 81.0%; Pred. No. 7.3e+03; Conservative 0; Mismatches 4; Indels C
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75:0%; Pred. No. 9.1e+03;
tive 0; Mismatches 6
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Best Local Similarity 75:0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-936457
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; ORGANISM: Mus musculus
US-10-719-900-298398
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Best Local Similarity
Matches 17; Conserva
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US-10-719-900-298398
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APPLICANT: Wyeth
APPLICANT: MOUNTS, William
APPLICANT: MOUNTS, William
APPLICANT: MOUNTS, William
APPLICANT: MOUNTS, WILLIAM
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARES PATENTIN VERSION 3.2
SEQ ID NO 177036
LENGTH: 25
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                                                                                                                                                                                                                       Sequence 564538, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 564538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 25;
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    Length 25;
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Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6;
Score 14.4; DB 22;
Pred. No. 9.1e+03;
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Pred. No. 9.1e+03;
0; Mismatches 6;
                                             0; Mismatches
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US-09-877-478-5195
; Sequence 5195, Application US/09877478
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ilarity 75.0%;
Conservative (
Query Match 60.0%;
Best Local Similarity 75.0%;
Matches 18; Conservative
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US-10-719-900-564538
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Best Local Similarity
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### APPLICANT: Renneth, wrapers
### APPLICANT: Renneth, wrapers
### APPLICANT: Elisabeth, Roberts
### TITLE OF INVENTION: OLIGONUCLECTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP9
### TITLE OF INVENTION: VIRUS REPLICATION
### FILE REFERENCE: 400/0420S (MARIBED: 249-E)
### FILE REPERENCE: 400/0420S (MARIBED: 249-E)
### CURRENT PAPLICATION WINDER: US/10/669,841
### CURRENT PAPLICATION WINDER: US/03-26
### RIOR PILING DATE: 2001-06-08
### RIOR PILING DATE: 2001-06-08
### RIOR PILING DATE: 2001-10-24
### RIOR PILING DATE: 2001-10-24
### RIOR PILING DATE: 2002-10-10-6
### RIOR PILING DATE: 2002-03-11-10-6
### RIOR PILING DATE: 2002-03-11-10-6
### RIOR PILING DATE: 2002-03-11-10-6
### RIOR PILING DATE: 2000-03-16
### RIOR PILING DATE: 2000-02-16
### RIOR PILING DATE: 2000-02-16
### RIOR PILING DATE: 2000-02-15
### RIOR PILING DATE: 2000
                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-10-342-902-5195
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9e+03;
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Pred. No. 9e+03;
0; Mismatches 6;
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Pred. No. 9e+03
0; Mismatches
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Publication No. US20040127446A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sirna Therapeutics, Inc. APPLICANT: Lawrence, Blatt
                                          NUMBER OF SEQ ID NOS: 6592
SOFTWARE: Patentin version 3.2
SEQ ID NO 5195
LENGTH: 31
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Best Local Similarity 75.0%;
Matches 18; Conservative (
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                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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David, Morrissey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pamela, Pavco
Patrice, Lee
Kenneth, Draper
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Best Local Similarity 75.0
Matches 18; Conservative
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                                                                             APPLICANT: Ribozyme Pharmaceuticals, inc.
APPLICANT: Ribozyme Pharmaceuticals, inc.
APPLICANT: Bratt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
FILE REFERENCE: Melholo 484-14 (400/029)
CURRENT APPLICANTION NUMBER: US/09/892,712
PRIOR PELING DATE: 2001-12-31
PRIOR PELING DATE: 2000-13-20
PRIOR PLING DATE: 2000-09-3-20
PRIOR PLING DATE: 2000-09-3-20
PRIOR PLING DATE: 2000-09-3-20
PRIOR PLING DATE: 2000-12-4
PRIOR PLING DATE: 1994-02-07
PRIOR PLING DATE: 1994-02-07
PRIOR PLING DATE: 1995-05-04
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APPLICANT: Draper, Kenneth
APPLICANT: Draper, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McMargen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McWiggen, Jim
APPLICANT: McWiggen, Jim
APPLICANT: 2001-06-08-15
PRIOR APPLICANT: 2001-06-08
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR PLICANT: WUMBER: US 09/636,385
PRIOR APPLICANT: 2000-08-09
PRIOR APPLICANT: 2000-08-09
PRIOR PILING DATE: 2000-08-09
PRIOR PILING DATE: 2000-08-09
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
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PRIOR FILING DATE: 2000-10-24
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US-09-877-478-5195
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ilarity 75.0%; Pred. No. 9e+03;
Conservative 0; Mismatches 6;
                           GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 1994-02-07
APPLICATION NUMBER: US 07/882,712
FILING DATE: 1992-05-14
APPLICATION NUMBER: US 09/436,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAAGGATCGCTACGGCTCCTGGAT 24
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; Publication No. US20040054156A1
Publication No. US20030068301A1
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 18; Conserv
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TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE MICROARRAY Probe Sequence Listing Generator V 1.1
LENGTH: 25
Indels
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. 9
0; Mismatches
                                                                                                                                                                                                                                                                      APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Kjacrulff, Soren
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/10/980,923
CURRENT FILING DATE: 2003-09-19
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28357, Application US/10098263B publication No. US20030104410A1 GENERAL INFORMATION:
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                                          1 CAAGGATCGCTACGGCTCCTGGAT 24
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; Sequence 44, Application US/10980923
; Publication No. US20050084937Al
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2%;
Matches 16; Conservative
18; Conservative
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ORGANISM: Homo sapien
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Pred. No. 8.9e+03;
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Pred. No. 8.9e+03;
0; Mismatches 6; Indels
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APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Djarne
APPLICANT: Nielsen, Djarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Kjaerulff, Soren
TITLE CP INVENTION: Alpha-Amulase Mutants
FILE REPERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/09/769,864
PRIOR PILING DATE: 2003-09-19
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PASSEQ for Windows Version 3.0
SSOFTWARE: PASSEQ for Windows Version 3.0
SSOFTWARE: 132
                                                                                                                                                                                                                            APPLICANT: Borchilds
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nissen, Torben L.
APPLICANT: Kjaerniff, Soren
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REPERENCE: 5368.200-US
CURRENT FILING DATE: 2001-01-25
FRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44
                                                            6 CAAGGCTAGCTACAACGACTGGAT 29
                    CAAGGATCGCTACGCTCCTGGAT 24
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US-10-665-667-44/C
Sequence 44, Application US/1066567; Publication No. US2004003386A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
                                                                                                                                                                 Sequence 44, Application US/09769864
Patent No. US20010039253A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.0 Matches 18; Conservative
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CTHER INFORMATION: Primer
US-10-665-667-44
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; Sequence 70024, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196
; FILOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: PSESEQ for Windows Version 4.0
; SEQ ID NO 70024
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RESULT 38
US-10-809-189-70013
Sequence 70013, Application US/10809189
Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Nockhart
APPLICANT: David Nockhart
FILE REFERENCE: 3101.1
CURRENT APPLICATION: Methods of Genetic Analysis
CURRENT APPLICATION NUMBER: US/09/396,196
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SSOFURRE: FASESEQ for Windows Version 4.0
SEQ ID NO 70013
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Matches 16, Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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CORGANISM: mus musculus
US-10-809-189-70013
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; ORGANISM: mus musculus
US-10-809-189-70024
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US-10-809-189-70024
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RESULT 40 US-10-956-157-168189/c

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Sequence 168189, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION.

APPLICANT: Wyeth

APPLICANT: Worth

APPLICANT: WORTHON: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARER: PatentIn version 3.2

SEQ ID NO 168189

LENGTH: 25
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Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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AX956456 Sequence
AX137780 Sequence
BD192813 Improved
AX035617 Sequence
AX033626 Sequence
AX035617 Sequence
AX0356419 Sequence
AX152460 Sequence
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AX15269 Sequence
AX23269 Sequence
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AX23649 Sequence
AX26402 Sequence
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Seidman, C., Seidman, J., Watkins, H. and Rosenzweig, A.
Method for detecting hypertrophic cardiomyophathy associated
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.larity 100.0%; Pred. No. 0.0063;
Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
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Sequence 2 from patent US 5429923.
112895
112895.1 GI:910872
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Patent: US 5429923-A 2 04-JUL-1995;
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AX955017
AR071455
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AR12460
AX456419
AR132695
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AR160328
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Pseudomonas aeruginosa
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JP 2000308489-A/4.
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Unknown.
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Best Local Similarity
Matches 30; Conserv
Unknown.
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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AX35198 Sequence
E31326 Process for
AX301265 Sequence
E31327 Process for
E3127 Process for
E3127 Process for
AX647902 Sequence
E51133 A carcino
AX453416 Sequence
E51173 Method for
E51191 Process for
EX1173 Sequence
AX137508 Sequence
AX137508 Sequence
AX137508 Sequence
AX137508 Sequence
AX137508 Sequence
                                                                               November 18, 2005, 11:12:34; Search time 832.357 Seconds (without alignments) 1746.433 Million cell updates/sec
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                            GCGGATCCAGGTAGGCAGACTTGTCAGCCT 30
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PAT 26-JUL-1995

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Gaps

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linear

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PI KEIICHI YOKOYAMA,NAMI NAKAMURA,TETSUYA MIWA,KATSUYA SEGURO PC C12N15/09,C12N1/21,C12N1/21,C12N1/21,C12N1:19),(C12N1/2), C12N15/00 PC C12N15/00 CC Strandedness: Single; CC Topology: Linear; FH Key FT Source
                                                                                                                                                                                                                                                                                                                                                                                                                                   E31326 45 bp DNA linear PAT 18-JUN-2001
Process for producing novel microbial transglutaminase.
E31326
                                                                              Unclassified.

1 (bases 1 to 41)
Lupton, S. D., Allen, J.M. and Feldhaus, A.L.
Hybrid genes for expression of stimulatory factors in activated
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Keilchi, Y., Nami, N., Tetsuya, M. and Katsuya, S.
Process for producing novel microbial transglutaminase
Patent: JP 1999075876-A 25 23-MAR-1999;
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                                                                                                                                                                                                                                                                       52.0%; Score 15.6; DB 6; Length 41; 81.8%; Pred. No. 4.2e+04;
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Location/Qualifiers
1. .45
                                                                                                                                                          Patent: US 6593124-A 14 15-JUL-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                             1. .41
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                  GI:33765364
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JP 1999075876-A/25.
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Best Local Similarity 81.8<sup>3</sup>
Matches 18, Conservative
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AR359198.1
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AR301265/c
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E31326/c
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
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Glazebrook,J., Katagiri,F., Kreps,J., Provart,N., Ricke,D. and
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/organism='Pseudomonas aeruginosa'
Location/Qualifiers
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    Organism="Pseudomonas aeruginosa"
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/db_xref="taxon:287"

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Yokota, H. and Goto, K. Method for detecting micromutated DNA Method for detecting micromutated DNA DAI ICHI SEIYAKU CO LTD OS Pseudomonas aeruginosa PN JP 2000308489-A/4

DO 07-NOV-2000
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                  TITLE
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TITLE JOURNAL FEATURES REFERENCE AUTHORS

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Novel methods for the identification of ligand and target biomolecules.
                                  PAT 12-JUN-2003
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RP 20-JUL-1998 DK PA 199800956, 29-JUL-1998 US 60/094868 PI

TORBEN HALKIER, LENE JESPERSEN, ALLAN JENSEN

PC GOLN33/50, GOLN33/50, C1201/02, C12Q1/25, GOLN33/15, PC

GOLN33/68//
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Description of Artificial Sequence: Synthetic DNA primer FH
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other sequences; artificial sequences.

1 (bases 1 to 29)
Halkier, T., Jespersen, L. and Jensen, A.

Novel methods for the identification of ligand and target
Patent: JP 2002521652-A 17 16-JUL-2002;
M AND E BIOTECH AS
OS Artificial Sequence
PN JP 2005251652-A/17

PD 16-JUL-2002
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                                  linear
                                                                                                                                                                                                    Unclassified.
1 (bases 1 to 50)
Yokoyama,K., Nakamura,N., Miwa,T. and Seguro,K.
Process for producing microbial transglutaminase
Patent: US 6538122-A 27 25-MAR-2003,
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                                  DNA
                       Sequence 27 from patent US 6538122. AR301266
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/organism="unknown"
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                                                                                                          AR301266.1 GI:31689039
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Best Local Similarity 76.0
Matches 19; Conservative
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       PAT 12-JUN-2003
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File Process for producing novel microbial transglutaminase Patent: JP 1999075876-A 26 23-MAR-1999;

AUTHOR PATENTIAL PATENTAL 
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Process for producing novel microbial transglutaminase.
E31327
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  linear
                                                                                                                                                                                               1 (bases 1 to 45)
Yokoyama, K., Nakamura, N., Miwa, T. and Seguro, K.
Process for producing microbial transglutaminase
Patent: US 6538122-A 26 25-MAR-2003;
Location/Qualifiers
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/organism='Unidentified'.
Location/Qualifiers
     DNA
AR301265 45 bp
Sequence 26 from patent US 6538122.
AR301265.1 GI:31689038
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Best Local Similarity 81.8
Matches 18; Conservative
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 7

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REFERENCE AUTHORS

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RESULT 8

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FEATURES

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Gaps

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S E51173.1 GI:18629490
S UP 2001046073-A/10.
Synthetic construct
other sequences; artificial sequences.
Other sequences; artificial sequences.
CE 1 (bases 1 to 42)
RAMASHITA, Yamaguchi, I., Yoshioka, K. and Doi, Y.
Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
Mathod for transforming plant and transformed plant
RIKAGAU KENKYUSHO, HIDDO NAKASHITA
OS Attificial Sequence
PN JP 2001046073-A/10
PP 09-AUG-1999 JP 1999225832
PR HIDBO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI
PC C12N15/09, A01H5/00, C12N5/10, C12N5/10,
                                                                                                                                                                 PAT 06-JUL-2002
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Location/Qualifiers
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                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                       Deleersnijder,W., Blockx,H. and de Moor,L. Human g-protein coupled receptor and uses thereof Patent: WO 0244212-A 5 06-JUN-2002; SOLVAY PHARMACEUTICALS B V (NL) Location/Qualifiers
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Pred. No. 5.4e+04;
0; Mismatches 6;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Primer"
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/organism="synthetic construct"
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synthetic construct
other sequences; artificial sequences.
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Sequence 5 from Patent W00244212.
AX453416 GI:21712729
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/db_xref="taxon:32630"
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Best Local Similarity 76.0%;
Matches 19; Conservative
                                            GGCAAACTTGTCAGCCT
GGCAGACTTGTCAGCCT
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Best Local Similarity
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ORGANISM
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E51173
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AX453416
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synthetic construct
other sequences; artificial sequences.
( Dasses 1 to 30)
Enjoji,T., Todo,N. and Imamura,M.
A carcinostatic or antiviral agent containing IRG27 protein or gene
Patent: WO 0187349-A 5 22-NOV-2001;
SUMITOWO PHARMACEUTICALS CO LTD, TAKASHI ENJOJI,NAOKI TODO, MOTOAKI
                                              PAT 03-MAR-2003
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A carcinostatic or antiviral agent containing IRG27 protein or
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19-MXY-2000 JP 00P 149097
TAKASHI ENJOYI,WAOXI TODO,WOTOAKI IMAMURA
A61K48/00,A61K38/17,A61P31/12,A61P35/00//C12N15/12,C07K16/18
Description of Artificial Sequence: a sequence of primer 4U
                                                                                                                                                                                                                                                    Jensen, A., Halkier, T. and Jespersen, L. Methods for the identification of ligand and target biomolecules Patent: EP 1270746-A 18 02-JAN-2003; Inoxell A/S (DK)
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                                              linear
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/noTe="Synthetic DNA primer"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                            AX647902 29 bp
Sequence 18 from Patent EP1270746.
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WO 0187349-A/5
22-NOV-2001
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synthetic construct
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Best Local Similarity 76.0
Matches 19; Conservative
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BD103433/c
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Matches

RESULT 14 E51191 LOCUS

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REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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1 (bases I to 29)
Yu,L., Fu,Q., Zhao,Y., Zhang,H. and Bi,A.
A novel human lysozyme gene, its encoded polypeptide and the method for preparing them
Patent: JP 2002523097-A 4 30-JUL-2002;
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A novel human lysozyme gene, its encoded polypeptide and the method
                                                                                                                                                   PAT 30-MAY-2001
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PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/36,C12P21/08//C12O1/
PC (C12N1/21,C12R1:19),(C12N5/10,C12R1:91),(C12N9/36,C12R1:19),
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PN JP 2002523097-A/4
PD 30-UUL-2002
PD 30-UUL-2002
PR 31-AUG-1999 JP 2000567703
PR 31-AUG-1999 CN 98 1 11044.4
PI LONG YU,QIANG FU,YONG ZHAO,HONGLAI ZHANG,ANDING BI PC
C12N15/09,A61K38/43,A61K39/395,A61K39/395,A61P31/04,A61P35/00, PC
     Gaps
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Patent: EP 1076095-A 10 14-FEB-2001;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="reaxon:32630"
/note="synthetic DNA"
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1. .29
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Pred. No. 6.6e+04;
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     Mismatches
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Sequence 10 from Patent EP1076095.
AX137508
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JP 2002523097-A/4.
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ilarity 71.4%;
Conservative
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     20; Conservative
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Best Local Simil
Matches 20; C
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BD240955
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AUTHORS
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Yamaquchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.
Methods for transformation of plants, transformed plants and
processes for preparation of polyesters

Patent: US 6620601-A 10 16-SEP-2003;
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/organism='Artificial Sequence'
Location/Qualifiers
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syntheric construct
synthetic construct
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(barses 1 to 42)
Nakashita,H., Yamaguchi,I., Yoshioka,K. and Doi,Y.
Process for producing polyester
Patent: JP 2001046074-A 10 20-FEB-2001;
RIKAGAKU KENKYUSHO
                                                                                                                                                   linear
   8; Indels
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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 0; Mismatches
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    .42
    /organism="unknown"
    /mol_type="genomic DNA"

                                                                                                                                                42 bp
Process for producing polyester.
E51191
                              2 CGGATCCAGGTAGGCAGACTTGTCAGCC
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E51191.1 GI:18629508
JP 2001046074-A/10.
20; Conservative
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Unclassified.
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Best Local Similarity
Matches 20; Conserv
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FEATURES

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KEYWORDS

RESULT 15 AR399392

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AUTHORS TITLE

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REFERENCE

PAT 20-APR-2002

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Microsatellite markers for genetic analyses and the differentiation of roses
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids I; Rosales, Rosaceae, Rosoideae, Rosa.
                                                                                                                                                                                                                                  Superantigen based methods and compositions for treatment of diseases
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48.7%; Score 14.6; DB 6; Length 24;
Best Local Similarity 81.0%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 4; Indels
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Location/Qualifiers
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AR137780.1 GI:14479289
                                                                                                                                                                                                                                                                   Patent: US 6340461-A 68 22-JAN-2002;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                   1. .37
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                  37 bp | Sequence 68 from patent US 6340461.
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Sequence 6 from Patent WO03097869.
AX956456
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/mol_type="unassigned I
/db_xref="taxon:36598"
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       4 AGGTCGACAGACTTGTCA 21
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                                                                                                                             AR183091.1 GI:20226684
                                                                                                                                                                             Unknown.
Unclassified.
1 (bases 1 to 37)
Terman,D.Stephen.
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 88.9
Matches 16; Conservative
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Unclassified.
Unclassified.
1 (bases 1 to 29)
Yu,L., Fu,Q., Zhao,Y., Zhang,H. and Bi,A.
Human lysozyme gene, it's encoded polypeptide and the method of preparing them
Preparing them to 660512-A 5 09-DEC-2003;
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Friedman, S. M., Crow, M. K., Li, Y., Tumang, J. R. and Sun, G.-R.
Conserved T-call receptor sequences
Patent: US 6303750-A 20 16-OCT-2001;
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                                                                                                                             Query Match 50.0%; Score 15; DB 6; Length 29; Best Local Similarity 78.3%; Pred. No. 8.4e+04; Matches 18; Conservative 0; Mismatches 5; Indels
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/organism='Unidentified'...
1. .29
1. .20
| / Organism="unidentified"
| / mol_type="genomic DNA"
| / db_xref="taxon:32644"
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Sequence 5 from patent US 6660512.
AR437642
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                         /organism≈"Homo sapiens"
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Sequence 1 from Patent EP1029923.
AX033626
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81.0%;
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synthetic construct
                                               Molday, R.S., Ahn, J.
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Best Local Similarity 81.0%
....hes 17; Conservative
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PD 21-MAY-2002
PF 19-MAY-1998 JP 1998550503
PR 19-MAY-1998 UP 208/85811
PR 19-MAY-1998 UP 208/85811
PR 19-MAY-1999 UP 208/85811
PR 19-MAY-1999 UP 208/85811
PC C12P13/04,C12P7/26,C12P7/62,C12N15/63,C12N9/88,C12N9/10 CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'synthetic oligonucleotide'
FH Key
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1 Similarity 69.0%; Pred. No. 1.3e+05;
20; Conservative 0; Mismatches 9; Indels
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Staphylococcus aureus
Bacteria, Firmicutes, Bacillales, Staphylococcus.
1 (bases 1 to 31)
Fotheringham, I.G.
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Improved transaminase biotransformation process
BD192813
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    .31
    Corganism="Staphylococcus aureus"
/mol type="genomic DNA"
/db_xref="taxon:1280"

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/desc = 'synthetic oligonucleotide'
Key
Location/Qualifiers
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Fotheringham, 1. G.
Transaminase biotransformation process
Patent: US 6197558-A 14 06-MAR-2001;
Location/Qualifiers
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                                                                                                                                                 /organism="unknown"
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JP 2002514921-A/14.
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Homo sapiens
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Best Local Similarity 69.0
Matches 20; Conservative
                              Unknown.
Unclassified.
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            Unknown.
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ORGANISM
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BD192813
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AX955017
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Unclassified.
In (bases 1 to 31)
Miller,W.Allen. and Wang,S.
Cap-independent translation sequences derived from barley yellow
dwarf virus
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Patent: EP 1029923-A 1 23-AUG-2000;
HAVE D J VAN DER BV (NL)
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                   Expression system for large functional proteins Patent: WO 03093468-A 13 13-NOV-2003; University of British Columbia (CA) Location/Qualifiers
                                                                                                                                                                                                                         Score 14.6; DB 6;
Pred. No. 1.3e+05;
0; Mismatches 4;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer P1"
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and Hauswirth, W.S.
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Sequence 19 from patent US 5910628.
AR071455
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/db_xref="taxon:9606"
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    PAT 06-JUL-2002
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Synthetic nucleic acid molecule compositions and methods of
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      linear
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48.0%; Score 14.4; DB 6;
Best Local Similarity 93.8%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                            /organism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"
|noTe="An oligonucleotide"
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                                                                                                          other sequences; artificial sequences.
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Patent: WO 0216944-A 277 28-FEB-2002;
PROMEGA CORPORATION (US)
Location/Qualifiers
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40 bp I
Sequence 277 from Patent WO0216944.
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Sequence 34 from patent US 6204371.
AR145578.1 GI:15104864
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/mol_type="unassigned DNA"
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                                               AX456419.1 GI:21715323
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                                                                              synthetic construct
synthetic construct
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1 (bases 1 to 44)
Levinson, D.Adam.
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1 (bases 1 to 44)
Levinson, D.Adam.
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AR143578/c
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Miller,W.Allen. and Wang,S.
Cap-independent translation sequences derived from barley yellow
dwarf virus
Patent: US 5910628-A 8 08-JUN-1999;
Location/Qualifiers
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Wong, A.K.C., Bartel, P.L., Teng, D.H.-F. and Tavtigian, S.V.
Carboxy-terminal BRCAl interacting protein
Patent: US 6235263-A 28 22-MAY-2001;
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                                               Query Match 48.0%; Score 14.4; DB 6; Length 31; Best Local Similarity 75.0%; Pred. No. 1.6e+05; Matches 18; Conservative 0; Mismatches 6; Indels
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/organism="unknown"
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    /mol_type="unassigned DNA"
                                                                                                                                                                                                               AR071444 33 bp
Sequence 8 from patent US 5910628.
AR071444 GI:7222332
                                                                                                          2 CGGATCCAGGTAGGCAGACTTGTC 25
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                                                                                                                             8 CGGATCCTGGGAAACAGGCTTGAC 31
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Best Local Similarity 75.0
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Patent: JP 2003000279-A 65 07-JAN-2003;
SUMITOWO CHEMICAL CO LTD
SUMITOWO CHEMICAL CO LTD
SON Artificial Sequence
PN JP 2003000279-A/65
PD 07-JAN-2003
PP 27-DEC-2001 JP 2001396288
PP 27-DEC-2001 JP 2001396288
PP 27-DEC-2001 JP 2001396288
PP C 12N15/09, A61K38/00, A61P25/28, C07K14/47, C07K16/18, PC
C12N1/19,
PC C12N1/19,
PC C12N1/19,
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447,C12N15/00,
C12N5/00,A61K37/02,G01N27/26,G01N27/26
Besigned oligomuclectide primer for PCR
Key
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bHLH-PAS proteins, its gene and use thereof.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                           mRNA
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JP 2003000279-A/65.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 45)
                                                                                                                                                                                                                                                                                      Patent: US 6562343-A 34 13-MAY-2003;
Location/Qualifiers
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AR316574.1 GI:33695435
                    40 TGCAGGTGTGCAGACTTGGGATCC 17
      TCCAGGTAGGCAGACTTGTCAGCC 29
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/mol_type="mRNA"
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Unclassified.
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BD188256/C
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AR316574/c
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Compositions and methods for the treatment and diagnosis of immune disorders
Patent: US 6288218-A 34 11-SEP-2001;
Location/Qualiflers
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Kingsbury, G.A. and Leiby, K.R.
Nucleic acid molecules encoding a 103 gene product and uses
therefor
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48.0%; Score 14.4; DB 6; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                  6; Indels
                                                                                                                                   Query Match 48.0%; Score 14.4; DB 6; Best Local Similarity 75.0%; Pred. No. 1.6e+05; Matches 18; Conservative 0; Mismatches 6;
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Location/Qualifiers
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Sequence 27 from patent US 6323334.
AR262637
AR262637.1 GI:28074173
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                                                                                                                                                                                                                                                                                                 44 bp
Sequence 34 from patent US 6455685.
AR232695.
AR232695.1 GI:27274972
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/mol_type="genomic DNA"
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Levinson, D.A.
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Unclassified.
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Query Match

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PAT 21-NOV-2002
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Affinium Pharmaceuticals, Inc. (CA)
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Lusis,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
Gene and sequence variation associated with lipid disorder
Patent: WO 0220847-A 214 14-MAR-2002;
THE RECENTS OF THE UNIVERSITY OF CALIFORNIA (US)
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AX526499
AX526499.1 GI:25171306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bodnar, J.S., Castellani, L.W., Chatterjee, A., de Jong, P., Lusis, A.J., Ohmen, J., Ross, D., Tafuri, S. and Wu, C. Gene and sequence variation associated with cancer Patent: WO 0220848-A 214 14-MAR-2002, THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) Location/Qualifiers
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Patent: WO 0216944-A 260 28-FEB-2002;
PROWEGA CORPORATION (US)
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Sequence 214 from Patent WO0220848.
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Sequence 260 from Patent WO0216944.
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NCE I (bases 1 to 28)

JORS Altieri,D.C.

LE Method for selectively modulating the interactions between survivin and tubulin

JRNAL Patent: US 6346389-A 12 12-FEB-2002;

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 Sequence 12 from patent US 6346389.
AR184482
AR184482.1 GI:20230447
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Human BRC Synthetic

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Reverse p 3' primer Mouse 103

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3' oligon Mouse 103

Murine

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Listing first 45 summaries
                                             nucleic search, using sw model
                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
        GenCore (c) 1993
                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
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                  Copyright
                                                                                                                                                                                                                        length: 0
length: 50
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Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy; Beta-cardiac myosin heavy chain PCR primer B. BP. AAQ91122 standard; cDNA; 30 (first entry) 19-FEB-1996 AAQ91122; RESULT

diagnosis; primer; mutation; detection; ss 04-JUL-1995. US5429923-A. Synthetic.

(HARD) HARVARD COLLEGE. (BGHM) BRIGHAM & WOMENS HOSPITAL. (GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA. 92US-00989160. 11-DEC-1992;

92US-00989160.

11-DEC-1992;

Watkins H, Rosenzweig A; Seidman C, Seidman J,

WPI; 1995-245715/32.

Non-invasive method for diagnosis of hypertrophic cardio-myopathy useful for testing asymptomatic individual(s)

Example 1; Col 10; 22pp; English.

AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-sasociated mutations in the beta-cardiac myosin heavy-chain obstained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

geneseqn2003ds:* geneseqn2004as:* geneseqn2003cs:* N_Geneseq_16Dec04:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2004bs: geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* 10: Database

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Scoring table:

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A228442 FIRMES US Aba96284 Human IRG Abk87354 Human G p Aa445207 Sequence Aaf4520 Poly-3-hy Aaa07726 Human lys Aat04797 T cell re Adp13952 Renal cel Adr05298 Human bet Aaf27237 Pseudomon Aaf82378 Human C-r Transglut Oligonucl Transglut for Aaq91122 Beta-card Human agg Aca63112 Human bet Oligonucl Human Description Abk88923 I Abt32007 I Aaq77830 I Aav81531 C Aaa73048 7 Aav81532 C SUMMARIES ADR05298 ABT32007 AAQ77830 AAV81532 AAA73049 AAA07726 AAT04797 ADP13952 AAF82378 AAA73048 **ABK88923** AAV81531 AAQ45507 а 001549800000000004 12 В Length Query 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 555.3 55 Score Result So. υ υ טט

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asymptomatic individuals suspected of having the disease. The method has a broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B. Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease and phenylketonuria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    familial hypertrophic cardiomyopathy; SHC; Gaucher's disease; sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia; buchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease; phenylketonuria; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting a presence or absence of a mutation associated with hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or hemophilia, by detecting a mutation in an amplified product of a beta cardiac myosin heavy-chain DNA.
                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
                                                                                                                                                     Length 30;
                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human beta cardiac myosin heavy chain PCR primer B.
                                                                                                               Sequence 30 BP; 6 A; 8 C; 10 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                   100.0%; Score 30; DB 2; 100.0%; Pred. No. 0.0015;
                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                             1 GCGGATCCAGGTAGGCAGACTTGTCAGCCT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 5; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                               ACA63112 standard; DNA; 30 BP
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                                                                                                                                                                                          30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-512374/48.
                                                                                                                                                     Query Match
Best Local Similarity
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oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain DNA. The method is useful for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. This method is especially useful for diagnosing off and FHC, as well as for determining the estimated the life expectancy of a person with familial hypertrophic cardiomyopathy. In particular, the method is useful for determining an individual's genetic information, and diagnosing e.g. Gaucher's disease, haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease, phenylketonuria or cystic fibrosis. The present sequence is a PCR primer used to amplify a region of the beta cardiac myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (familial or sporadic, FHC, SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy, comprising amplifying beta-cardiac myosin heavy-chain DNA forming an associated with hypertrophic cardiomyopathy in the amplified product, thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also included are a set of DNA oligonuclectide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting mutations associated with hypertrophic cardiomyopathy to diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac myosin heavy-chain DNA and detecting the mutation in the amplified
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, beta cardiac myosin, heavy chain, PCR, primer; ss, FHC, SHC, familial hypertrophic cardiomyopathy, sporadic hypertrophic cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human beta cardiac myosin heavy chain mutation detection primer B.
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                                                                                                                                                                                                                                               Score 30; DB 9; Length 30;
Pred. No. 0.0015;
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                                                                                                                                                                                                             Sequence 30 BP; 6 A; 8 C; 10 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                            chain cDNA containing an FHC-associated mutation
                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                 100.0%;
100.0%;
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95US-00469172.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR05298 standard; DNA; 30
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                                                                                                                                                                                                                                                                                30; Conservative
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SEIDMAN J.
WATKINS H.
                                                                                                                                                                                                                                                                Similarity
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Best Local {
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(WATK/)
(ROSE/)
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oligonucleotide primers being useful for facilitating the diagnosis of hypertrophic cardiomyopathy by being capable of detecting a hypertrophic cardiomyopathy by being capable of detecting a hypertrophic cardiomyopathy (comprising a first container diagnosis of hypertrophic cardiomyopathy (comprising a first container bolding an RNA probe completely hybridisable to the beta-cardiac myosin heavy chain DNA, where the RNA probe is capable of detecting a hypertrophic cardiomyopathy-associated mutation, a second container by principle of a maplifying beta-cardiac myosin heavy-chain DNA and instructions for using the components of the kit to detect the presence or absence of a hypertrophic cardiomyopathy-associated mutation in detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy for facilitating the diagnosis of hypertrophic cardiomyopathy for facilitating the diagnosis of hypertrophic cardiomyopathy refreshed to the presence of the kirch hypertrophic cardiomyopathy refreshed to hypertrophic cardiomyopathy refreshed to hypertrophic cardiomyopathy refreshed to hypertrophic cardiomyopathy relies on the presence of typical calling hypertrophic cardiomyopathy relies on the presence of typical calling hypertrophic cardiomyopathy relies on the presence of typical calling hypertrophic cardiomyopathy relies on the presence of typical calling hypertrophy. The present invention is non-invasive and based, at least in the hypertrophy and the demonstration of unexplained ventricular and the diagnosis of the transfer of the hypertrophy. ö caused by point mutations in the beta cardiac myosin heavy-chain gene. The present sequence is a PCR primer used to amplify a region of the beta part, on the discovery that hypertrophic cardiomyopathy is caused by point mutations in the beta cardiac myosin heavy-chain gene. Prior art reveals that there are no extensive studies involving a large number of families which established that this particular disease or disorder was Selective cloning, mismatch detection; mismatch binding protein; MutS; mutant gene; strain PAO128; bacterial infection; ss. Gaps chain having a disease-related point mutation. ö amplify beta-cardiac myosin heavy-chain DNA (the set of 100.0%; Score 30; DB 13; Length 30; 100.0%; Pred. No. 0.0015; ive 0; Mismatches 0; Indels Pseudomonas aeruginosa strain PAO128 oligonucleotide. Sequence 30 BP; 6 A; 8 C; 10 G; 6 T; 0 U; 0 Other; 1 GCGGATCCAGGTAGGCAGACTTGTCAGCCT 30 GCGGATCCAGGTAGGCAGACTTGTCAGCCT 30 Pseudomonas aeruginosa; strain PAO128 99JP-00121957, (first entry) 30; Conservative (revised) cardiac myosin heavy Best Local Similarity Matches 30; Conserv JP2000308489-A 28-APR-1999; 11-SEP-2003 24-APR-2001 07-NOV-2000. AAF27237; Query Match which ð 셤

Detection of minutely mutated DNA useful for detection and treatment of Pseudomonas aeruginosa, and development of antibacterial agents comprises cloning a structurally characterized DNA. Example 6; Fig 6; 13pp; Japanese. AAF27237/c ID AAF27237 standard; DNA; 34 BP 99JP-00121957. (DAUC) DAIICHI PHARM CO LTD. WPI; 2001-127778/14. 28-APR-1999;

region by concentrating the DNA of interest using a substance which specifically recognises the structurally characterised region or a fragment thereof, and selectively cloning only the DNA of interest by subtraction treatment. The invention especially relates to a method for cloning or detecting a minutely mutated DNA by concentrating the mutated DNA using a substance (such as a mismatch repair protein) which capecifically recognises mismatched DNA, and selectively cloning only the mutant DNA. Such a method of detection may also be used in the diagnosis of disease associated with DNA mutations. The method was exemplified by the cloning and sequencing of DNA from the PAO128 strain of Pseudomonas aeruginosa using an immobilised maltose binding protein (MBP)-MutS fusion protein, and the corresponding DNA from pseudomonas aeruginosa strain PAO1 (which was designated as the wild-type). The MutS portion of the fusion protein recognised mismatches in PAO1/PAO128 DNA duplexes. The mutant (i.e., PAO128) DNA was thus concentrated, amplified via PCK, and contaminating DNA removed by RDA. A Pseudomonas aeruginosa strain PAO128 library was constructed and its genome sequenced. Such a protocol may be development of an unidentified gene from Pseudomonas aeruginosa strain capened on 11-SEP-2003 to standardise OS field)

Sequence 34 BP; 4 A; 11 C; 13 G; 6 T; 0 U; 0 Other;

Gaps ö 55.3%; Score 16.6; DB 5; Length 34; 82.6%; Pred. No. 1.5e+03; 4; Indels 0; Mismatches Local Similarity 82.6 es 19; Conservative Query Match Matches

8 CAGGTAGGCAGACTTGTCAGCCT 30

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AAF82378 standard; DNA; 37 AAF82378; RESULT 5 AAF82378

(first entry) 25-JUN-2001

Human C-reactive protein 5' primer.

Human, C-reactive protein, CRP; chicken embryo lethal orphan virus; CELO; recombinant avian egg; chicken adenovirus expression vector; AdCEV; recombinant protein production; vaccine; gene therapy; PCR primer; ss. Human;

Homo sapiens

WO200119968-A1.

22-MAR-2001.

15-SEP-2000; 2000WO-US025489.

99US-0154393P.

17-SEP-1999;

(CHEM-) CHEMOGEN INC

Grabko VI,

Blyden ER;

WPI; 2001-328015/34.

Use of avian adenovirus for producing recombinant proteins by mixing vector containing avian adenovirus DNA with purified adenovirus DNA, introducing DNA mixture into embryonated avian egg, and harvesting proteins.

Example 5; Page 22; 70pp; English.

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The invention relates to a method of cloning a a structurally characterised DNA or a flanking DNA containing part of the characterised

The present sequence was used in the construction of recombinant human C-reactive protein (CRP). It was used in an example illustrating an invention relating to the use of avian adenovirus for producing

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recombinant proteins in an avian egg. The method involves preparing a vector containing avian adenovirus DNA, preparing a mixture of vector DNA with purified adenovirus DNA or adenovirus particles, introducing mixture into embryonated avian egg or avian cell culture, incubating, and harvesting fluids from egg containing recombinant protein molecule encoded by vector DNA. The method is useful for producing recombinant proteins such as therapeutic proteins, immunostimulatory proteins, or tumour antigens in an avian egg. The eggs may be used as a vaccine to elicit an immunological response to the antigenic portion of the protein encoded by the DNA present in the chimeric gene of a prepared infectious adenovirus. The chicken adenovirus expression vector (AdGEV) egg system is simple, and economical and allows isolation of the protein in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a purified aggrecanase polypeptide and the polypurlectide encoding it. The polypeptide is useful in a method for developing inhibitors of aggrecanase, where the method comprises three dimensional structural analysis or computer aided drug design. The sequences of the invention are useful for inhibiting or preventing the effects of aggrecanase. The sequences and for inhibiting the proteolytic activity of aggrecanase. The sequences and the inhibitors are useful for treating various aggrecanase-associated conditions such as osteoarthritis, conditions characterised by the degradation of articular cartilage, or diseases characterised by degradation of aggrecan and/or an upregulation of aggrecanase, and also for detecting or diagnosing genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel purified aggrecanase polypeptide useful for developing inhibitors of aggrecanase for treating various aggrecanase-associated conditions such as osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, aggrecanase, primer, computer aided drug design, osteoarthritis, aggrecan; genetic disorder; proteolytic activity, articular cartilage, osteopathic; antiarthritic; ss; PCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 55.3%; Score 16.6; DB 4; Length 37; Best Local Similarity 82.6%; Pred. No. 1.5e+03; Matches 19; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37 BP; 11 A; 8 C; 12 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biologically active form, free of endotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human aggrecanase cDNA PCR primer #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK88923;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acids encoding polypeptides that mediate phosphate uptake into plant cells, useful in plant biotechnology, particularly in regulating transport and translocation of phosphorus in photosynthetic
disorders in which aggrecanase is irregularly transcribed or expressed. This sequence represents a PCR primer used to amplify human aggrecanase
                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant growth regulant; phosphate uptake; plant; mycorrhizal fungus; phosphate deficiency; phosphate sufficiency; plant biotechnology; transport; translocation; photosynthetic plant; rice; PCR; primer; ss.
                                                                                                                                        Gaps
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I, Ricke D,
                                                                                                  54.0%; Score 16.2; DB 6; Length 26; 85.7%; Pred. No. 2.2e+03; live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 23;
                                                                   Seguence 26 BP; 7 A; 8 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 4 A; 5 C; 6 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goff SA,
Provart 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.0%; Score 15.6;
                                                                                                                                                                                                                                                                                                                                                                                                         RubQ1 forward PCR primer SEQ ID No 72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Briggs S, Cooper B,
Katagiri F, Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Page 93; 235pp; English.
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                                                                                                                                                                           8 CAGGTAGGCAGACTTGTCAGC 28
                                                                                                                                                                                               CATCTATGCAGACTTGTCAGC 26
                                                                                                                                                                                                                                                                                                 BP
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26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332064P.
21-MAR-2002; 2002US-0361819P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-2002; 2002WO-EP006967.
                                                                                                                                                                                                                                                                                 ABT32007/c
ID ABT32007 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                     08-MAY-2003 (first entry)
                                                                                                                                        Conservative
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                                                                                                                    Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003000897-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paszkowski U,
Glazebrook J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2003
                                                                                                                                                                                                                                                                                                                                    ABT32007;
                                                                                                      Query Match
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Query Match

involving aggrecanase or disorders involving cellular, organ or tissue

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AAV81521-60 were used for construction of a synthetic Streptoverticillium sp. transglutaminase gene (see AAV81508). The synthetic gene is codon altered for high expression in Escherichia coli. The specification describes a new microbial transglutaminase that has the N-terminal aspartic acid of transglutaminase deleted. Eliminating the N-terminal Asp from microbial transglutaminase allows efficient removal of the terminal Met residue added when the protein is expressed in E. coli. The E. coli methionine aminopeptidase acts well on Met-Ser but only poorly on Met-Asp, so problems of antigenicity associated with Met-terminated proteins are avoided. Recombinant transglutaminase is used to produce gelled foods (jellies, yogurt and cheeses) or cosmetics, to improve the quality of meet, in the production of materials for microcapsules of high thermal stability and as a carrier for immobilised enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New microbial transglutaminase with N-terminal aspartic acid deleted -allowing high level recombinant production without added methionine in E. coli, useful in production of gelled foods, cosmetics etc.
                                                                                   Transglutaminase, microbial; gelled food; jelly; yogurt; cheese; cosmetic; meat quality; microcapsule production; high thermal stability; carrier; immobilised enzyme; codon optimised; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transglutaminase; gelled food; jelly; yoghurt; gelled cosmetic; cheese;
                                               Oligonucleotide used for codon optimisation of transglutaminase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transglutaminase related oligonucleotide sequence SEQ ID NO:24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.6; DB 2; Length 45; Pred. No. 4.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45 BP; 14 A; 10 C; 8 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ATCCAGGTAGGCAGACTTGTCA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                         Yokoyama K, Nakamura N, Miwa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 34; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 Arccaegraaecaearrcarca
                                                                                                                                                                                                                                                                                                                   98EP-00112315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.0%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA73048 standard; DNA; 45
      01-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                (AJIN ) AJINOMOTO CO INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-062664/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                            Streptomyces sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200040706-A1.
                                                                                                                                                                                                                                                                                                                 02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                          04-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                  EP889133-A2
                                                                                                                                                                                                                                                                        07-JAN-1999
                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The human CTLA-1 transcriptional control region was amplified directly from human genomic DNA by PCR using oligonuclectides AAQ77829 and AAQ77830. The amplified product was operatively linked to a reporter gene encoding chloramphenicol acctyl transferase (CAT) in a HyTK plasmid. A fragment spanning the HCWV IE94 enhancer was ligated upstream of the CTLA-I-CAT. The plasmid was electroporated into human Jurkat cells. The CTLA-1 transcriptional control region in combination with the CMV enhancer mediates activation-induced expression in human T lymphocytes. (Updated
                                                                                                                                                                                                                                                                                                                                                                                            Human CTLA-1; granzyme B; transcription control region; cytomegalovirus;
HUMV; immediate early gene IE94 enhancer;
chloramphenicol acetyl transferase reporter construct; T cell expression;
T cell activation-induced expression; ss.
                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant polynucleotide encoding stimulatory factor poly:peptide under control of region causing activation-induced expression in T lymphocytes to reduce their dependence on helper cells.
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                         Indels
                                                                                                                                                                                                                                                                                                                                                   Human CTLA-1 transcriptional control region PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 41 BP; 9 A; 12 C; 13 G; 7 T; 0 U; 0 Other;
                         4;
81.8%; Pred. No. 4e+03;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feldhaus AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 15; Page 33; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGATCCAGGAAGGCTGCCTG 29
                                                             8 CAGGTAGGCAGACTTGTCAGCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CGGATCCAGGTAGGCAGACTTG 23
                                                                                       23 CAAATAGGCAGACTTGTGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TARG-) TARGETED GENETICS CORP.
                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                           AAQ77830 standard; DNA; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV81531 standard; DNA; 45
                                                                                                                                                                                                                                                                                                             (first entry)
                     18; Conservative
                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lupton SD, Allen JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-332835/41.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9422489-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-1994;
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                                                                                                                                                                                                                                                                                       25-MAR-2003
16-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                               AAQ77830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV81531;
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AAV81531/c
ID AAV8153
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AC AAV8153
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                     Matches
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AAV81521-60 were used for construction of a synthetic Streptoverticillium sp. transglutaminase gene (see AAV81508). The synthetic gene is codon deltered for high expression in Escherichia coli. The specification describes a new microbial transglutaminase that has the N-terminal aspartic acid of transglutaminase deleted. Eliminating the N-terminal from microbial transglutaminase deleted. Eliminating the N-terminal Asp from microbial transglutaminase allows efficient removal of the terminal Met residue added when the protein is expressed in E. coli. The E. coli methionine aninopeptidase acts well on Met-Ser but only poorly on Methio, so problems of antigenicity associated with Met-terminated proteins are avoided. Recombinant transglutaminase is used to produce gelled foods (jellies, yogurt and cheses) or cosmetics, to improve the quality of meat, in the production of materials for microcapsules of high thermal stability and as a carrier for immobilised enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for producing active transglutaminase from denatured enzyme. The method comprises: (i) forming an intermediate structure of the enzyme having transglutaminase activity under acidic conditions in an aqueous medium; and (ii) forming a higher-level structure of the enzyme having transglutaminase activity under neutral conditions in an aqueous medium. The method can be used for industrial production of active transglutaminase from denatured material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Production of active transglutaminase from denatured enzyme by two-stage refolding process for industrial production of active enzyme for use in
New microbial transglutaminase with N-terminal aspartic acid deleted -allowing high level recombinant production without added methionine in coli, useful in production of gelled foods, cosmetics etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transglutaminase; gelled food; jelly; yoghurt; gelled cosmetic; cheese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transglutaminase related oligonucleotide sequence SEQ ID NO:25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.0%; Score 15.6; DB 2; Length 50; 81.8%; Pred. No. 4.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 50 BP; 12 A; 11 C; 11 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 59; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ATCCAGGTAGGCAGACTTGTCA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arccaegraagcagarrcarca 34
                                                                                           Example 1; Page 34; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ejima D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-JP007250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA73049 standard; DNA; 50
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Best Local Similarity 81.8
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      food production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200040706-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA73049;
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                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for producing active transglutaminase from denatured enzyme. The method comprises: (i) forming an intermediate structure of the enzyme having transglutaminase activity under acidic conditions in an aqueous medium, and (il) forming a higherneutral conditions in an aqueous medium; and (il) forming a higherneutral orditions in an aqueous medium. The method can be used for industrial production of active transglutaminase from denatured material (such as recombinant transglutaminase) which can be used in the food chock industry for the production of gelled foods such as jellies, yoghurts and cheeses, and for the production of gelled cosmetics. The present sequence represents an objective which is used in the exemplification from
                                                                                                                                                                                                                                                                                two-stage
or use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transglutaminase; microbial; gelled food; jelly; yogurt; cheese; cosmetic; meat quality; microcapsule production; high thermal stability; carrier; immobilised enzyme; codon optimised; ss.
                                                                                                                                                                                                                                                                              n of active transglutaminase from denatured enzyme by two-st process for industrial production of active enzyme for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide used for codon optimisation of transglutaminase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.6; DB 3; Length 45;
Pred. No. 4.3e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 45 BP; 14 A; 10 C; 8 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguro K;
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 59; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 ATCCAGGTAGGCAGACTTGTCA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 Arccaegraaccaearrcarca 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miwa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV81532 standard; DNA; 50 BP.
                                                                                                                                                                                    ů,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-00180010.
                                             99WO-JP007250
                                                                                           98JP-00373131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98EP-00112315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.0%;
ilarity 81.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura N,
                                                                                                                                       (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention
                                                                                                                                                                                                                                                                              Production of active
                                                                                                                                                                                    Ono K,
                                                                                                                                                                                                                                  WPI; 2000-475826/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-062664/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                           food production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUL-1997;
                                             24-DEC-1999;
                                                                                           28-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yokoyama K,
13-JUL-2000
                                                                                                                                                                                    Yokoyama K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP889133-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JAN-1999
                                                                                                                                                                                                                                                                                                   refolding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV81532;
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Matches

RESULT 11 AAV81532

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Gaps

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Gaps

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Indels

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0; Mismatches

19; Conservative

Matches

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(such as recombinant transglutaminase) which can be used in the food industry for the production of gelled foods such as jellies, yeghurts and cheeses, and for the production of gelled cosmetics. The present sequence represents an oligonucleotide which is used in the exemplification from
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel screen comprising a pool of vectors with randomly modified nucleotide sequences, useful for identifying modulators of enzyme activity useful for selecting antibiotic agents.
                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chymotrypsin inhibitor; CI-2A; barley; plasmid pCMVbipep; endoplasmic reticulum retention signal; CellScreen; enzyme activity modulator; enzyme inhibitor; drug discovery;
                                                                                                                                            52.0%; Score 15.6; DB 3; Length 50; 81.8%; Pred. No. 4.4e+03; ive 0; Mismatches 4; Indels
                                                                                                            Sequence 50 BP; 12 A; 11 C; 11 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29 BP; 9 A; 6 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                in pCMVbipepER/CI-2A construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ligands using the methods of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1-c; Page 73; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jensen A;
                                                                                                                                                                                                                      5 ATCCAGGTAGGCAGACTTGTCA 26
                                                                                                                                                                                                                                                          13 Arccaggraagcagarrcarca 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide library; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98DX-00000956.
98US-0094868P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-DK000408
                                                                                                                                                                                                                                                                                                                                                    AAZ58442 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                               Local Similarity 81.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jespersen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MEBI-) M & B BIOTECH AS
                                                                        the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-182719/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200005406-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer used
                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                        AAZ58442;
                                                                                                                                              Query Match
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                  AAZ58442
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DB 3; Length 29;

Score 15.4; DB Pred. No. 5e+03;

51.3%; 76.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carcinostatic or anti-viral agents comprising a IRG27 polypeptide, useful for the treatment of cancer and viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, 88; PCR; G protein-coupled receptor; GPCR; IGS70; CNS; primer;
psychiatric disorder; central nervous system disorder; schizophrenia;
Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to carcinostatic, cytostatic or anti-viral agents comprising an IRG27 polypeptide that is induced by a mutated or modified cancer controlling gene p53, a cytokine that controls cell growth and/or by differentiation and is increased in cancer tissue. The gene and IRG27 are useful for treatment and prevention of cancer and viral infection. The present sequence is that of a PCR primer for amplifying the IRG27 encoding polymucleotide
                                                                                                                                                                                                                            Human, IRG27, carcinostatic, cytostatic, anti-viral, cancer, cytokine, cell growth, differentiation, p53, infection, PCR primer, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.3%; Score 15.4; DB 6; Length 30; 94.1%; Pred. No. 5.1e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human G protein-coupled receptor IGS70 PCR primer IP15,490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30 BP; 8 A; 5 C; 9 G; 8 T; 0 U; 0 Other;
3 GGATCCAGGTAGGCAGACTTGTCAG 27

    s egarccargaagacagagreeccag

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 94; 104pp; Japanese.
                                                                                                                                                                                              Human IRG27 PCR primer SEQ ID NO 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                              (SUMU ) SUMITOMO PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 GGCAGACTIGICAGCCT 30
                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-2000; 2000JP-00149097.
                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2001; 2001WO-JP004155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                   ABA96284 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gechakerrereageer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK87354 standard; DNA; 33
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tohdoh N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-114218/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                       WO200187349-A1.
                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                 15-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-2002
                                                                                                                                                                                                                                                                                                                                     22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enjoji T,
                                                                                                                                   ABA96284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK87354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
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ABK87354
                                                                                     ABA96284/
ID ABA9
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The invention relates to a G protein-coupled receptor (GPCR) IGS70

polypeptide including sequences that are 98-99.6% identical. Also
included are the polymucleotide encoding IGS70 (including sequences 98-
09.6% identical to the polymucleotide or the DNA insert contained in
plasmid CBS 109818), a hybridisation probe derived from the
comprising the expression system producing IGS70, a host
comprising the expression system IGS70 receptor membrane preparation
derived from the cell, an antibody immunospecific for IGS70, IGS70 is
comprising the expression or activity of the IGS70 polypeptide in a
cusful for diagnosing a disease or a susceptibility to disease in a
cubject related to expression or activity of the IGS70 polypeptide in a
cubject by determining the presence or absence of mutation in the
cubject by determining the presence or absence of entail mentifying agonist
contained from the subject. IGS70 is also useful identifying agonist
contained from the subject. IGS70 is also useful identifying agonist
cor antagonists. The IGS70 protein, polymucleotide, antibody and identified
contained are useful for treating psychiatric and central nervous
contained percents, myocardial infarction, kidney disease such as
continue, angina pectoris, myocardial infarction, kidney disease such as
crenal failure, gastrointestinal disorders such as jastric ulcer,
contained (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,
contained (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,
contained protozoal) especially human immunodeficiency virus infection
(HIV), diabetes, osteoporosis and allergies. The present sequence is a
contained to isolate the CDNA encoding the human GPCR IGS70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
heart failure; angina pectoris; myocardial infarction; kidney disease; renal failure; gastrointeetinal disorder; irritable bowel syndrome; IBS; inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer; asthma; infection; human immunodeficlency virus infection; HIV; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel G-protein coupled receptor IGS70 polypeptide useful for treating dysfunctions, disorders or disease related to lung, bone marrow, spinal cord immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.3%; Score 15.4; DB 6; Length 33; 76.0%; Pred. No. 5.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33 BP; 8 A; 9 C; 7 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        De Moor L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GGATCCAGGTAGGCAGACTTGTCAG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 dgarccagcrcrgaaagcrrgrcag 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 33; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ45507 standard; DNA; 33 BP.
                                                                                                                                                                                                                                                                23-NOV-2001; 2001WO-EP013706.
                                                                                                                                                                                                                                                                                                            2000EP-00204280.
                                                                                                                                                                                                                                                                                                                              05-DEC-2000; 2000US-0251045P
                                                                                                                                                                                                                                                                                                                                                                                                                     Blockx H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 76.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                          (SOLV ) SOLVAY PHARM BV
                                                                                       osteoporosis; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-527703/56.
                                                                                                                                                                                                                                                                                                                                                                                                                        Deleersnijder W,
                                                                                                                                                                            WO200244212-A2
                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                            30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
30-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ45507
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                                                                                                                                                                                                                                                                                                       Recombinant and chimeric antibodies to C-ERBB-2 - used as therapeutic and diagnostic agents for tumours expressing C-ERBB-2.
                                       variable region; therapy; diagnosis; cancer; mammary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant; polyester synthase; alkyl 3-hydroxyalkanoic acid; PCR primer; phbC; poly-3-hydroxybutyrate synthase; plastid; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.7%; Score 15.2; DB 2; Length 33;
                                                                                                                                                                                                                                                   Parkes DL, Mcbrogan MP, Brandis JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33 BP; 7 A; 10 C; 7 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 6.3e+03;
0; Mismatches 8
             Sequence of a kappa constant region 3' primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGATCCAGGTAGGCAGACTTGTCAGCCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 69; 106pp; English.
                                                     primer; ss.
                                                                                                                                                                 92WO-US010437.
                                                                                                                                                                                             91US-00808462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF84270 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                         (BERL-) BERLEX LAB INC.
                                                                                                                                                                                                                                                   Shawver LK, Liu HC,
                                                                                                                                                                                                                                                                             WPI; 1993-214162/26.
                                       Antibody; c-erbB-2;
ovary; tumour; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
tes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ralstonia eutropha
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                                                                                                                                                                   04-DEC-1992;
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                                                                                                           WO9312220-A1
                                                                                                                                                                                              12-DEC-1991;
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                                                                                                                                       24-JUN-1993
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                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF84270;
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Matches
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Gaps

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Lysoenzyme is useful in cleavage of glycosidic bonds in the cell walls of bacteria, causing lysis. The LYC4 polypeptide can be used in preserving the freshness of foods including meat and wine. It may also be used as an antibacterial agent through its ability to cleave glycosidic bonds to antibacterial ealer. LYC4 is also a non-specific immune molecule, inhibitor of tumour growth e.g. stoanch cancer and mammary cancer. Sequences AAA07726-27 represent PCR primers for amplifying LYC4 CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT04796 and AAT04797 are primers used to amplify T cell receptor (TCR) DNA sequences from rheumatoid arthritis (RA) patients, for analysis of the TCR alpha rearrangements. The amplified sequences are derived from synovial tissue T cells and encode the alpha region of the CDR3 region of the TCR. Both alpha and beta chain DNA can be used as probes in the diagnosis of RA and can also be used for immunotherapy for RA, e.g. by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using them as blocking antigenic peptides, activation of immunoregulatory cells, induction of an anti-TCR antibody or in monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T cell; receptor; rheumatoid arthritis; CDR3; V-beta region; homologous; synovial; immunotherapy; probe; diagnosis; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New conserved T cell receptor sequences in rheumatoid arthritis - used develop prods. for the diagnosis and therapy of rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T cell receptor CDR3 alpha constant region antisense PCR primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mediated detection of the pathogenic V gene expressing T cells
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                                                                                                                                                                                                            5; Indels
                                                                                                                                                                          Length
                                                                                                                                        Sequence 29 BP; 5 A; 7 C; 9 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                      Score 15; DB 3; I
Pred. No. 7.6e+03;
); Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                   ВР.
                                                                                                                                                                                                                                                                                                                                                                 AAT04797 standard; cDNA to mRNA; 25
                                                                                                                                                                                                                                                                           3 GCGGATCCATGAAGGCATCCGTG 25
                                                                                                                                                                                                                                            1 gcggarccaggraggcagacrrg 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NYRU-) NEW YORK SOC RUPTURED
                                                                                                                                                                          50.0%;
78.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                            18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-373796/48.
                                                                                                                                                                          Query Match
Best Local Similarity
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hes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Friedman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                   AAT04797;
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Matches
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ID AAT(
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                                                                                                                                                                                 The present invention relates to methods for transformation of plants. The methods comprise ligating an operon containing a promoter and 2-100 genes of interest, to a vector and integrating the resulting recombinant vector into a plastid chromosome. The methods are useful for transforming brassicaceae, Composites, Pedaliaceae, Olacecae, Maraceae, Rosaceae, Theaceae, Composites, Pedaliaceae, Olacecae, Myraceae, Rosaceae, Theaceae, Leguminosae, Palmae, Sterouliaceae or Rubiaceae, in particular objoyester at abacum of Solanaceae family, for producing polyester, which is polyester synthase genes were used in the method to generate a plant which produces polyester. The present sequence is a PCR primer for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lysoenzyme; LYC4; glycosidic bond; food preservation; antibacterial; tumour inhibition; stomach cancer; mammary cancer; human; PCR primer; ss.
                                                                                  Transforming plants for producing polyester, involves ligating an operon containing a promoter and several genes of interest to a vector and integrating the recombinant vector into a plastid chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel gene of human lysozyme family with human LYC4 protein activity, antibacterial effect and function of inhibiting tumor growth, useful e.g. in anti-bacterial and anti-cancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a human lysoenzyme polypeptide LYC4. The LYC4 polypeptide can be expressed by standard recombinant methodology.
                                                                                                                                                                                                                                                                                                                                                                                 polyester synthase gene poly-3-hydroxybutyrate synthase (phbC:
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0
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Pred. No. 6.5e+03;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42 BP; 11 A; 10 C; 17 G; 4 T; 0 U; 0 Other;
                 Doi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lysoenzyme LYC4 cDNA amplifying primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cedarccaeeceaarcareeceaec 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CGGATCCAGGTAGGCAGACTTGTCAGCC 29
                 Χ,
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                 Yoshioka
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                                                                                                                                                        Example 1; Page 10; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                쁌.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.7%;
Best Local Similarity 71.4%;
Matches 20; Conservative
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                 Nakashita H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA07726 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-237878/20.
                                                  WPI; 2001-292601/31
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                 Yamaguchi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-1999;
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Gaps

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us-10-788-779-2.rng

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rCR; multiple sclerosis; MS; brain; amplification; primer; ss.
                                                                                                                                                                                                 l-cell receptor C-alpha primer.
                     AAQ15070 standard; DNA; 26
                                                                                                                      25-MAR-2003
19-FEB-1992
                                                                                                                                                                                                                                                                                                                                                       W09117268-A
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                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                          AAQ15070;
AAQ15070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample is a whole blood sample (Calaimed). (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples is solated at different stages of progression, development or treatment of RCC and/or other solid tumors. This sequence corresponds to a probe to detect a gene that is differentially expressed and detected by the method
                                                                                                                                                                                                                                             ss; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stover JA;
                                                                                                                                                                                                 Renal cell carcinoma differentially expressed gene probe #357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dorner A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 25 BP; 5 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burczynski ME, Trepicchio WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 688; 350pp; English.
                                            ADP13952 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-2002; 2002US-0427982P.
03-APR-2003; 2003US-0459782P.
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88.9%;
                                                                                                                                                 (first entry)
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Best Local Similarity 88.9
Matches 16; Conservative
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BURCZYNSKI M E.
TREPICCHIO W L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TWIN/) TWINE N C.
(BURC/) BURCZYNSKI N
(TREP/) TREPICCHIO V
(DORN/) DORNER A.
(STOV/) STOVER J A.
(SLON/) SLONI D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-460799/43
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STOVER J A.
                                                                                                                                                                                                                                                                                                                                                                                                       WO2004048933-A2.
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                 26-AUG-2004
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                                                                                               ADP13952
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               ADP13952/
XX ADP13952/
XX ADP1
XX ADP1
XX ADP1
XX ADP1
XX BS;
XW BS;
XW BS;
XW WOOO
XX HOMO
XX HOMO
XX HOWO
YX WOOO
YX WOOO
YX WOOO
YX WOOO
YX WP 10-J
XX YOO
YX WP 11-N
YX YOO
YX WP 11-N
YX YOO
YY YOO
YX YOO
YY YOO
YX Y
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90US-00517245.

(first entry)

(revised)

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TCR V-alpha and V-beta rearrangements were studied in 16 MS brains and in 10 control brains. TCRValpha-dalpha-Calpha and Vbeta-Dbeta-Dbeta-Carbeta decrarangements were confirmed with Southern blotting and hybridisation of the PCR product obtained by amplification using a Calpha or Cbeta primer and a Valpha or a Vbeta specific primer. See AAQ15052-92 for Valpha, Vbeta, Calpha and Cbeta primers. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                  Method for diagnosing T-cell associated disease - comprises identifying rearranged variable region of appropriate T-cell also T-cell compsns. for treating neo:proliferative conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T cell receptor; beta chain; variable region; rheumatoid arthritis; synovial joint fluid; PCR; amplification; primer; immunogen; vaccine; immune disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.3%; Score 14.8; DB 2; Length 26; 88.9%; Pred. No. 9.2e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26 BP; 8 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                Bernard C;
                                     (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                       Disclosure; Page 31; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-cell receptor primer C beta 3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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90US-00517245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT10374 standard; cDNA; 26
                                                                                  Oksenberg J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 88.5
nes 16; Conservative
                                                                                                                            WPI; 1991-353787/48.
01-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09523164-A1
                                                                                  Steinman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT10374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 22
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Gaps

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CAGGTAGGCAGACTTGTC 25 caggaaggcagacrcgrc

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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B Virus (HBV) RNA. The nucleic acid molecules include antisense and enzymes, zinzymes, amberzymes, and enzymes, also disclosed and enzymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptenners that bind to HBV reverse transcriptase and/or HBV reverse transcriptase and/or HBV reverse transcriptase and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and method for screening compounds of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocallular expression and acceptables of the HCV DNAZyme or arciname. The present sequence represents one of the HCV DNAZyme or
                                                                                                                                                                                                treating cirrhosis, liver failure, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                  ٠<u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       minus strand DNAzyme sequences disclosed in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzymatic nucleic acid, RNA cleavage, hepatitis C virus, HCV, infection, type I interferon, DNAzyme.
                                                                                                    ree
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.3%; Score 14.8; DB 8; Length 31;
                                                                                                  Mcswiggen J, Morrissey D, Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.4e+03;
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31 BP; 7 A; 9 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 9.4e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CGGATCCAGGTAGGCAGACTTGTCAG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 CGGATCGTTGTAGCTAGCCTTGCCAG 2
                                                                                                                                                                                                                                                                          Claim 1; Page 234; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI87346 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2000; 2000US-00740332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2000; 2000US-00740332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.18;
                                                                                                                                                                                              Novel compound useful for hepatocellular carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV DNAzyme sequence #37.
                                                                                              Macejak D,
Roberts E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLATT L.
MCSWIGGEN J.
ROBERTS E.
PAVCO P A.
                                                                                                                                                         WPI; 2003-229207/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                      (DRAP/) DRAPER K. (ROBE/) ROBERTS E.
                    LEE P.
DRAPER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus
  PAVCO P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003125270-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUL-2003,
                                                                                              Blatt L, N
Draper K,
                                                                                                                                                                                                                                       infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI87346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MCSW/)
(ROBE/)
(PAVC/)
PAVC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BLAT/)
                  (LEEP/)
                                                                                                                                                                                                Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 24
ADI87346/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB; HCV
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                         The primers AAT10352-97 were used to PCR amplify the T cell receptor beta chain variable regions from T cell culture clones, isolated from the synovial joint fluid of 11 patients suffering from rheumatoid arthritis. The coding sequences were shown to contain the nucleotide sequence AAT07409. The encoded polypeptide can be used as an immunogenic cpd. the detection of or predisposition to an immune disease, or for use as a
                                                                                                                                                                                                           Peptide contained in the variable region of a T-cell receptor beta chain - specifically associated with immune disease, esp. rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 49.3%; Score 14.8; DB 2; Length 26; Best Local Similarity 88.9%; Pred. No. 9.2e+03; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine for prevention or treatment of an immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26 BP; 9 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                   Graus JPM;
                                                                                                                                 Rijnders AWM,
                                                                                                                                                                                                                                                                      Example 2; Page 24; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virucide; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AGGTAGGCAGACTTGTCA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 AGGCAGACAGACTTGTCA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΒÞ
                95WO-EP000670.
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08-UUN-2001; 2001US-00877478.
08-UUN-2001; 2001US-0296876P.
24-0CT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-0337055P.
                                                     94EP-00200454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002; 2002WO-US009187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACD56891/c
ID ACD56891 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV DNAzyme sequence #37.
                                                                                        (ALKU ) AKZO NOBEL NV
                                                                                                                                                                      WPI; 1995-311502/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCSWIGGEN J. MORRISSEY D.
                                                                                                                                 Van Der Maaden JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLATT L.
MACEJAK D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200281494-A1
                                                     23-FEB-1994;
                23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACD56891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BLAT/)
(MACE/)
(MCSW/)
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RESULT 23

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Query Match
                                                                                                     response
                                                                                                                                                                                                                                                                                                                                                                                                    Rosa sp.
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                                                                                                                                                                  Matches
                                                                                                                                                                                                                                            RESULT 26
                                                                                                                                                                                                                                                        ADH68394
 888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primers AAV42608-11 were used to amplify the T cell receptor (TCR) alpha chain cDNA. The products were used to prepare effector T cells with tumour specificicity. The specification describes a method for treatment
                                                              Enzymatic nucleic acid molecules which specifically cleave RNA derived from hepatitis C virus (HCV), useful for the treatment of HCV infections, especially in combination with type I interferon therapy.
                                                                                                                             The invention relates to an enzymatic nucleic acid molecule which specifically cleaves RNA derived from hepatitis C virus (HCV), in which the binding arms of the enzymatic nucleic acid molecule comprises sequences complementary to any of the defined substrate sequences given in the specification. The nucleic acid molecule may be administered for the treatment of HCV infections, especially in combination with type I interferons. The present sequence represents a HCV DNAzyme sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ror treatment of cancer, infection, autoimmune disease and graft rejection, also treatment by administering lymphocytes treated in vitro by these antigens.
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superantigen; treatment; cancer; tumour-specific antigen; autoimmune disease related antigen; infection; bacterial; viral; eukaryotic; autoimmune disease; inhibit; pathological response; immune response; mouse; I cell receptor; TCR; PCR primer; se.
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                                                                                                                                                                                                                                        49.3%; Score 14.8; DB 12; Length 31; 73.1%; Pred. No. 9.4e+03; ive 0; Mismatches 7; Indels (
                      Macejack D;
                                                                                                                                                                                                                     Sequence 31 BP; 7 A; 9 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer used to amplify TCR alpha chain cDNA.
                      Pavco PA,
                                                                                                          Claim 2; SEQ ID NO 4834; 198pp; English
                                                                                                                                                                                                                                                                                       2 CGGATCCAGGTAGGCAGACTTGTCAG 27
                                                                                                                                                                                                                                                                                                          27 cedarcerreraecraecerreceae 2
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                      Roberts E,
                                                                                                                                                                                                                                                                                                                                                                AAV42608 standard; DNA; 37 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US023637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0033172P
97US-0044074P
                                                                                                                                                                                                                            Query Match
Best Local Similarity 75....
Best Local Similarity 75....
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                     Mcswiggen J,
                                          WPI; 2004-031273/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-362497/31.
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S
(MACE/) MACEJACK D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TERM/) TERMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1996;
17-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9826747-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                            07-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Terman DS;
                    Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                      AAV42608;
                                                                                                                                                                                                                                                                                                                                             RESULT 25
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microsatellite markers and used for the amplification of the rose genome.

The invention also describes a test kit for genetic analysis of cultured or wild forms of the genus Rosa sp. that contains at least one of the new oligonucleotide primers and preparing microsatellite markers of Rosa sp. by PCR amplification of hypervariable genomic regions, using at least one primer pair, to produce polymorphic fragments which are separated and etected. The primer pair, fragments which are separated and amplified. The amplified markers are separated by electrophoresis, especially on high-resolution agarose or native or denatured polyacrylamide gels, or by mass spectrometry. After separation, the amplicons are detected by staining (ethidium bromide or silver), radioactive labelling and autoradiography, automated sequencing using radioactive labelling and autoradiography, automated sequencing using primers labelled with dyes or fluorophores or by mass spectrometry. A genomic library of 0.5-1.5 kb fragments from the rose variety inchtblick was constructed in pUC18 and used to transform Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
of cancer which comprises incubating lymphocytes with a tumour-specific antigen or autoimmune disease related antigen and a superantigen. The treated cells are then introduced into the patient. The superantigen and the tumour-specific antigen or autoimmune disease related antigen can be conjugated together. The products are used to treat cancer (carcinoma, melanoma, lymphoma etc.), infections (bacterial, viral or eukaryotic) and autoimmune disease (e.g. idiopathic thrombocytopaenic purpura, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis etc.). The antigens either induce an immune response or inhibit a patholgical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligonucleotides from rose microsatellite markers, useful for genomic analysis, including identification of varieties and hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microsatellite marker; rose genome; PCR; hypervariable region; genetic mapping; relatedness analysis; hybrid identification; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.8; DB 2; Length 37;
Pred. No. 9.7e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosa sp reverse PCR primer for microsatellite marker RMS003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37 BP; 10 A; 8 C; 10 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AGGTAGGCAGACTTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH68394 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CONC-) CON CIPIO GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 breeding; primer; ss.
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ses 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to preparation of natural and unnatural amino acids that (a) reacting a first amino acid and a keto acid with transaminase enzyme to produce an amino acid and pyruvate, and (b) reacting pyruvate with acetolactate synthase enzyme to produce a compound that does not react with transaminase enzyme. The amino acids produced in these processes are useful as flavouring agents, sweeteners, nutritional supplements, synthetic intermediates in the preparation of pharmaceuticals. Acetolactate synthase enzyme eliminates the keto acid produced by the transaminase enzyme reaction, thus preventing the production to completion. The preparation and driving the amino acid production to completion. The preparations are especially used to produce but an acid by achieves sequences AXV65623-24 represent PCR primers used for generating the E. coli K12 ilvA gene fragment. This is used in the
              microsatellites. Inserts in plasmids that hybridised were sequenced and the identified sequences selected for ability to differentiate between a set of 30 rose varieties. The oligonucleotides are used for genetic analysis of cultivated and wild types of roses, particularly for genetic mapping and labelling of mono- or poly-genic traits, selection, analysis of relatedness, identification of varieties and evaluation of varietial purity, identification of hybrids and plant breeding. The oligonucleotides are useful in automated processes, do not require commercial rose varieties. AbH68075-AbH68674 represent the PCR primers used to amplify the Rose microsatellite regions described in the method
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flavouring agent; sweetener; nutritional supplement; pharmaceutical; L-2-aminobutyrate; ilvA gene; PCR primer; ss.
coli and the cells tested against a high-density array of synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparation of amino acid - which does not react with transaminase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transaminase; enzyme; pyruvate; acetolactate synthase; keto acid;
                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                          Score 14.6; DB 12; Length 24; Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                    Sequence 24 BP; 10 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli K12 ilvA gene fragment generating primer.
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       9 AGGTAGGCAGACTTGTCAGCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AGGTAGGCAGAGTGACAGAC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 20; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00858111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US010169
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX05623 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-070156/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MONS ) MONSANTO CO
                                                                                                                                                                                                                                            the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fotheringham IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9853088-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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The present invention describes a nucleic acid composition (I) for the expression of a functional member of the ATP-binding cassette (ABCA) subfamily of ABC transporters in a host cell comprises two or more different nucleic acid molecules, each of which encodes one or more different nucleic acid molecules, each of which encodes one or more compensation of an ABC transporter, where the domains are functionally comprising of an ABC transporter of the ABCA subfamily of ABC transporters in a host cell; (3) a system for expressing a functional member of the ABCA subfamily of ABC transporters in a host cell comprising to comprising to a method of treating a mammal in need of functional member of the ABCA subfamily of ABC transporters; (6) a pharmaceutical composition of system; (5) a method of transporters; (6) a pharmaceutical composition of the ABCA subfamily of ABC transporters in a host cell. The nucleic acid composition (I) can be used for the expression of a functional member of the ABCA subfamily of ABC transporters in a host cell, which is useful in treating a mammal in need of functional member of the ABCA subfamily of ABC transporters in a host cell, which is useful in treating a mammal in need of functional member of the ABCA subfamily of ABC transporters in a host cell, which is useful in treating a mammal in need of functional member of the ABCA subfamily of ABC transporters. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid composition for expression of a functional member of the ATP-binding cassette (ABCA) subfamily of ABC transporters in a host celluseful in treating a mammal in need of the member of the ABCA subfamily
                                                                                                                                   Gaps
construction of an expression vector pIF347 comprising the ilvA gene encoding threonine deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                               subfamily; ABCA subfamily; ABC transporter;
                                                                                                                       . 0
                                                                                             Length 31;
                                                                                                                                 Indels
                                                     G; 5 T; 0 U; 0 Other;
                                                                                         48.7%; Score 14.6; DB 2;
69.0%; Pred. No. 1.2e+04;
iive 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                       Human ABCA1 C-half PCR primer SEQ ID NO:13.
                                                                                                                                                                       29
                                                                                                                                                                                                             30
                                                                                                                                                                       1 GCGGATCCAGGTAGGCAGACTTGTCAGCC
                                                                                                                                                                                                             GCGGATCCATCGCTGACTCGCAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 13; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ahn J, Hauswirth WS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2002; 2002CA-02385110.
27-JUN-2002; 2002US-0391644P.
                                                       Sequence 31 BP; 6 A; 13 C; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2003; 2003WO-CA000633
                                                                                                                                                                                                                                                                                                         ADE94330 standard; DNA; 44
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                               Local Similarity 69.0
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cassette su
human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of ABC transporters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-903674/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003093468-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molday RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
                                                                                                                                                                                                                                                                                                                                               ADE94330;
                                                                                           Query Match
                                                                                                                                   Matches
                                                                                                                                                                                                                                                                   RESULT 28
                                                                                                                                                                                                                                                                                         ADE94330
ន្តដូន
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library.

Compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises comparises of at least one target sequence. The method of analysis comprises more compounds. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence or specific contactions of any gene, in mapping the 5' termin of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones contacting sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence contacting format directly from LSPTO at seedles uncapproce or pecific contacting the microarray. Note: The sequence or specific contact the sequence or specific contact the microarray. Note: The sequence or specific contact the seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
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                                           48.7%; Score 14.6; DB 10; Length 44; 81.0%; Pred. No. 1.2e+04;
                                                                                              4; Indels
Sequence 44 BP; 13 A; 10 C; 15 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human microarray DNA oligonucleotide SEQ ID NO 3116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 4 A; 8 C; 8 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for this patent can also be obtained in USPTO at segdata.uspto.goc/seguence.html
                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 3116; 9pp; English
                                                                                                                                            3 GGATCCAGGTAGGCAGACTTG 23
                                                                                                                                                                          24 GAATCCAGAGAGACAGACTTG 44
                                                                                                                                                                                                                                                                                                                       ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                                                                    ACI03125 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                              17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-567953/53.
                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003104410-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     13-OCT-2003
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                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conveying resistance to beet necrotic yellow vein virus (BNYVV) to sugar beet (Beta vulgaris) comprises introducing a DNA fragment having a nucleotide sequence which is homologous to the sequence of the genomic RNA 1 of BNYVV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beet necrotic yellow vein virus (BNYVV) causes rhizomania disease in sugar beet plants. The present sequence is a PCR primer for BNYVV. The resulting PCR fragment was cloned and used to convey resistance to BNYVV to a sugar beet plant, to result in production of a transgenic BVYVV-resistant sugar beet plant
                                                                                                                                                                                                                                                           BNYVV-resistance; rhizomania; sugar beet; transgenic plant; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                            Gaps
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  Length 25;
                            Indels

    untranslated region sequence of a viral genome.

Query Match
48.0%; Score 14.4; DB 9;
Best Local Similarity 93.8%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 BP; 5 A; 9 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Dun CMP;
                                                                                                                                                                                                                                Beet necrotic yellow vein virus PCR primer Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guilley H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 12; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCGGATCCAGGTAGGCAGACTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deddarceaedadarredr
                                                                                                                                                                                                                                                                                                  Beet necrotic yellow vein virus.
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                                                                                                                                                                                                                                                                                                                                                                                                          99EP-00200236
                                                      2 CGGATCCAGGTAGGCA 17
                                                                               2
                                                                                                                                                 AAA74492 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX60078 standard; RNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                     01-DEC-2000 (first entry)
                                                                               cedacccaeeraeeca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jonard G,
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SESE-) SES EURO NV SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-505981/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                             WO200044915-A1
                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1999;
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04-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richards K,
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                                                                               20
                                                                                                                                                                            AAA74492;
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                                                                                                                        RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 31
                                                                                                                                      AAA74492
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Gaps

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Length 33; 6; Indels

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The invention relates to nucleic acid molecules that modulate replication treating a condition related to WNV infection e.g. pancreatitis, encating a condition related to WNV infection e.g. pancreatitis, encaphalitis, myocarditis, meningitis, neurologic infection, hepatitis, molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least the 2'-O-methyl modifications, phosphorothicate linkages on at least three of the 5' terminal nucleocides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
                                            The specification describes a method for producing a protein in a eukaryotic cell, from an uncapped mRNA using sequences derived from the barley yellow dwarf virus PAV serotype (BYDV-PAV). The sequences are useful for increasing the production of a protein translated from an uncapped eukaryotic mRNA. Ax60064-74 represent 3 untranslated regions of viral genomes, and were used in the course of the invention. (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; viruoids; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; encephalitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
                                                                                                                                                                           Sequence 33 BP; 9 A; 7 C; 13 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                       Score 14.4; DB 2;
Pred. No. 1.4e+04;
3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 24; SEQ ID NO 17179; 495pp; English.
                                                                                                                                               on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                          2 CGGATCCAGGTAGGCAGACTTGTC 25
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                Example 5; Fig 4; 49pp; English.
                                                                                                                                                                                                           48.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-OCT-2001; 2001WO-US048350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNV Inozyme SEQ ID NO 17179.
                                                                                                                                                                                                                                                                                                                                                                                        ACN17176 standard; RNA; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-2004 (first entry)
                                                                                                                                                                                                           Query Match
Best Local Similarity 62.5
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcswiggen JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amberzyme; Zinzyme; ss
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MCSWIGGEN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-706994/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                West Nile Virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                       ACN17176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RIBO-)
                                                                                                                                                                                                                                                                                                                                                        RESULT 33
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                                                                                                                                                                                                                                                                                                                                                                  The specification describes a method for producing a protein in a everaryotic cell, from an uncapped mRNA using sequences derived from the barley yellow dwarf virus PAV serotype (BYDV-PAV). The sequences are useful for increasing the production of a protein translated from an uncapped eukaryotic mRNA AXK60075-85 represent 3' untranslated regions of viral genomes, and were used in the course of the invention. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 48.0%; Score 14.4; DB 2; Length 31; Local Similarity 62.5%; Pred. No. 1.4e+04; les 15; Conservative 3; Mismatches 6; Indels
 Protein production; eukaryotic cell; uncapped mRNA;
barley yellow dwarf virus PAV serotype; BYDV-PAV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein production; eukaryotic cell; uncapped mRNA; barley yellow dwarf virus PAV serotype; BYDV-PAV; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31 BP; 9 A; 7 C; 11 G; 0 T; 4 U; 0 Other;

    untranslated region sequence of a viral genome.

                                                                                                                                                                                                         (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CGGATCCAGGTAGGCAGACTTGTC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cap-independent in eukaryotic cells.
                                            unidentified tobacco necrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unidentified tobacco necrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cap-independent in eukaryotic cells.
                                                                                                                                                                                                                                                                                                                                    Example 19; Fig 13; 49pp; English.
                                                                                                                                          97US-00858623
                                                                                                                                                                           96US-0017199P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-00858623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0017199P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX60067 standard; RNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                      WPI; 1999-356844/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-356844/30.
                                                                                                                                                                                                                                       Miller WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miller WA;
                                                                                                                                          20-MAY-1997;
                                                                                                                                                                         20-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-1996;
                                                                            US5910628-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5910628-A.
                                                                                                          08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX60067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                        Wang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX60067
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us-10-788-779-2.rng

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Preparing a synthetic nucleic acid molecule with reduced inappropriate transcriptional characteristics when expressed in a cell, for e.g making fusion proteins, by altering a wild type or another synthetic nucleic
                                                                                           Luciferase, synthetic nucleic acid, transcriptional characteristic, transcription; codon usage, PCR, primer; ss.
                                                                 Synthetic Renilla luciferase preparation oligo SEQ ID NO:277.
                                                                                                                                                                                                                          24-AUG-2001; 2001WO-US026566.
                                                                                                                                                                                                                                                    24-AUG-2000; 2000US-00645706
                                       27-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                             (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                WPI; 2002-304140/34
                                                                                                                                                                                                                                                                                                     KV, Wood MG,
                                                                                                                                                                       WO200216944-A2.
                                                                                                                                                                                                                                                                                                                                                                                               acid sequence.
                                                                                         Luciferase;
                                                                                                                                                                                                 28-FEB-2002
                                                                                                                                  Renilla sp.
Synthetic.
                ABL99294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT38282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                               Renilla
                                                                                                                                                                                                                                                                                                      Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT38282,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a human BRCA1 interacting protein, designated B112. BRCA1 is a tumour suppressor protein. Methods and compositions from the present invention are useful for diagnosis of, determining predisposition to or lack of predisposition to, and treatment of human cancer, such as breast or pancreatic cancer, as a result of a nutation in C1IP or BRCA1. The methods and compositions can also be used in rational drug design for cancer therapeutics. The present sequence represents a PCR primer for B112 which is used in an example from the
                                                                                                                                                                                                                                                                                                                              interacting protein; B112; CtIP; tumour suppressor; cancer;
 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid
                                                                                                       Gaps
                                                                                                       ;
                                                                                                                                                                                                                                                                                                    Human BRCA1 interacting protein gene B112 PCR primer B112.2T
                                                                          48.0%; Score 14.4; DB 6; Length 38; 60.0%; Pred. No. 1.5e+04; live 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.0%; Score 14.4; DB 2; Length 40; ilarity 75.0%; Pred. No. 1.5e+04; Conservative 0; Mismatches 6; Indels
                                                   Sequence 38 BP; 8 A; 12 C; 11 G; 0 T; 6 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40 BP; 15 A; 10 C; 7 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tavtigian SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A carboxy-terminal BRCA1 interacting protein.
                                                                                                                               4 GATCCAGGTAGGCAGACTTGTCAGC 28
                                                                                                                                              Example 4; Page 42; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHF,
                                                                                                                                                                                                                        AAX76467 standard; DNA; 40 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US024831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                          (first entry)
             in the specification. The molecule of the invention
                                                                                                     15; Conservative
                                                                                                                                                                                                                                                                                                                                           primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bartel PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-357827/30.
                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
Les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention
                                                                                                                                                                                                                                                                                                                              Human; BRCA1
therapy; PCR
                                                                                                                                                                                                                                                                           05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                        WO9927075-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wong AKC,
                                                                                                                                                                                                                                                 AAX76467;
                                                                            Query Match
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                                                                                                     Matches
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Paguio A;

Zhuang Y,

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                                        The present invention relates to the preparation of synthetic nucleic acid molecules which have altered transcriptional regulatory sequences compared to the wild-type. These sequences are then transcribed with less frequency compared to the wild-type. In particular, the invention relates to altered luciferase sequences. This can be used to detect wask promoter activity, to express fusion proteins, to detect and/or measure levels of gene expression, subcellular localisation or targeting, in life science research, agrogenetics, gene therapy, developmental science and pharmaceutical development. The present sequence is an oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T helper cell; TH cell; T-cell; T-lymphocyte; 103 gene; differential expression; immune disorder; multiple sclerosis; asthma; lepromatous leprosy; diagnosis; therapy; primer; PCR; polymerase chain reaction; transgenic mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine 103 gene 3' primer for construction of transgenic clone
                                                                                                                                                                                                                                                                                                                                                                                    48.0%; Score 14.4; DB 6; Length 40; 93.8%; Pred. No. 1.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1.; Indels
                                                                                                                                                                                                                                                                                                                                    Sequence 40 BP; 7 A; 14 C; 10 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
Example 1; Fig 10; 294pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GGATCCAGGTAGGCAG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 GGCTCCAGGTAGGCAG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT38282 standard; DNA; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 15; Conserv
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Gaps

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Matches

ABL99294 ID ABL99294 standard; DNA; 40 BP.

RESULT 35

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Genes which are differentially expressed within and among T helper (TH) cells and TH cell subpopulations, e.g. THO, TH1 and TH2 subpopulations, can be used diagnostically or as targets for therapeutic intervention. The polypeptides are useful for treating and diagnoshing of immune disorders, especially T lymphocyte-related disorders. These disorders include chronic inflammatory diseases and disorders (e.g. Crohn's disease, reactive arthritis, Lymme disease, Hashimoto's thyroidit's or Grave's disease), or atopic conditions (e.g. asthma and allergy, including allergic rhintis or food allergies). Also included are certain bathogen susceptibilities (e.g. leishmaniasis), and viral (e.g. HUV) or bacterial (e.g. tuberculosis or lepromatous leprosy) infections
                                            New isolated human 200 gene products or polypeptides, useful for treating and diagnosing immune disorders, especially T helper lymphocyte-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 gene, immune disorder, T helper lymphocyte 2 related disorder; TH2; ST2; T1; Fit-1; therapy, asthma; allergy, IgB; IL-4; antiviral; fimunoglobulin E mediated condition; interleukin-4 mediated condition; crohn's disease; arthitis; insulin-dependent diabetes; antihelminthic; multiple sclerosis; Hashimoto's thyroiditis; Grave's disease; contact dermatitis; psotiasis; allergic rhinitis; conjunctivitis; glomerular nephritis; systemic lupus erythematosus; eosinophilia; neuroprotective; ophthalmological; antibacterial; immunosuppressive; sarcoidosis; scleroderma; murine; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New 103 gene products and immunospecific antibodies, useful for the diagnosis and treatment of T helper lymphocyte 2 (like) related immune disorders e.g. asthma, allergy, immunoglobulin E and interleukin-4 mediated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.0%; Score 14.4; DB 3; Length 44; 75.0%; Pred. No. 1.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3' primer, to amplify long form of murine 103 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 TCCAGGTAGGCAGACTTGTCAGCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 recadererecadacrirecarce 17
                                                                                                                                            Example; Col 91; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD03383 standard; DNA; 44 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-1999; 99US-0155862P.
28-APR-2000; 2000US-00560639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-2000; 2000WO-US026555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 75.0 tes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leiby KR, Kingsbury GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-211462/21.
  WPI; 2000-464385/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2001.
                                                                                               disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD03383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fatches
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AAD03383/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A 5' primer (AAT38281) and 3' primer (AAT38282) contg. 5' Spel and 3' bamHI sites were used to amplify the murine 103 gene (see also AAT38272) that is differentially expressed in T helper TH2 cells. Murine TH2-type cell line D1064 cDNA was used as template. The PCR product was used to replace the IL-10 gene in plasmid pCIL-10. The final construct, pCD2-1031-GH, contained the human CD2 enhancer and Pmu promoter and the murine 103 gene coding sequence. It was used to produce transgenic mice that expressed the 103 gene product (see also AAT38283-84). Such mice can be used as models of TH2 cell subpopulation-related disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thelper cell; differential expression; 200 gene; immunomodulator; anti-inflammatory; anti-arthritic; antibacterial; immunosuppressive; thyromimetic; anti-thyroid; anti-asthmatic; anti-allergic; antiviral; protozoacide; lymphocyte; modulator; gene therapy; primer; ss.
                                                                                                                                                                                                                                                                                                                                                   Genes and their products differentially expressed in T helper cells useful in diagnosis and treatment of immune disorders, e.g. multiple sclerosis, asthma, lepromatous leprosy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reverse primer to construct a murine 103 gene transgenic clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.0%; Score 14.4; DB 2; Length 44; 75.0%; Pred. No. 1.5e+04; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 11, Page 167; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 TCCAGGTAGGCAGACTTGTCAGCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA51915 standard; DNA; 44 BP
                                                                                                                                         95US-00398633,
95US-00487748,
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                                                                                             96WO-US002798
                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00829525
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96US-00609583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 75.0
nes 18; Conservative
                                                                                                                                                                                                                                                                                                            WPI; 1996-433404/43
WO9627603-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAR-1995;
07-JUN-1995;
                                                                                           01-MAR-1996;
                                                                                                                                         03-MAR-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                             Levinson DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6084083-A.
                                              12-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA51915;
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The present invention describes a method for ameliorating a symptom of ischaemic disorder or injury in a mammal. The method comprises administering a 200 gene product, a nucleic acid encoding (S1) or an antibody directed against (S1). The method is useful for treating a symptom of an ischaemic disorder such as ischaemic renal disease or myocardial ischaemia (such as angina pectoris), myocardial or cortical infarction. The method is also useful for treating a symptom of an ischaemic injury occurring due to transplantation of a kidney. The present sequence represents a PCR primer which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cysteine protease; immune disorder; T lymphocyte; Crohn's; arthritis; diabetes; multiple sclerosis; viral infection; bacterial; HIV; ds.
                                                                                                                                                                                                                                                                                                   48.0%; Score 14.4; DB 4; Length 44; 75.0%; Pred. No. 1.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3' oligonucleotide used in construction of 103 gene clone.
                                                                                                                                                                                                                                                        Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                           exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                            6 TCCAGGTAGGCAGACTTGTCAGCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                           40 TGCAGGTGTGCAGACTTGGGATCC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00398633.
95US-00487748.
96US-00609583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF23475 standard; DNA; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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07-JUN-1995;
01-MAR-1996;
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       8866666666666888
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                                                             diagnosis of immune disorders, especially T lymphocyte-related disorders.

The methods and compositions of the present invention particularly
relates to detection and/or modulation of expression and/or activity of
103 gene. This gene is alternatively referred as ST2, T1 and Fit-1 and is
differentially expressed in T helper lymphocyte 2 (TH2) cells Antibodies
gpecific for 103 gene are useful for the treatment and prevention of
immune disorders in humans, preferrably TH2 related disorders, such as
asthma, allergy, immunoglobulin E (IgE) mediated conditions and
interleukin-4 (IL-4) mediated conditions. Modulators of 103 gene such as
antibodies, ribozymes, antisense oligomucleotides and peptides are useful
for the treatment and diagnosis of immune disorders such as Crohn's
disease, archritis, insulin-dependent diabetes, multiple sclerosis,
Hashimoto's thyroidiis, Grave's disease, graft rejection, contact
dermatitis, psoriasis, allergic rhintis, conjunctivitis, graft- versus-
host disease, glomerular nephritis, sarcoidosis, eosinophilia, systemic
lupus erythematosus, scleroderma and helminthic (e.g leishmaniasis),
viral and bacterial infections (e.g. tuberculosis and lepromatous
mirria 101 genesont sequence is 3' primer used to amplify long form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment, diagnosis, immune disorder; mast cell related disorder, T-helper lymphocyte-related disorder; ischaemic disorder; identification, sasodilator; cardiant; antianginal, angina pectoris, ischaemic renal disease; myocardial ischaemic senal disease; myocardial ischaemic cenal disease; myocardial ischaemic infarction; schaemic injury; kidney transplant; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                            methods and compositions for treatment and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.0%; Score 14.4; DB 4; Length 44; larity 75.0%; Pred. No. 1.5e+04; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse 103 gene PCR primer SEQ ID NO:34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 TCCAGGTAGGCAGACTTGTCAGCC 29
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  Example; Page 112; 197pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC92152 standard; DNA; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                            The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine 103 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 39
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AAC92152/

g

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The present invention relates to a novel cysteine protease. The protein of the invention is useful for treating and diagnosing immune disorders, especially Tlymphocyte-related disorders. In particular, the polypeptide is useful for treating or diagnosing Thelper (TH) cell or TH cell subpopulation-related disorders. These disorders include Crohn's disease, reactive arthritis, Lyme disease, insulin-dependent diabetes, organspecific autoimmunity, multiple sclerosis, Hashimoto's thyroiditis, Grave's disease, context dermatitis, psoriasis, graft rejection, graft versus host disease, sarcoidosis, atopic (e.g. asthma or allergy), eosinophilia, conjunctivitis, glomerular nephritis, or helminthic (e.g. leishmaniasis), viral (e.g. HU) (human immunodeficiancy virus) or bacterial (e.g. tuberculosis or lepromatous leprosy) infections
                                                                                                                                                                                                                                                                                                         polypeptide exhibiting cysteine protease activity, useful for
ing and diagnosing immune disorders, especially T lymphocyte-related
ders, e.g. Crohn's disease, multiple sclerosis, graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Col 93; 107pp; English.
(MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                            treating and diagnosi. disorders, e.g. Crohn disease or allergies.
                                                                                                                                                                                                                 WPI; 2001-101473/11.
                                                                                                                                                                                                                                                                                                                          Novel
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Ameliorating a symptom of an ischemic disorder or injury in a mammal e.g. ischemic renal disease or myocardial ischemia, by administering a 200 gene product (S1), a nucleic acid encoding (S1) or an antibody directed

Example 6; Page 190; 309pp; English

(81)

against

Mccarthy SA;

Levinson DA, Lloyd CM, WPI; 2001-016510/02.

31-MAY-2000; 2000WO-US014986

WO200073498-A1

07-DEC-2000

99US-00324986

02-JUN-1999;

(MILL-) MILLENNIUM PHARM INC.

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SQ Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
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0; Gaps Query Match 48.0%; Score 14.4; DB 4; Length 44; Best Local Similarity 75.0%; Pred. No. 1.5e+04; Matches 18; Conservative 0; Mismatches 6; Indels

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6 TCCAGGTAGGCAGACTTGTCAGGC 29

ò qq Search completed: November 18, 2005, 11:52:20 Job time : 209.578 secs

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SALK 1117 SALK 0164 0057a07.s qe29c04.s AU107828 AU107829

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AA932841 0057307 5 A1185949 qe29c04 s AU107828 AU107828 AU107829 AU107829 BZ586756 3590 1 20 AU260098 AU260058 AU52435 Drosophil B1080927 602878838 H40051 y144410.r1 BX948677 Arabidops AU102393 AU102393 AU10419 AU10419 AW507292 EST00720 BX893038 Arabidops AW507292 EST00720

Arabidops

Arabidops 1M0226106

Drosophil 602878838

OM nucleic

Run on:

Sequence:

Searched:

Database

Result Š.

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Bmail: info@genetrap.de
UJCEO gene trap. Sequence tag generated by 5'RACE. Additional
uJCEO gene trap. Sequence found at:
'http://genetrap.gsf.de/project/web_new/database/result clone.html?
'http://genetrap.gsf.de/project/web_new/database/result
clone_id=G050F11'ES cell line harboring insertion mutation of
target gene is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 16659
Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 45) 1 (bases 1 to 45) 4 Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P. A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Embryonic stem cell"
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/note="Vector: U3CEO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jun 30, 2004 this sequence version replaced gi:40729685
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    .45
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="129 Sv"

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/clone="G050F11"
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CR137702
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CC057135
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AA9135441
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AU107829
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Mus musculus
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A4836932 of36c11.8
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                                                                   November 18, 2005, 11:22:09; Search time 1434.98 Seconds (without alignments) 795.779 Million cell updates/sec
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Compugen Ltd.
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       GenCore version
Copyright (c) 1993 - 2005
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                                                 nucleic search, using sw model
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AI312023
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Gapop 10.0 , Gapext 1.0
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KEYWORDS

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REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

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AG264147 25-JUL-2003
Lotus corniculatus var. japonicus DNA, clone:LjT59109_sfi, genomic
                                                                                                                                                                                                                                                                         AJ428912 Hordeum vulgare subsp. vulgare primary leaf 7-day old seedling Hordeum vulgare subsp. vulgare cDNA clone CE8-3, mRNA
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Eckey,C., Korell,M. and Kogel,K.H.
Identification and characterisation of powdery mildew-induced genes
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Stragtota, Viridiplantae; Stregtotophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantaer, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="primary leaf"
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7-day old seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Eckey C Contact: Eckey C Contact: Eckey C IPAZ) Institute for Phytopathology and Applied Zoology (IPAZ) Justus-Liebig-University Giessen Heinrich-Buff-Ring 26-32, 35392 Giessen, Germany. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.3%; Score 14.8; DB 1; Length 39; 73.1%; Pred. No. 1.2e+05; ive 0; Mismatches 7; Indels
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/organism="Hordeum vulgare subsp. vulgare"
                                             Indels
                       71.4%; Pred. No. 8.2e+04; ive 0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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                                                                                               1 GCGGATCCAGGTAGGCAGACTTGTCAGC 28
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AG264147
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AJ428912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnarces/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E I (bases 1 to 45)
E I (bases 1 to 45)
S Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Tingey, A., von Diasmid inserts
D lunnamid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Urah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                    GSS 29-SEP-2000
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                                                                                                                                                                                                                                                                              AZ331000 45 bp DNA linear GSS 29-SEP-200
1M0056F24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus G57BL/6J (male) was obtained from the Jackson
                                                  Gaps
                                                  ö
Pred. No. 3.7e+04;
                                                                                                                                                                                                                                                                                                                                   clone UUGC1M0056F24 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                  0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0056F24"
/sex="Male"
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Location/Qualifiers
                                                                                                    2 CGGATCCAGGTAGGCAGACTTGTC 25
                                                                                                                                                  1 cegarcraegarescrercriere 24
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Mus musculus
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Plate: 0056 row: F c
                       79.2%;
                                                     19; Conservative
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Fax: 801 585 7177
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                       Best Local Similarity
Matches 19; Conserv
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84112, USA
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Gaps

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50.7%; Score 15.2; DB 8; Length 45;

Query Match

ORIGIN

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fragment (a) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. Es cell lines harboring insertion mutation of target
are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
                                                                                                                                                                                                                                                                                                                 /note=""PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 '(bases 1 to 46)
BayGenomics.
  MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-keeln.mpg.de/GABI-Kat/. Location/Qualifiers
                                                                                                                                              /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="columbia 0"
/db_xref="taxon:3702"
/clone="GK-688E05-023078"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/note="Vector: pGT0Lxf"
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Bay Area Functional Genomics Consortium (BayGenomics)
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69.0%; Pred. No. 1.5e+05;
ive 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.6; DB 9;
Pred. No. 1.4e+05;
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Location/Qualifiers
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="129 ola"
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                                                                                                                                                                                                                                                                                                ecotype="Col-0"
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Best Local Similarity
Matches 20; Conserv
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TITLE
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KEYWORDS
SOURCE
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CG784706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX662359 31 bp DNA linear GSS 05-APR-2004 Arabidopsis thaliana T-DNA flanking sequence GK-688E05-023078,
                 Direct Submission
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research; 2-6-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                          Kazüsa-kamatari, Kisarazu, Chiba 292-0818, Japan
(B-mail:sastoekazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,
Tel:81-418-52-3935(ex.3136), Fax:81-438-52-3934)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/strain="Miyakojima MG-20"
/variety="japonicus"
/db_xreef="taxon:34305"
/clone="LjT99109_8fi"
/clone_lib="genomic_TAC library"
/note="VBCTOR:pYLTAC7-synonym: Lotus japonicus"
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Weisshaar, B.

    .25
/organism="Lotus corniculatus var. japonicus"

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Rosso, M.G., Li, Y., Strizhov, N. and Weisshaar, B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.6; DB 9;
Pred. No. 1.4e+05;
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BX662359
BX662359.1 GI:37618781
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Best Local Similarity 81.0%;
Matches 17; Conservative
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AA996291

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 38)
S Salland,C., Gay.C., Larmande,P., Bes,M., Piffanelli,P., Piegu,B.,
Droc,G., Regad,F., Bourgeois,B., Meynard,D., Perin,C.,
Ghesquiere,A., Delseny,M., Glaszmann,J.C. and Guiderdoni,E.
High throughput T-DNA insertion mutagenesis in rice: A first step
towards in silico reverse genetics
Contact: Guiderdoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PCR was performed on DNA of primary transformants of Orysa sativa plants. The DNA fragment(s) resulting of Orysa sativa plants. The DNA fragment(s) resulting of determine the apequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding muctant line and a link to a database providing a graphical display is available from june 2004 at http://genoplante-info.infobiogen.fr/oryzatagline/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of36cll.sl NCI CGAP Kid6 Homo sapiens cDNA clone IMAGE:1423220 similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B ABARAGO," mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/cultivar="Nippone"
/db xref="traxon:39947"
/clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 33467615629
Fax: 33467615605
Email: emmanuel:guiderdoni@cirad.fr
Class: TDNA tagged.
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Best Local Similarity
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                                                                                                                                                                               AA996291 34 bp mRNA linear EST 27-AUG-1998 os19b04.sl NCI CGAP Kid5 Homo sapiens cDNA clone IMAGE:1605775 3' similar to WP:ZK863.6 CE15445 DPY-30: DPY-30 PROTEIN ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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/tissue_type="2 pooled tumors (clear cell type)"
/lab host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trace considered overall poor quality Insert Length: 757 Std Error: 0.00 Seq primer: -40m13 fwd. Er from Amersham High quality sequence stop: 1.
                                              1 GCGGAAGCCGGAGGCCATGGCGGCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                               AA996291.1 GI:3182780
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Homo sapiens
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Unpublished (1997)
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RESULT 8 CL522268/c LOCUS

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Length 50;

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A1312023 49 bp mRNA linear EST 03-FEB-1999 qp78b08.xl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1929111 3' similar to TR:Q60980 Q60980 BASIC KRUPPEL-LIKE
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1 (bases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This Clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1440 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                  /clone_11b="CAS11861"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.7%; Score 14; DB 1; Length 49; 77.3%; Pred. No. 2.7e+05; 2.1ve 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1929111"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                     48.0%; Score 14.4; DB 1; 93.8%; Pred. No. 1.8e+05; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
             /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                               Query Match
Best Local Similarity 93.8°
Matches 15; Conservative
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Best Local Similarity
Matches 17; Conserv
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp Ostoria.
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1199-156 (1997).
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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., 1sogal, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Pred. No. 1.8e+05;
                                                                                                                                                                                                                Trace considered overall poor quality
Insert Length: 589 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1423220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GATCCAGGTAGGCAGACTTGTCAG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 daaccredeadecadagerrrcae 10
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Location/Qualifiers
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Best Local Similarity 75.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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/organism="Homo sapiens"

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/organism="Trypanosoma brucei"
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/strain="TREU927"
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/clone="21h09"
                                                                                               genomic survey sequence
                                                                                                                                         AL454798.1 GI:11844296
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                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musns.
E 1 (bases 1 to 29)
S Dunn, D. Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R.,
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
C Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                              GSS 03-OCT-2000
                                         AZ441837 190234007F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0234007 F, genomic survey sequence.
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84112, USA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0234 row: O column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
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'mol_type="genomic DNA"
'strain="C57BL/63"
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High quality sequence stop: 29.
Location/Qualifiers
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clone="UUGC1M0234007"
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                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
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RESULT 12
AZ441837/c
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KEYWORDS
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The longest 1 (2011) Atkin, R., Chillingworth, C., Crmond, D., Harris, B., El-Sayed, N., Hou, L., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

Libract Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: Darrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Cofford University Press, 1999).
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602499583F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613012 5',
GSS 13-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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11 H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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TA21H09P 31 bp DNA linear GSS 13-D
T. brucei sheared genomic DNA clone 21h09, forward sequence,
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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Best Local Similarity 88.2
Matches 15; Conservative
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AZ303920/c
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                                                                                                                                                                                                                                                                                                                                                   /clone="Invariant properties" / clone="Invariant properties" / clone="Invariant properties" / lab_host="DH10B (TI phage-resistant)" |
/clone="Invariant properties" / clone the="Invariant properties" / clone | fall properties | f
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CELL_LINE&KEY=TEA007
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43)
BayGenomics.
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Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@bayGenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. Es cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov.f consortium/LLNL at: Plate: LLCM1362 row: f column: 21
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/clone_lib="BayGenomics Gene Trap Library pGTlLxf"
/note="Vector: pGTlLxf"
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46.0%; Score 13.8; DB 4; Length 40;
Best Local Similarity 72.0%; Pred. No. 3.2e+05;
Matches 18; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
/strain="129 ola"
                                                                                                                                           High quality sequence stop: 40.
Location/Qualifiers
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Unpublished (2001)
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GSS.
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46.0%; Score 13.8; DB 8; Length 43;

Query Match

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84112, USA
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Dunn, D., Aoyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid innerts

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
                                                                                                                                                                                   AZ303920

1M0003F19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0003F19 R, genomic survey sequence.
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                   Indels
88.2%; Pred. No. 3.2e+05; vative 0; Mismatches 2;
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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: F column: 19
Seq primer: CACAAGABAACAGCTAATGACC
Class: plasmid ends
High quality sequence stop: 32.
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/strain="C57BL/6J"
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/clone="UUGC1M0003F19"
                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
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                                                      6 TCCAGGTAGGCAGACTT
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AZ352257

MO090G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0090G11 R, genomic survey sequence.
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Ball: Shirokamedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitcomo.Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                             AU103363 Sugano Homo sapiens CDNA library Homo sapiens CDNA library Homo sapiens CDNA clone
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 33)
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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of manA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
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0; Mismatches
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                                           Score 13.6; DB 9;
Pred. No. 3.9e+05;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
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80.0%;
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                                             Query Match 45.3
Best Local Similarity 67.9
Matches 19; Conservative
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/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone are described in References 1-3. The sequences are generated at the Protocools used for generation of the sequence are described in References 1-3. The sequences are generated at the project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                         AL953049 43 bp DNA linear GSS 02-APR-2004 Arabidopsis thaliana T-DNA flanking sequence GK-348B03-016247,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis
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| clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                           4; Indels
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Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
Direct Submission
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/mol_type="genomic DNA"
/strain="Columbia 0"
80.0%; Pred. No. 3.7e+05;
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22755829
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Arabidopsis thaliana
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                                                                      3 GGATCCAGGTAGGCAGACTT 22
                                                                                                                    30 GGACCCAGGTGAGAGACTT 11
                                                                                                                                                                                                                                                                                                genomic survey sequence.
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                           16; Conservative
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UNCEO gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone id=G061A09' ES cell line harboring insertion mutation of target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.html' Inhouse Sequence Identifier: 18060
Class: Gene Trap.
Location/Qualifiers
  Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P. A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
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1006017F11.y1 1006 - RescueMu Grid G Zea mays genomic, genomic
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/cell_line="ES cells [C57BL/6J x 12986/SvEvTac] Fl"
/clone lin="GGTC Gene Trap Library GV07C05"
/note="Vector: U3CEO"
                                                                                                                                                         On Jun 30, 2004 this sequence version replaced gi:42743355.
Contact: GGTC
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/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
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Stanford University
BSS California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: Walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

44.7%; Score 13.4; DB 9;
Best Local Similarity 65.4%; Pred. No. 4.7e+05;
Matches 17; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                       German Genetrap Consortium (GGTC)
Email: info@genetrap.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 ATCCAGGTAGGCAGACTTGTCAGCCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 Arccaggargrcaganngnrgaggcr 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="129 Sv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="G061A09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: transposon-tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ920008.1 GI:13390291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
                                                                                                                                          12904583
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AZ920008/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
// Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
// Clone lib="Mouse 10kb plasmid UUGCIM library
// Clone lib="Wouse 10kb plasmid UUGCIM library
// Inde="Wector: PWD4Zuv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4772114|gb|AR129072.1); a copy-number.
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                  Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CL302526

39 bp mRNA linear GSS 30-JUN-2004 G061A09 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone G061A09, mRNA sequence.
CL302526
CL302526.2 GI:49489458
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 39)
                      Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mose whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.7%; Score 13.4; DB 8; Length 33; 73.9%; Pred. No. 4.6e+05; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Exror: 0.00
Plate: 0090 row: G column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="UUGC1M0090G11"
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                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Conservative
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Matches 17; Conserv
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us-10-788-779-2.rst

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Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Oryctolagus cuniculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 48)
Zhang, B., Wang, Z. and Zhu, P.
Cloning and identification of injury-related gene(s) in the process of fetal rabbit skin healing
Unpublished (2002)
                                                                                                                                                                                                                                                                                68 bp mRNA linear EST 18-SEP-2002 Oryctolagus cuniculus adult subtractive hybridization library BU582005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU104377 50 bp mRNA linear EST 28-JAN-2004 AU104377 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP21718, mRNA sequence.
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: PUCm-T; inserts-subtractive hybridization
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
                                                                                         Gaps
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/dev stage="adult"
/lab_host="E.coli HB101"
/clone llb="Oryctolagus cuniculus adult subtractive
hybridIzation library"
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0
                                          Length 45;
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Changliangzhilu 10, Chongqing, P.R.China., 400042
Tel: 86-23-68757444
Fax: 86-23-68819750
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                                                                                         Indels
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Pred. No. 5.8e+05;
0; Mismatches 8;
                                          Score 13.2; DB 8;
Pred. No. 5.8e+05;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: john power1201@hotmail.com.
Location/Qualifiers
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                                                                                                                                        5 ATCCAGGTAGGCAGACTTGTCAGCCT 30
                                                                                                                                                                     1 AACAATGTAGGCAGAATTTGAATCCT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9986"
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                                            44.0%;
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Best Local Similarity 69.2
Matches 18; Conservative
                                                                                         18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Zhang Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department 4
                                     Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU104377
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BU582005/c
LOCUS
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AUTHORS
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AU104377
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                                                                                         pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BZ764481
SALK 124922.26.85.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_124922.26.85.x, genomic survey sequence.
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/clone="SALK 124922.26.85.x"
/clone="salk 124922.26.85.x"
/clone="lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

| (bases 1 to 45)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                /clone lib="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         벙
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Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Nor. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Matches 17; Conserv
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 36)

Humphray, S. J., Huckle, E. and Hunt, S. E.

Birect Submission

Direct Submission

Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinton, Cambridgeshire, CB10 1SA, UK. E-mail contact: hunguery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 43H15. 43H15 is part of the Danlokey BAC Library created by R. Plasterk and N.V.
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                                                                                                                                                                                                                                                 CR127702

Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP408a08, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J., and Bradley, A.
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
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             Length 50;
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         Score 13.2; DB 1; 1
Pred. No. 5.9e+05;
0; Mismatches 8;
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69.2%; Pred. No. 5.9e+05;
iive 0; Mismatches 8;
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GSS; genome survey sequence; MICER.

    .50
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Mus musculus
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         44.0%;
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Matches 18; Conserv
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                                                                                                                                                                       Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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AU107676
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Institute of Medical Science, University of Tokyo
A-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitono-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a S.-end-enriched cDNA library. Gene 200 (1-2),
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1 (Dass 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Bata,H., Ota,T., Isogal,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
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                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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/clone="HBP21286"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

44.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 5.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels
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/organism="Homo sapiens"
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                                                                  mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Location/Qualifiers
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/clone="SALK O16405.53.70.x"
/clone="SALK Analytication of the process of the pro
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                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
SALK 016405.53.70.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_016405.53.70.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is single pass sequence recovered from the left border TDNA. This sequence lies within 300 bases of the 5' end of Atlg10190. Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Pax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Arabidopsis thaliana"
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/ecotype="Col-0"
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                                                                                                                                 BH857661.1 GI:21708482
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                                                                                                                                                                                                                                    Arabidopsis thaliana
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Unpublished (1997)
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                                                                    survey sequence.
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Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 6379
Email: ecker@salk.edu
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/clone="SALK 111730.14.10.n"
/clone="Parabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana lines
/clone lib="PcR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used car
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g48010.
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larity 76.2%; Pred. No. 6.9e+05;
Conservative 0; Mismatches 5; Indels
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/mol type="genomic DNA"
/ecotype="Col-0"
                                                                                                                                                                   Score 13; DB 9; I
Pred. No. 6.8e+05;
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/clone="DKEY-43H15"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
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hes 16; Conserv
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/organism="Homo sapiens"
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CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 bp mRNA linear EST 29-OCT-1998 ge29c04.s1 Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:1740390 3' Similar to SW:RL2B_HUMAN P29316 60S RIBOSOWAL PROTERN L23A.;, mRNA sequence.
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NCI-CRAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 360 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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43.3%; Score 13; DB 1; Length 46;
Best Local Similarity 76.2%; Pred. No. 7.1e+05;
Matches 16; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                  Trace considered overall poor quality Insert Length: 1206 Std Brror: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
Email: cgapbs-r@mail.nih.gov
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AI185949.1 GI:3736587
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Homo sapiens
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Unpublished (1997)
                                                                                                                                                                                                                                                                                 . source
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AI185949/c
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DEFINITION
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Bacil: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzukieims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Onkagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AULO/1828 50 bp mRNA linear EST 28-JAN-2004 AULO/1828 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAE00112, mRNA sequence.
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Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
43.3%; Score 13; DB 1; Length 49;
Best Local Similarity 76.2%; Pred. No. 7.1e+05;
Matches 16; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.3%; Score 13; DB 1; Length 50; 76.2%; Pred. No. 7.1e+05; ive 0; Mismatches 5; Indels
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/moi type="genomic DNA"
/wol type="aminays"
/wol type="aminays"
/wol type="aminays"
/wol type="leaf"
/tissue_type="leaf"
/tissue_type="leaf"
/dev_stage="adult"
/lab host="whitos"
/lab host="whitos"
/clone_lib="3590 - RescueMu Grid M"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: BglII;
RescueMu is a 4: 9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units: For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
rescueMu. Grid M was grown at University of Arizona in
2001. DNA was extracted from leaf punches, double digested
using BamHI and BglII, and ligated to form circular
plasmids. DH108 cells were transformed and then screened
on LB plates with ampicillin."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
E 1 (bases 1 to 27)
S Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain
L Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ביה באים באקר 27 bp mRNA linear EST 25-APR-2002 AU260098 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0016170 3', mRNA sequence.
               Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 3590_1_20_1 column: 7 Class: transposon-tagged.
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/clone_lib="3'-directed mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.3%; Score 13; DB 8; Length 50; 76.2%; Pred. No. 7.1e+05; Live 0; Mismatches 5; Indels
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URL:http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
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/db_xref="taxon:10090"
                                                                                                                                                                'organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="BED0016170"
                                                                                                                     Location/Qualifiers
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walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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Best Local Similarity
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 bp DNA linear GSS 17-DEC-2002 3590 1 20 1 GOB.2EL_Y_1 3590 - RescueMu Grid M Zea mays genomic, genomic survey sequence.
                                                                   50 bp mRNA linear EST 28-JAN-2004
AU107829 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZRV61043, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Virology Institute of Medical Science, University of Tokyo for Medical Science, University of Tokyo Medical Science, University of Tokyo Bazuki, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitcomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2),
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Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
Zea mays
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.3%; Score 13; DB 1; Length 50; 76.2%; Pred. No. 7.18+05; rive 0; Mismatches 5; Indels
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/db_xref="taxon:9606"
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Location/Qualifiers
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BZ586756.1 GI:27221817
                                                                                                                                                                                            AU107829.1 GI:13557351
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. B 1 (bases 1 to 37)
S NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
L Unpublished (1999)
C Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://inage.linl.gov
Plate: LiAM11058 row: k column: 10
High quality sequence stop: 37.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 bp mRNA linear EST 31-JUL-1995 y144d10.rl Soares breast 3NDHBst Homo sapiens cDNA clone IMAGE:161107 5' similar to SP:S29539 S29539 BASIC PROTEIN, 23K - ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_trpe="lunor, biopsy sample"
/dev stage="5 months"
/dev stage="5 months"
/lab_host="DHIOB"
/clone_lib="NCI CGAP Mam2"
/note="Organ: mammary; Vector: pCNV-SPORT6; Site 1: Sall;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Loases I to 43)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Taryaskis, E., Materston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 42.7%; Score 12.8; DB 4; Length 3 I Similarity 70.8%; Pred. No. 8.3e+05; 17; Conservative 0; Mismatches 7; Indels

    .37
    /organism="Mus musculus"
/mol type="mRNA"
    /strain="FVB/N-3"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:5010561"
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High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TCCAGGTAGGCAGACTTGTCAGCC 29
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Insert Size: 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 recaderecredecarereage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Best Local Similarity
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                                                    AUTHORS
TITLE
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COMMENT
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JOURNAL
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H40051/c
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AUTHORS
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                                                                                                                                                                                                                                       AJ622435 28-JAN-2004 DNA linear GSS 28-JAN-2004 Drosophila melanogaster flanking sequence of RS P element insertion P{RS5}5-HA-2412, clone library P{RS5}, genomic survey sequence.
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                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Russell, S. Mapping of RS P element insertions in Drosophila melanogaster for the Drosoel second generation deficiency kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (19-307-2004) Ryder B.J., Department of Genetics,
University Of Cambridge, Downing Street, CB23EH, UNITED KINGDOM
The insertion point of the P element is before base I of the
agequance. Further information about this P element insertion line
can be found at http://www.flyseq.org.uk and
http://www.drosdel.org.uk.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

    .28
/note="P element insertion in the 3' to 5' orientation"

                             Gaps
                                                                                                                                                                                                                                                                                                                                                          GSS; genome survey sequence.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Sukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ryder, B.J., Ashburner, M., Bagunya, J., Blows, F., Bucheton, A., Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N., Hafen, B., Hall, S., Helsenberg, M., Lepesant, J. A., Maroy, P., Mechler, B., O'Kane, C., Pflugfelder, G., Rasmuson-Lestander, A. Reuter, G., Roote, J., Szidonya, J., Wang, S., Webster, J. and
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
|chromosome="žL"
                           7;
    Pred. No. 8e+05;
                           0; Mismatches
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/clone lib="P{RS5}"
                                                                        4 GATCCAGGTAGGCAGACTTGTCAG 27
                                                                                                                  1 darccaagaagaagccrrarrag 24
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Similarity 70.8%;
17; Conservative (
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BI080927
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Best Local Similarity
  Best Local Similarity
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BI080927/c
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AJ622435
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AUTHORS
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1902009.

Sily, Strizhov,N., Rosso,M.G. and Weisshaar,B.

Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.

Direct Submission

Submitted (11-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion within the locus defined by BAC clone

T20F20. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-keln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        finites (T1) which were transformed with the T-DNA from plants (T1) which were transformed with the T-DNA from vector pAcific (GenBank accession number: 4M537514). The lines contain one or T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 bp mRNA linear EST 28-JAN-2004 AU102393 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone COLF942, mRNA sequence.
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Barai: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Ysbhitokno-Vakkagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.

1 (Dasea I to SO)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3702"
/clone="GK-792A06-025017"
/clone lib="Arabidopsis thaliana T-DNA insertion lines"
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Pred. No. 8.7e+05;
0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Arabidopsis thaliana"
     BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic_DNA"
/strain="Columbia 0"
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hes 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                     Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX948677 49 bp DNA linear GSS 05-APR-2004 Arabidopsis thaliana T-DNA flanking sequence GK-792A06-025017,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infCominage.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Insert Length: 910 Std Error: 0.00 Seg primer: M13Rev High quality sequence stop: 1.
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High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
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Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
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Pred. No. 8.5e+05;
0; Mismatches 2;
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Arabidopsis thaliana
                                                                                                                                                                                                                      /organism="Homo sapiens"
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clone="IMAGE:161107"
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BX948677
BX948677.1 GI:42598363
                                                                                                                                                                                                                                                                                                                                                /sex="Female"
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Best Local Similarity 87.5%;
Matches 14; Conservative (
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TITLE
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/organism="Homo sapiens"
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Search completed: November 18, 2005, 21:12:37 Job time : 1437.98 secs

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                                                                       November 18, 2005, 00:26:13 ; Search time 58.289 Seconds (without alignments) 842.154 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-213-993-14

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US-09-448-310-26

US-09-884-948-26

US-09-884-948-25

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US-09-983-121-10

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US-09-31-10-27

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US-09-396-196G-18196
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US-08-858-623A-8
US-08-975-703-28
US-09-515-884-28
US-08-829-525-34
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1 GCGGATCCAGGTAGGCAGACTTGTCAGCCT 30
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                                                                                                                                                                                                                  1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
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Match Length
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4 Sequence 34, Appl Sequence 10.784, Sequence 10.784, Sequence 42, Appl Sequence 42, Appl Sequence 757, Appl Sequence 757, Appl Sequence 757, Appl Sequence 526, Appl Sequence 526, Appl Sequence 526, Appl Sequence 536, Appl Sequence 536, Appl Sequence 536, Appl Sequence 536, Appl Sequence 5363, Appl Sequence 5363, Appl Sequence 6, Appl Sequ	ONS
3 US-08-609-583A-34 3 US-09-50-399-34 3 US-09-50-639-27 3 US-09-032-337-34 4 US-09-032-337-34 4 US-09-464-231-34 4 US-09-464-231-34 4 US-09-283-144-12 1 US-09-283-144-12 1 US-09-283-144-12 1 US-09-283-144-12 1 US-09-283-144-12 1 US-09-283-144-12 1 US-09-283-144-12 1 US-09-396-1966-1077-1078-108-108-1966-1966-1966-1966-1966-1966-1966-196	ALIGNMENTS US/07989160 CHRISTINE JOHN HUGH G, ANTHONY A METHOD FOR DETECTING 10 S: CCCKFIELD TREET, Suite 510 TABETH ANS CONPALIDE C-1993 5 ATION 33,505 MBER: GWL-111 ROBMATION: 27-7400 -5941 NO: 2: ILCS: IL
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44444444444444444444444444444444444444	RESULT 1 US-07-989-160-2 Sequence 2, Application Patent No. 5429923 PAPLICANT: SEIDMAN APPLICANT: SEIDMAN APPLICANT: SEIDMAN APPLICANT: ROSENZM TITLE OF INVENTION: TOOPHOTER: BOSTON STREET: GO STATE COUNTRY: U.S.A. COMPUTER: READABLE FOOTON STREET: GO STATE COMPUTER: END PC COMPUTER: INPO CO
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Length 30; Indels

Query Match 100.0%; Score 30; DB 1; I Best Local Similarity 100.0%; Pred. No. 0.00022; Matches 30; Conservative 0; Mismatches 0;

1 GCGGATCCAGGTAGCCAGACTTGTCAGCCT 30

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STRANDEDNESS: single
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US-08-244-548-14
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US-08-244-548-14
IS-08-244-548-14

Sequence 14, Application US/08244548

Patent No. 5874556

GENERAL INFORMATION:
APPLICANT: LUPTON, STEPHEN D.
TITLE OF INVENTION: OF TH-INDEPENDENT CYTOTOXIC T CELLS
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
CITY: Palo Alto
CITY: Palo Alto
CITY: Palo Alto
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COUNTRY: USA

ZIP:

STATE:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentin Release #1.0, Version #1.30

CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/08/244,548

FILING DATE: 06-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INTORMATION:

NAME: DYLAN, TYLER M.

REGISTRATION INDERER: 37,612

REGISTRATION INDERER: 37,612

REGISTRATION INDERER: 37,612

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 494-0792
                                                                             US-01-12

Sequence 80578, Application US/09396196G

Sequence 80578, Application US/09396196G

FARTERL No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFRENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR PILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOSTWARE: FASESQ for Windows Version 4.0
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79.2%; Pred. No. 5.4e+02;
iive 0; Mismatches 5;
1 GCGGATCCAGGTAGGCAGACTTGTCAGCCT 30
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
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Best Local Similarity 79.2
Matches 19, Conservative
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ORGANISM: mus musculus
US-09-396-196G-80578
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LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LUPTON, STEPHEN D.
ALLEN, JAMES M.
Feldhaus, Andrew L.
TITLE OF INVENTION: PYERID GENES FOR USE IN THE PRODUCTION
OF TH-INDEPENDENT CYTOTOXIC T CELLS
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Query Match 52.0%; Score 15.6; DB 2; Length 41; Best Local Similarity 81.8%; Pred. No. 9.1e+02; Matches 18; Conservative 0; Mismatches 4; Indels
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PPC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 16-Feb-1998

CLASSIFICATION NUMBER: US/09/213,993

FILING DATE: 6-JUN-1994

APPLICATION NUMBER: US 08/244,548

FILING DATE: 6-JUN-1994

APPLICATION NUMBER: US 08/044,539

FILING DATE: 6-JUN-1993

ATTORNEY/AGRAT INFORMATION:

NAMM: POLIZI, CATHERINE M.

RECISTRATION NUMBER: 40,130

REPERENCE/DOCKET NUMBER: 40,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: bingle required required required requirements bescription: SEQ ID NO: 14: US-09-213-993-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (650) 813-569
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 41 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 81.8<sup>3</sup>
Matches 18; Conservative
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APPLICANT: YOKOYAMA, KEIICHI
APPLICANT: NAKAMURA, NAMI
APPLICANT: MIWA, TETSUYA
APPLICANT: SEGURO, KATSUYA
       NAKAMURA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-109-063-27
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APPLICANT: NAKAMURA, NAMI
APPLICANT: NAKAMURA, NAMI
APPLICANT: MIWA, TETSUYA
TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
FILE REFERENCE: 0010-0937-0
CURRENT APPLICATION NUMBER: US/09/109,063
CURRENT APPLICATION NUMBER: US/09/109,063
EARLIER PILING DATE: 1998-07-02
EARLIER PILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 62
SOFTWARE PARENTIN VET: 2.0
SOFTWARE PARENTIN VET: 2.0
SEQ ID NO 26
LENGTH: 45
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                  Sequence 26, Application US/09109063
Patent No. 6013498
GENERAL INFORMATION:
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Patent No. 6538122
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; Sequence 26, Application US/09884948
; Patent No. 6821763
                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
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GENERAL INFORMATION:
US-09-109-063-26/c
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APPLICANT: MIWA, TETSUTA
APPLICANT: SEGURO, KATSUYA
TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
TITLE OF INVENTION: PROCESS
FILE REFERENCE: 0010-0937-0
CURRENT PILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 09/448,310
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTI VET: 2.0
SEQ ID NO S: 62
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA US-09-884-948-26
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| Sequence 25, Application US/09892864A
| Sequence 25, Application US/09892864A
| Patent No. 683328
| GENERAL INFORMATION:
| APPLICANT: VOKOYAMA, Keiichi
| APPLICANT: ONO, Kunio
| APPLICANT: BJIMA, Daisuke
| TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUTAMINASE
| FILE REFERENCE: 2095-244050CONT |
| CURRENT APPLICATION NUMBER: US/09/892,864A
| CURRENT FILING DATE: 2001-66-28
| PRIOR APPLICATION NUMBER: PCT/JP99/07250
| PRIOR PILING DATE: 1999-12-24
| PRIOR APPLICATION NUMBER: JP 10-373131
| PRIOR PILING DATE: 1998-12-24
| PRIOR PILING DATE: 1998-12-24
| PRIOR PELING DATE: 1998-12-28
| NUMBER OF SEQ ID NOS: 58
| SOFTWARE: PatentIn version 3.1
| SEG ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.0%; Score 15.6; DB 4; Length 45;
81.8%; Pred. No. 9.3e+02;
tive 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic DNA US-09-892-864A-25
                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 81.8%
Matches 18; Conservative
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FEATURE:
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APPLICANT: VOKOYAMA, KEIICHI
APPLICANT: NAKAMURA, NAMI
APPLICANT: NAKAMURA, NAMI
APPLICANT: MAKAMURA, NAMI
APPLICANT: MIWA, TETSUYA
APPLICANT: GEGURO, KATSUYA
TILLE OF INVENTUDIO: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
FILE REFERENCE: 0010-0937-0
CURRENT PILING DATE: 1999-11-24
FRIOR APPLICATION NUMBER: 09/109,063
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
SOFTWARE: PACENTIN OF: 2.0
SOFTWARE: PACENTIN OF: 2.0
SEQ ID NO 27
LENGTH: 50
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APPLICANT: NAKAMURA, NAMI
APPLICANT: MIWA, TETSUYA
APPLICANT: SEGURO, KATSUYA
TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
FILE REPERENCE: 0010-0937-0
CURRENT APPLICATION NUMBER: US/09/884,948
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 09/448,310
TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE FILE REFERENCE: 0010-0037-0
CURRENT APPLICATION NUMBER: US/09/109, 063
CURRENT FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: J97-07-04
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 50
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Patent No. 6821763
GENERAL INFORMATION:
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US-09-884-948-27
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GENERAL INFORMATION:
APPLICANT: YAMAGUCHI, ISAMU
APPLICANT: YORAGHIA, HIDEO
APPLICANT: YOSHIOKA, KEIKO
APPLICANT: DOI, YOSHIHARU
TITLE OF INVENTION: METHODS FOR TRANSFORMATION OF PLANTS, TRANSFORMED
TITLE OF INVENTION: PLANTS AND PROCESSES FOR PREPARATION OF POLYESTERS
FILE REFERENCE: 081356/0148
FILE REFERENCE: 081356/0148
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: JP 11-225832
PRIOR APPLICATION NUMBER: JP 11-225839
PRIOR APPLICATION NUMBER: JP 11-225839
PRIOR FILING DATE: 1999-08-09
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US-09-982-864A-26

Sequence 26, Application US/09892864A

Sequence 26, Application US/09892864A

Sequence 26, Application US/09892864A

GENERAL INFORMATION:

APPLICANT: WOW, Kunio

APPLICANT: WOW, Kunio

FILE REFRENCE: 2095-24USCOUT

CURRENT APPLICATION: PROCESS FOR PRODUCING TRANSGLUTAMINASE

FILE REFRENCE: 2095-24USCOONT

CURRENT APPLICATION NUMBER: US/09/892,864A

CURRENT FILING DATE: 1999-12-24

PRIOR FILING DATE: 1999-12-24

PRIOR FILING DATE: 1999-12-24

SPRIOR FILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 58

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                           52.0%; Score 15.6; DB 4; Length 50; ilarity 81.8%; Pred. No. 9.5e+02; Conservative 0; Mismatches 4; Indels
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; Sequence 10, Application US/09635132
; Patent No. 6620601
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ORGANISM: Artificial Sequence
                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 62
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 50
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Best Local Similarity
Matches 18; Conserv
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Best Local Similarity
Matches 18; Conserv
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RESULT 16
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APPLICANT: Yu, Long
APPLICANT: Fu, Oiang
APPLICANT: Fu, Oiang
APPLICANT: Fu, Oiang
APPLICANT: Bi, Anding
ITILE OF INVENTION: POLYPEPTIDE AND THE METHOD FOR PREPARING
ITILE OF INVENTION: POLYPEPTIDE AND THE METHOD FOR PREPARING
ITILE REPRENCE: 1990-08-30
CURRENT APPLICATION NUMBER: US/09/786,025A
CURRENT APPLICATION NUMBER: US/09/786,025A
FILE REPRENCE: 1999-08-30
PRIOR APPLICATION NUMBER: US/09/186,025A
PRIOR APPLICATION NUMBER: CN98111044.4
PRIOR APPLICATION NUMBER: CN98111044.4
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 5.
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US-08-963-121C-20
; Sequence 20, Application US/08963121C
; Patent No. 6084087
; GENERAL INFORMATION:
; APPLICANT: Friedman, Steven M
; APPLICANT: Tumang, Joseph
; APPLICANT: Tumang, Joseph
; APPLICANT: Tumang, Joseph
; TITLE OF INVENTION: Conserved T-Cell Receptor Sequences
; MUMBER OF SEQUENCES: 23
; CORRESPONDENCES 23
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 15; DB 4; Length 29; 78.3%; Pred. No. 1.6e+03; tive 0; Mismatches 5; Indels
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Pred. No. 1.4e+03;
0; Mismatches 8;
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US-09-786-025A-5
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Patent No. 6660512
                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                Query Match 50.7%;
Best Local Similarity 71.4%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                      SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.3°
Matches 18; Conservative
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-786-025A-5
                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                  FEATURE:
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Gaps
                                                                                                         SUFWAKE: PACENTIN MELEABE #1.0, VETBION #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/963,121C

FILING DATE: October 28, 1997

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/427,009

FILING DATE: April 18, 1994

APPLICATION NUMBER: 08/229,285

FILING DATE: April 18, 1994

APPLICATION NUMBER: 07/766,751, Patent No. 6084087 5,480,895

FILING DATE: September 27, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 5983/17499-US1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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APPLICANT: Crow, Mary K
APPLICANT: Crow, Mary K
APPLICANT: Tunang, Joseph
APPLICANT: Tunang, Joseph
APPLICANT: Sun, Guang-Rong
TITLE OF INVENTION: Conserved T-Cell Receptor Sequences
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby & Darby PC
STREET: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.8; DB 3; Length 25; Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/09543513; Patent No. 6303750; GENERAL INFORMATION:
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ilarity 88.9%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: TCRa 3'antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-753 6237
TELEX: 23687
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10022
COMPUTER READABLE FORM:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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US-08-992-877-68
          APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.3%; Score 14.8; DB 4; Length 25; 88.9%; Pred. No. 1.9e+03; live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application PC/TUS9504803
GENERAL INFORMATION:
APPLICANT: New York Society For the ruptured and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6441
FILLING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/963,121
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 5983/17499-US1
TELECOMMUNICATION INFORMATION:
TELEBHONE: 212-57-7700
TELEBHONE: 212-57-7700
TELEBHONE: 212-57-7700
TELEBHONE: 212-57-7700
TELEBHONE: 212-57-7700
TELEBHONE: 212-57-7700
TELEBK: 236697
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STREE: Annobing aingle
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15-09-396-196G-6441/c
7. Sequence 6441, Application US/09396196G
7. Patent No. 6821724
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                                                                                                                                                                                                                                                                                                                                                                                       CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: TCRa 3'antisense
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                                                                                                                                                                                                                                                                                                                                                                linear
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                STRANCE TOPOLOGY: 11Dear MOLECULE TYPE: CD?
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PCT-US95-04803-21
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Sequence 68, Application US/08992877

Sequence 68, Application US/08992877

Setent No. 6340461

GENERAL INFORMATION:

PAPLICANT: Terman, David S

TITLE OF INVENTION: SUPERANTIGEN BSED METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: TRREATMENT OF INFECTIOUS DISEASE

FILE REPERENCE: Superantigen

CURRENT FILING DATE: 1997-12-17

PRIOR PAPLICATION NUMBER: 08/084,074

PRIOR PAPLICATION NUMBER: 60/044,074

PRIOR FILING DATE: 1997-04-17

NUMBER OF SEQ ID NOS: 78

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 68

LENGTH: 37
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                                                                                                            APPLICANT: Yi, Y.
APPLICANT: Tumang, Joseph
APPLICANT: Tumang, Joseph
APPLICANT: Tumang, Joseph
APPLICANT: Tumang, Joseph
APPLICANT: Sun, Guang-Rong
ITILE OF INVENTION: Conserved T-Cell Receptor Sequences
ITILE OF INVENTION: Conserved T-Cell Receptor Sequences
INVENTION: 2 January PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.8; DB 5; Length 25; Pred. No. 1.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: PCT/US95/04803
FILING DATE:
CLASSIFICATION:
Crippled Maintaining The Hospital for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                  Special Surgery
INVENTORS: Friedman, Steven M
Crow, Mary K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5983/09449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 5983,
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPHONE: 212-537-7700
TELEPK: 212-537-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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ilarity 88.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: TCRa 3'antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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Patent No. 6197558
GENERAL INFORMATION:
TITLE OF INVENTION: PROCESS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-858-623A-19

Sequence 19, Application US/08858623A

Patent No. 5910628

GENERAL INFORMATION:

APPLICANT: Miller, W.A., and Wang, S.

TITLE OF INVENTION: Cap-Independent Translation Sequences

TITLE OF INVENTION: Derived From Barley Yellow Dwarf Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.7%; Score 14.6; DB 3; Length 31;
69.0%; Pred. No. 2.5e+03;
ive 0; Mismatches 9; Indels
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDIUM TYPE: Cloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,111
FILING DATE: 19-MAY-1997
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: Golden, Matchew J.
REGISTRATION NUMBER: 25,161
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 218-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic oligonucleotide"
         4.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
STREET: 8011 Candle Lane
CITY: Houston
       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCGGATCCAGGTAGGCAGACTTGTCAGCC 29
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
       17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Te
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       Matches
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                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: primer; OTHER INFORMATION: sequences
US-08-992-877-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 48.7%; Score 14.6; DB 4; Length 25; Best Local Similarity 81.0%; Pred. No. 2.4e+03; Matches 17; Conservative 0; Mismatches 4; Indels
                                                                                                                                                             Query Match

49.3%; Score 14.8; DB 3; Length 37;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-05-36-196G-18196/C
Sequence 18196, Application US/09396196G
Sequence 18196, Application US/09396196G
GENERAL INCORMATION:
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-17
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15342/c
Sequence 15342 Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 15342
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18196
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TCCAGGTAGGCAGACTTGTCA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 rcradriadcadecercica 5
                                                                                                                                                                                                                                                       9 AGGTAGGCAGACTTGTCA 26
                                                                                                                                                                                                                                                                                                  16 AGGCAGACAGACTTGTCA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.7%;
81.0%;
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Mus musculus
US-09-396-196G-18196
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Gaps

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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017,199
FILING DATE: May 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5892
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEPHONE: (713) 777-6908
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIAINO JAINO STA
ATTORNEY/AGENT INFORMATION:
NAME: SARe, Stephen A.
REGISTRATION UNMBER: 38,609
REFERENCE/DOCKET NUMBER: 2318-0174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 CGGAUCCUGGGAAACAGGCUUGAC 32
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                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: genomic RNA (POTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.5*
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Ge; PUBLICATION INFORMATION: US-08-858-623A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: r
ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U. ZIP: 20004
                                                                                                                                                                                                                                                                                                          LENGTH:
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Sequence 8, Application US/08858623A
Patent No. 5910628
GENERAL INFORMATION:
APPLICANT: Miller, W.A., and Wang, S.
TITLE OF INVENTION: Cap-Independent Translation Sequences
TITLE OF INVENTION: Derived From Barley Yellow Dwarf Virus
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 48.0%; Score 14.4; DB 2; Length 31; Best Local Similarity 62.5%; Pred. No. 3.1e+03; Matches 15; Conservative 3; Mismatches 6; Indels
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    COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Wb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,623A
FILING DATE: May 20, 1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 06/017,199
FILING DATE: May 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFRENCE/DOCKET NUMBER: 35,423
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAN: (713) 777-2321
TELEPROME: (713) 777-6908
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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POSITION IN GENOME:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
SOFTMARE: Microsoft Word for Macintosh
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,623A
FILING DATE: May 20, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Houston.
STATE: Texas
COUNTRY: United States of America
ZIP: 77071
ZIP: 77071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic RNA
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PUBLICATION INFORMATION:

US-08-858-623A-19
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ORIGINAL SOURCE:
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HYPOTHETICAL: n
ANTI-SENSE: no
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MOLECULE TYPE:
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US-08-858-623A-8
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Gaps
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                                                                                                   GenBank Accession No. 5910628 X58455
                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C. STREET: 555 Thirteenth Street, N.W., Suite 701 East STREET: Tower CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,703
ANTI-SENDE.
FRAGMENT TYPE:
ORIGINAL SOURCE:
CANTERN TODACCO NECROSIS Virus Strain A
                                                                                                                                                                                         3; Mismatches
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Gaps

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Indels

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US-08-829-525-34/c

| Sequence 34, Application US/08829525 |
| Sequence 34, Application US/08829525 |
| Sequence 34, Application US/08829525 |
| Patent No. 6084083 |
| APPLICANT: Levinson, Douglas A. |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE |
| TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS |
| NUMBER OF SEQUENCES: 38 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Pennie & Edmonds |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 44;
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             75.0%; Pred. No. 3.2e+03;
                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FEALESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,525
FILING DATE: 28-MAR-1997
CLASSIPRICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,583
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: US 08/487,748
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/487,748
FILING DATE: 03-MAR-1995
ATTORNEY/AGBNT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 7853-081
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                          56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                           18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-869-8664
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 75.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
          Best Local Similarity
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MOLECULE TYPE:
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US-08-829-525-34
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                                           Matches
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Tavtigian, Sean V.
TITLE OF INVENTION: A Carboxy-Terminal BRCAl Interacting Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
Tower
                                                                                                                                                                                                                                                                                                                                                                                                                    48.0%; Score 14.4; DB 3; Length 40; 75.0%; Pred. No. 3.2e+03; Live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORPUTER: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/09/515,884
FILING DATE: 29-Feb-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION AND AND:
APPLICATION NUMBER: 08/975,703
FILING DATE: «Unknown»
ATTORNEY/AGBNT INFORMATION:
NAME: SAA-SPEPHEN A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2318-0174
TELEPHONE: 202-624-1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.0%; Score 14.4; DB 3; Length 40;
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DESCRIPTION: /desc = "Primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-515-884-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GGATCCAGGTAGGCAGACTTGTCA 26
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Patent No. 6235263
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
Bartel, Paul L.
                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                          TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 75.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 26
US-09-515-884-28/c
                                                                                                                                                                                                                                                                                                                                                    US-08-975-703-28
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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ORGANISM: Artificial Sequence
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-937-399-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Levinson, Douglas A.
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
  TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Best Local Similarity 75.0%; Pred. No. 3.3e
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FascESC Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,583A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,748
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/398,633
FILING DATE: 07-JUN-1995
ATCORNEY, LEGARATION:
NAME: CAPLAZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-048
TELEPHONE: 212-790-9090
TELEX: 66141 PERNIE
TELEX: 66141 PERNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CIIY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,399
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 TCCAGGTAGGCAGACTTGTCAGCC 29
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; Sequence 34, Application US/08937399
; Patent No. 6288218
                                                                                                                                             COUNTRY: USA
ZIF: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPES Diskette
COMPUTER: IBM COMPACTION
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY! linear
MOLECULE TYPE: CDNA
US-08-609-583A-34
TITLE OF INVENTION: TRI
NUMBER OF SEQUENCES: 3'
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 29
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Sequence 27, Application US/09560639

Sequence 27, Application US/09560639

Patent No. 632334

GENERAL INFORMATION:

APPLICANT: Kingsbury, G.

APPLICANT: Kingsbury, G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF INMUNE DISORDERS

FILE REPERENCE: 7853-1850-639

CURRENT FILING DATE: 2000-04-28

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 27

LENGTH: 44
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,583
FILING DATE: 01-MAR-1996
APPLICATION NUMBER: 08 08/487,748
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/399,633
FILING DATE: 03-WAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTAZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-048
TELEPHONE: 212-90-9090
TELEPHONE: 212-90-9090
TELEFAX: 212-869-8864
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LINCORMATION FOR SEQ ID NO: 34:
ELENEN: ABBREACTERISTICS:
CONTROL OF SEQUENCE CHARACTERISTICS:
CONTROL OF SEQUENCE CHARACTERISTICS
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US-09-310-367-34/c
; Sequence 34, Application US/09310367
; Patent No. 6414117
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
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US-09-464-231-34/c

| Sequence 34, Application US/09464231
| Patent No. 6562433
| Patent No. 65624343
| Patent INPORMATION:
| APPLICANT: Levinson, Douglas A. TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS |
| TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS |
| NUMBER OF SEQUENCES: 37 |
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Pennie & Edmonds |
| STREET: New York |
| CITY: New York |
| STARTE: New York |
| COUNTRY: USA |
| COMPUTER READABLE FORM: MEDIUM TYPES: Diseasette |
| COMPUTER: IBM Compatible |
| COMPUTER: IBM Compatible |
| COMPUTER: IBM Compatible |
| COMPUTER: FasteSEQ Version 2.0 |
| CURRENT APPLICATION NUMBER: US/09/464,231 |
| FILING DATES.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/609,583
FILING DATE: 01-MAR-1996
APPLICATION NUMBER: US 08/487,748
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/398,633
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
                          OPERATING SYSTEM: DOS
SOCTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,337
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic
STRANDEDNESS:
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                    COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
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Pred. No. 3.3e+03;
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Best Local Similarity 75.0%; Pred. No. 3.3e
Matches 18; Conservative 0; Mismatches
TITLE OF INVENTION: COMPOSITIONS AND METHY
TITLE OF INVENTION: TREATMENT AND DIAGNOS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036/Z111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COUNTRY: USA
ZIP: 10036/Z111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COUNTRY: USA
ZIP: 10036/Z111
COMPUTER: TAM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/310,367
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: US 08/487,748
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: US 08/487,748
FILING DATE: 03-MAR-1995
APPLICATION NUMBER: US 08/398,633
FILING DATE: 03-MAR-1995
APPLICATION NUMBER: US 08/398,633
FILING DATE: 03-MAR-1995
APPLICATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELEFAX: 212-86-8864
TELESPAX: 212-86-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: LENGTH: LAND ALLEST ALL
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-310-367-34
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Gaps
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FILING DATE:
CLASSIFICATION
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PILING DATE:
CLASSIFICATION NUMBER: US 08/409,583
FILING DATE: 01-MAR-1996
APPLICATION NUMBER: US 08/398,633
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/398,633
FILING DATE: 03-MAR-1995
APPLICATION NUMBER: US 08/398,633
REGISTRATION NUMBER: 30,742
REGISTRACION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7863-016
TELEPHONE:
TELEPHONE:
212.790-9090
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4 GATCCAGGTAGGCAGACTTGTCAGCCT 30
EARLIER APPLICATION NUMBER: US 60/031,435
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NAME: Pabst, Patrea L.
REGISTATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: TSII;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8794
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                  EARLIER FILING DATE: 1996-11-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.4%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-SEPT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 70.43
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-08-123-702-42
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ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Atlanta
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US-08-123-702-42
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                                                                                                                                       TYPE: DNA
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; Sequence 12, Application US/09283144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions
; TITLE OF INVENTION: between Survivin and Tubulin
; TITLE OF INVENTION: between Survivin and Tubulin
; FILE REFERENCE: 44574-5033-US
; CURRENT APPLICATION NUMBER: US/09/283,144
; CURRENT PILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: US 60/080,288
; EARLIER PILING DATE: 1999-04-01
; FARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER PILING DATE: 1997-11-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 107784, Application US/09396196G; Patent No. 6821724; GENERAL INFORMATION: Michael Mittmann; APPLICANT: Michael Mittmann; APPLICANT: David Mack; APPLICANT: David Lockhart; APPLICANT: David Lockhart; APPLICANT: Affymetrix, Inc.; ATPLE OF INVENTION: Methods of Genetic Analysis; FILER REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
47.3%; Score 14.2; DB 4;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 107784
LENGTH: 25
                     7853-048
                                                                                                                                                                                                                                                                                                                                                                                                                                      6 TCCAGGTAGGCAGACTTGTCAGCC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 TGCAGGTGTGCAGACTTGGGATCC 17
                REFERENCE DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAN: 212-90-9090
TELEFAX: 212-90-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear
NOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GGATCCAGGTAGGCAGACT 21
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    REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: mus musculus
US-09-396-196G-107784
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Matches
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Sequence 42, Application US/08123702
| Sequence 42, Application US/08123702
| Patent No. 5604131
| GENERAL INFORMATION:
| APPLICANT: Wadsworth, Samuel
| APPLICANT: Reddy, Vermuri, B. APPLICANT: Reddy, Vermuri, B. APPLICANT: Wei, Chamer
| APPLICANT: Wei, Chamer
| TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding APP770
| Patent No. 5604131
| TITLE OF INVENTION: Containing a Genomic DNA Insert of the KI and OX-2 Regions NUMBER OF SEQUENCES: 45
| CORRESPONDENCE ADDRESS: 45
| CORRESPONDENCE ADDRESS: 1201 West Patentic Center STREET: 2800 One Allantic Center STREET: 2000 One Allanti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer for
OTHER INFORMATION: cloning Survivin construct
US-09-283-144-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                        Length 28;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEACHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14.2; DB 1;
Pred. No. 3.8e+03;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                        47.3%; Score 14.2; DB 3; 70.4%; Pred. No. 3.7e+03; 7ative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CGGATCCAGGTAGGCAGACTTGTCAGC 28
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US-09-671-317-767/c

1 Sequence 767, Application US/09671317

1 Patent No. 6528260

2 GENERAL INFORMATION:

2 APPLICANT: Blumenfeld, Marta

3 APPLICANT: Blumenfeld, Marta

3 APPLICANT: Cohen, Annick

4 APPLICANT: Cohen, Annick

5 TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

7 TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

7 TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

7 TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

7 TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

7 TITLE OF INVENTION NUMBER: US 60/53,178

7 PRIOR FILING DATE: 2000-03-23

7 PRIOR FILING DATE: 1999-03-25

7 PRIOR FILING DATE: 1999-03-25

7 PRIOR FILING DATE: 1999-04-30

8 NUMBER OF SEQ ID NOS: 977

8 SOFTWARE: Patent.pm

8 SEQUENCE: Patent.pm
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COATION: 24
COCHEN INFORMATION: 12-603-191 : polymorphic base T or C
US-09-671-31'-767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
47.3%; Score 14.2; DB 3;
Best Local Similarity 84.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                         STATE: Massachusetts
COUNTRY: USA
ZIP: 00109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,333A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Catherine J. Kara
REGISTRATION NUMBER: 41,106
REFERRATION NUMBER: 41,106
REFERRATION NUMBER: 41,106
REFERRATION NUMBER: CPI-012CP5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
        ORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 TAGGCAGACTTGTCAGCCT 30
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens
                                                                                        Boston
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                                                              Sequence 41, Application US/08936632B

Sequence 41, Application US/08936632B

Patent No. 6159765

GENERAL INFORMATION:

APPLICANT: Truehart, Joshua

APPLICANT: Fuernkranz, Hans

APPLICANT: Paul, Jeremy I.

APPLICANT: Harinans, Debra

APPLICANT: Mathans, Debra

APPLICANT: ADIMES, Scott

TITLE OF INVENTION: INENTIFYING RECEPTORS

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTY: US

ZIP. ACCURATION OF SECONDENCES

COUNTY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'PERATING SISTEM: PC-UDS/NNS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,632B
FILING DATE: 24-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/718,910
FILING DATE: 24 SEPTEMER 1996
APPLICATION NUMBER: US 08/851,469
FILING DATE: 05 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: DECONTI, GIULIO A., JR.
REGISTRATION NUMBER: 31,503
REGISTRATION NUMBER: 27,7400
TELEPRONE; (617)/227-7400
TELEPRONE; (617)/24-4214
INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS:
LUNGTH: 39 DASE pairs
LUNGTH: 39 DASE pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 92, Application US/08582333A
Patent No. 6255059
GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Compositions for TITLE OF INVENTION: Jentifying Receptor Effectors NUMBER OF SEQUENCES: 98
4 GGTGGAGGTAGGTAAACTTGACTGCAT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 TAGGCAGACTTGTCAGCCT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.3
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                     US-08-936-632B-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-936-632B-41
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Gaps

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US-09-268-22
; Sequence 22, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: MONIA, Brett P.
; APPLICANT: MONIA, Brett P.
; TITLE OF INVENITON: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; TITLE OF INVENITON: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
LENGTH: 23
                                               Gaps
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Query Match 47.3%; Score 14.2; DB 4; Length 47; Best Local Similarity 76.2%; Pred. No. 4.1e+03; Matches 16; Conservative 1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GCGGATCCGCGTACTCAGAGTT 23
                                                                                FEATURE:
COTHER INFORMATION: PCR primer
US-09-209-668-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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25, Appl 621574,

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Scoring table:

Searched:

Database

score:

Perfect

Sequence:

OM nucleic

Run on:

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Sequence 839968,
Sequence 160368,
Sequence 127072,
Sequence 851373,
Sequence 806412,
Sequence 80578,
Sequence 81060, A
Sequence 17727,
Sequence 243203,
Sequence 72, Appl
Sequence 72, Appl
Sequence 172680,
Sequence 172680,
Sequence 634810,
Sequence 634810,
Sequence 588184,
Sequence 588184,
Sequence 588184,
Sequence 58186,
Sequence 588184,
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Sequence 588184,
Sequence 588184,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 303122,
Sequence 463637,
Sequence 606347,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence S
                                       Sequence
Sequence
Sequence
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| Sequence 2, Application US/08469172
| Publication No. US2003005433A1
| GENERAL INFORMATION:
| APPLICANT: SEIDMAN, CHRISTINE
| APPLICANT: SEIDMAN, JOHN
| APPLICANT: ROSENZWHIG, ANTHONY
| TITLE OF INVENTION: A METHOD FOR DETECTING
| TITLE OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS:
US-11-036-317-411291

US-11-036-317-635455

US-11-036-317-621574

US-11-036-317-621574

US-11-036-317-772779

US-11-036-317-772779

US-10-036-317-772779

US-10-036-317-772779

US-10-719-900-10072

US-10-719-900-10072

US-10-719-900-906412

US-10-719-900-906412

US-10-719-900-906412

US-10-719-966-127779

US-10-719-966-1277779

US-10-719-960-190832

US-10-719-900-190832

US-10-719-900-190832

US-10-719-900-190832

US-10-719-900-190832

US-10-719-900-190832

US-10-719-900-190832

US-10-719-900-15688

US-10-719-900-15688

US-10-719-966-17689

US-11-036-317-589184

US-11-036-317-791168
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-892-864A-25
US-09-892-864A-25
US-09-996-561-26
US-09-996-561-27
US-09-996-561-27
US-09-996-561-27
US-09-996-561-27
US-08-996-561-27
US-08-996-361-37
US-08-996-361-37
US-10-719-956-303122
US-10-719-956-465637
US-10-719-956-665347
US-10-719-956-66537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-719-900-539634
US-10-719-900-580775
US-11-036-317-217141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510
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APPLICATION NUMBER: US/08/469,172
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: LAHIVE & COCKFIELD
60 STATE STREET, Suite
     Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 60 STATE CITY: BOSTON STATE: Massachuse COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
US-08-469-172-2
     16.8
116.8
116.6
116.2
116.2
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Sequence 64086, A
Sequence 107278,
Sequence 28585, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Appli
                                                                                                                   November 18, 2005, 06:36:48; Search time 403.232 Seconds (without alignments) 615.265 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgn2_6/ptodata1/jubpna/USO7_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO6_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO6_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO6_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO7_NEW_PUB.seq:*

(cgn2_6/ptodata1/jubpna/USO8_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO8_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO8_PUBCOMB.seq:*

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(cgn2_6/ptodata1/jubpna/USO8_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO9_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO9_PUBCOMB.seq:*

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(cgn2_6/ptodata1/jubpna/USO9_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO9_NEW_PUB.seq:*

(cgn2_6/ptodata1/jubpna/USO9_NEW_PUB.seq:*

(cgn2_6/ptodata1/jubpna/USO9_NEW_PUB.seq:*

(cgn2_6/ptodata1/jubpna/USO9_PUBCOMB.seq:*

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(cgn2_6/ptodata1/jubpna/USO9_PUBCOMB.seq:*

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(cgn2_6/ptodata1/jubpna/USO0_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO0_PUBCOMB.seq:*

(cgn2_6/ptodata1/jubpna/USO0_NEW_PUB.seq:*

(cgn2_6/ptodata1/jubpna
                                                                                                                                                                                                                                                                                                                                                 11093112
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-11-036-317-64086
US-10-719-900-107278
US-11-036-317-28585
                                                                                                                                                                                                                      1 GCGGATCCAGGTAGGCAGACTTGTCAGCCT 30
                                                                                                                                                                                                                                                                                                                                            hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                             9794790 segs, 4134909567 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   nucleic search, using sw model
                                                                                                                                                                                                                                                        IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Match Length
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18.4 16.8 16.8

Score

Result Š.

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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             US-11-036-317-64086/c
; Sequence 64086, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
                                                                                                        100.0%; Scu-
100.0%; Pred
0; N
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                                                                                                                                                                                                          1 GCGGATCCAGGTAGGCAGAC
                                                                                                                  Query Match
Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.03
Matches 19; Conservative
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CORGANISM: Mus musculus
US-11-036-317-64086
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US-10-719-900-107278
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LENGTH: 25
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US-10-788-779-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
DISEASE-ASSOCIATED MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: Massachusetts
COMPUTE: MASSACHUSETTS
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/788,779
FILING DATE: 27-Feb-2004
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/469,172
FILING DATE: «Unknown»
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.

REGISTRATION NUMBER: 33,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCGGATCCAGGTAGGCAGACTTGTCAGCCT 30
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY: NIFORMATION:
NAME: HANLEY ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GML-111
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10788779
Publication No. US20040152121A1
GENERAL INFORMATION:
APPLICANT: SEIDWAN, CHRISTINE
SEIDWAN, JOHN
WATKINS, HUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-469-172-2
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPRENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 64086
LENGTH: 25
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     Length 30;
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILER REFERENCE: 35.201
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR PILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 98.2914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.3%; Score 18.4; DB 26; 95.0%; Pred. No. 4.4e+02;
Score 30; DB 20;
Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                              1 GCGGATCCAGGTAGGCAGACTTGTCAGCCT 30
                                                Mismatches
                                                                                                   TGTCAGCCT 30
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-635455
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US-11-004-843-25
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Sequence 411291, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25

LENGTH: 25
       Sequence 2855, Application US/11036317
Sequence 2855, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION UNMBER: US 60/536,639
PRIOR PLING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SSOTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION UNBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.8; DB 26;
Pred. No. 2.2e+03;
0; Mismatches 2;
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Sequence 635455, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
HAPLICANT: Blume, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 GTAGGCAGACTTGTCAGCCT 30
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Best Local Similarity 90.0%;
Matches 18; Conservative (
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Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-036-317-411291/c
US-11-036-317-28585
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WS-11-036-317-621574

Sequence 621574, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Williams, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT FILING DATE: 2005-01-13

PRIOR FILING DATE: 2005-01-13

PRIOR FILING DATE: 2004-01-13

NUMBER: OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 621574
                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                           Length 25;
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NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 635455
LENGTH: 25
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                                                                                                                                                                                           Score 16.8; DB 26;
Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/11004843
PUDLICATION NO. US20050239173A1
GENERAL INFORMATION:
TITLE OF INVERTION: PRODUCTION OF AMINO SUGARS
FILE REFRENCE: 023829/0393
CURRENT APPLICATION NUMBER: US/11/004,843
FURIOR APPLICATION NUMBER: 11/004,843
PRIOR APPLICATION NUMBER: 60/527,309
PRIOR FILING DATE: 2004-12-07
PRIOR FILING DATE: 2004-12-07
PRIOR FILING DATE: 2003-12-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN OFF: 3.3
                                                                                                                                                                       56.0%; Scor.
90.0%; Pred. No. 4...
0; Mismatches
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Best Local Similarity 90.0
Matches 18; Conservative
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us-10-788-779-2.rnpb

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Sequence 772379, Application US/11036317

Sequence 772379, Application US/11036317

Sequence 772379, Application US/11036317

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR RILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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BUDICACION NO. US20050214823A1

GENERAL INFORMATION.

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3664.

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13
                      Gaps
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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                      4; Indels
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82.6%; Pred. No. 2.7e+03;
                        Mismatches
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
                                                               6 TCCAGGTAGGCAGACTTGTCAGC 28
                                                                                     3 TCCAGGATGTCAGATTTGTCAGC 25
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                      ö
                      19; Conservative
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CORGANISM: Mus musculus
US-11-036-317-839968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-772379
Best Local Similarity
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US-10-719-900-160368/c
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US-11-036-317-839968
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LENGTH: 25
                      Matches
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TITLE OF INVENTION: WIlliam
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: OSTEOARTHISTIC AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 127072
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| Sequence 427846, Application WS/10719956
| Publication No. US20040146910A1
| GENERAL INFORMATION:
| APPLICANT: Vue Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Rat
| FILE REPERBENCE: 3527.1
| CURRENT PILING DATE: 2003-11-20
| PRIOR PFLICATION NUMBER: 60/427,836
| PRIOR FILING DATE: 2002 11-20
| NUMBER OF SEQ ID NOS: 699466
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                           Length 25;
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                 TITLE OF INVENTION: Methods of Genetic Analysis of Mouse FILE REPERSENCE: 3528.1

CURRENT APPLICATION UNDER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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85.7%; Pred. No. 4e+03;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                         54.0%; Score 16.2; DB 2
85.7%; Pred. No. 4e+03;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 127072, Application US/10956157; Publication No. US20050118625A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CCAGGTAGGCAGACTTGTCAG 27
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CRGANISM: Rattus norvegicus
US-10-719-956-427846
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Best Local Similarity 85...
Best Local Similarity 85...
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Best Local Similarity 85.7°
Matches 18; Conservative
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; ORGANISM: Probe Sequence
US-10-956-157-127072
                                                                                                                                                                                                                                                                                      ; ORGANISM: Mus musculus
US-10-719-900-160368
APPLICANT: Xue Mei Zhou
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                                                                                                                                                                                                              SEQ ID NO 160368
LENGTH: 25
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Matches

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Pred. No. 4.9e+03;
0; Mismatches 5; Indels
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Pred. No. 4.9e+03;
0; Mismatches 5; Indels
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CURRENT FILING DATE: 2003-11-20
PRIOR PPLICATION NUMBER: 00/427,836
PRIOR PILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 167727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 83060
LENGTH: 25
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FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR PELLING DATE: 2002 11 20
                   APPLICANT: David Lockhart
APPLICANT: Affwnetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
TITLE OF INVENTION: Methods of Genetic Analysis
TITLE OF INVENTION: Methods of Genetic Analysis
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1998-09-17
NUMBER OF SEC ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                           53.3%; Scor.
79.2%; Pred. No. 4...
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; Publication No. US20040146910A1
; APPLICANT: Xue Mei Zhou
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US-10-719-956-83060
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 79.29
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Best Local Similarity 79.2
Matches 19; Conservative
  David Mack
David Lockhart
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: mus musculus
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US-10-719-956-167727/c
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US-10-719-956-83060
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                                                                                                                                                                                                                                                                                                  SEQ ID NO 80578
LENGTH: 25
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; Sequence 906412, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR PILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 906412
; LENGTH: 25
54.0%; Score 16.2; DB 24; Length 25; 85.7%; Pred. No. 4e+03; 1ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.3%; Score 16; DB 22; Length 25; 79.2%; Pred. No. 4.9e+03; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                 APPLICANT: Xue Med Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 35.28.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 851373
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 53.3%; Score 16; DB 22; Length 25; Best Local Similarity 100.0%; Pred. No. 4.9e+03; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db -- 4.9e+03;
                                                                                                                                                                                                                                                  Sequence 851373, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
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Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 deaaccadeadrcacacrircica 1
                                                                                        9 AGGTAGGCAGACTTGTCAGCC 29
                                                                                                                                 3 AGCTCTGCAGACTTGTCAGCC 23
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Matches 19; Conservative
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus
US-10-719-900-851373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus US-10-719-900-906412
                     Local Similarity
Les 18; Conserv
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US-10-719-900-851373/c
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US-10-809-189-80578/c
  Query Match
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US-10-19-900-190832
IS-20-19-900-190832
Sequence 190832, Application US/10719900
Sequence 190832, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
GURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
FRIOR FILING DATE: 2002-11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 190832
FENCH: 25
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| Sequence 244203. Application US/10719900
| Publication No. US20050026164A1
| GENERAL INFORMATION:
| APPLICANT: Vue Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| FILE REFERENCE: 3528.1
| CURRENT APPLICATION NUMBER: US/10/719,900
| CURRENT FILING DATE: 2003-11-20
| PRIOR PFLICH DATE: 2002-11-20
| NUMBER OF SEQ ID NOS: 982914
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.7%; Score 15.8; DB 22; Length 25; 89.5%; Pred. No. 6e+03; tive 0; Mismatches 2; Indels
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Pred. No. 6e+03;
0; Mismatches 2; Indels
                                                                              Query Match 53.3%; Score 16; DB 24; Length 25; Best Local Similarity 79.2%; Pred. No. 4.9e+03; Matches 19; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                    7 CCAGGTAGGCAGACTTGTCAGCCT 30
                                                                                                                                                                                                24 CCAGGTAGCCAGCCTAGTCAAACT 1
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89.5%;
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-167727
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Best Local Similarity 89.5
Matches 17; Conservative
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Matches 17; Conservative
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CORGANISM: Mus musculus
US-10-719-900-243203
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CORGANISM: Mus musculus
US-10-719-900-190832
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RESULT 22 US-11-036-317-475065

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APPLICANT: Ricker, Nicolas
APPLICANT: Ricke, Darrell
APPLICANT: Case 60145USPCT
CURRENT APPLICATION NUMBER: US/10/481,113
CURRENT APPLICATION NUMBER: US 60/300,112
PRIOR APPLICATION NUMBER: US 60/300,112
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-01-121
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2002-03-21
PRIOR FILING DATE: 2002-03-21
PRIOR FILING DATE: 2002-03-21
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/361,819
PRIOR FILING DATE: 2002-06-24
SHOR FILING DATE: 2002-06-24
SHOR FILING DATE: 2002-06-24
SHOR FILING DATE: 2002-06-24
SEQ ID NO 7:
LENGTH: 23
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; Sequence 475065, Application US/11036317; Publication No. US20050214823A1; GENERAL INFORMATION:
; APPLICANT: Williams, Alan; APPLICANT: Williams, Alan; APPLICANT: Williams, Alan; APPLICANT: Williams, Alan; APPLICANT: Blume, John TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse; FILE REPERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13; PRIOR APPLICATION NUMBER: US 60/536,639; PRIOR PLING DATE: 2004-01-13; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 475065
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Pred. No. 6e+03;
0; Mismatches 2;
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Pred. No. 7.4e+03;
0; Mismatches 4;
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89.5%;
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81.8%;
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Moughamer, Todd
Glazebrook, Jane
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Best Local Similarity 81.8
Matches 18; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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Cooper, Bret
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US-10-481-113-72
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APPLICANT:
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APPLICANT:
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Matches 18; Conserv
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LENGTH: 25
SEQ ID NO 634810
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                      LENGTH:
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                                      Sequence 156288, Application US/10719900
; Sequence 156288, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Kue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: WHORER: US/10/719,900
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR PILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SEQ ID NO 156288
; LENGTH: 25
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Fublication No. US20040146910A1
Fublication No. US20040146910A1
FUBLICANT: Kue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: 057211-20
FRIOR PFLING DATE: 2003-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Yue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4;
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; ORGANISM: Rattus norvegicus
US-10-719-956-172680
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
               RESULT 24
US-10-719-900-156288/c
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US-10-719-956-172680/c
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US-10-719-956-634810/c
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US-11-036-317-90978
; Sequence 90978, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFRENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: MICROARRAY Probe Sequence Listing Generator V 1.1
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Sequence 588184, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
FRIOR PELING DATE: 2004-01-13
FRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOSTWARE MICROARTS Probe Sequence Listing Generator V 1.1
                                                                                                                                      Gaps
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                                                                                           Length 25;
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Pred. No. 7.4e+03;
0; Mismatches 4;
                                                                                       Query Match 52.0%; Score 15.6; DB 24 Best Local Similarity 81.8%; Pred. No. 7.4e+03; Matches 18; Conservative 0; Mismatches 4
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TYPE: DNA
CORGANISM: Rattus norvegicus
US-10-719-956-634810
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Best Local Similarity 81.8
Matches 18; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-588184
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APPLICANT: MINA, TETSUTA
APPLICANT: SEGURO, KATSUYA
TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
FILE REFERENCE: 0010-0037-0
CURRENT APPLICATION NUMBER: US/09/996,561
CURRENT FILING DATE: 2001-11-30
PRIOR PRILING DATE: CURRENT APPLICATION NUMBER: US/09/448,310
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver: 2.0
                                                ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-254016
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
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US-11-036-317-791169

Sequence 791169, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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            Sequence 791168, Application US/11036317
; Bublication No. US20050214823A1
; Publication No. US20050214823A1
; GENERAL INCORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR PILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 791168
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CURRENT APPLICATION NUMBER: US/11/060,756
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Publication No. US20050221354A1
PUBLICANT. UNFORMATION:
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Matches 18; Conservative
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US-11-036-317-791168
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US-11-060-756-254016/c
US-11-036-317-791168
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APPLICANT: YOKOYAMA, Keiichi
APPLICANT: YOKOYAMA, Keiichi
APPLICANT: YOKOYAMA, Keiichi
APPLICANT: ONO, Kunio
TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUTAMINASE
FILE REPERENCE: 2092AUSRCONT;
CURRENT APPLICATION NUMBER: US/09/892,864A
CURRENT FILING DATE: 2001-06-28
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1998-12-28
NUMBER: OF SEQ ID NOS: 58
SOFTWARE: PATCHTION VUMBER: JP 10-373131
PRIOR FILING DATE: 1998-12-28
SOFTWARE: PATCHTION VUMBER: JP 10-373131
                                                                                                                                                                                             Length 25;
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Pred. No. 7.4e+03;
0; Mismatches 4;
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Pred. No. 7.2e+03;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                      24 AGGGAGGTAGACTCGTTAGCCT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic DNA US-09-892-864A-25
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81.8%;
CURRENT FILING DATE: 2005-02-1
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 254016
LENGTH: 25
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81.8%;
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Best Local Similarity 81.8°
Matches 18; Conservative
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Best Local Similarity 81.8
Matches 18; Conservative
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Gaps

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APPLICANT: MIWA, TETSUYA
APPLICANT: SEGURO, KATSUYA
TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
TITLE REFERENCE: 0010-0937-0
CURRENT PELLIGATION NUMBER: US/09/996,561
CURRENT PILING DATE: 2011-30
PRIOR PELICATION NUMBER: US/09/996,561
PRIOR PELICATION NUMBER: 09/109,063
PRIOR FILING DATE: CURRENT PILING DATE: 1999-11-24
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 62
SOFTWARE PACENTION OF 27
LENGTH: 50
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Patent No. US20020173021A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VAKOYANA, KEIICHI
APPLICANT: MAKAMURA, NAMI
APPLICANT: SEGURO, KATSUYA
APPLICANT: SEGURO, KATSUYA
APPLICANT: SEGURO, PRODUCING MICROBIAL TRANSGLUTAMINASE
FILE REFERENCE: 0010-0937-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-996-561-27
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                                                                     Score 15.6; DB 9;
Pred. No. 7.1e+03;
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CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 09/448,310
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VET: 2.0
LENGTH: 50
                                                                                                                                                                     5 ATCCAGGTAGGCAGACTTGTCA 26
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                                                                                                                                                                                                                                                                                                                                           ; Sequence 27, Application US/09996561; Patent No. US20020151703A1
GENERAL INFORMATION: APPLICANT: YOKOYAMA, KEIICHI
OTHER INFORMATION: Synthetic DNA
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ORGANISM: Artificial Sequence
                                                                   Query Match 52.0%;
Best Local Similarity 81.8%;
Matches 18; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 81.89
Matches 18; Conservative
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     ) UINER ANY 200 US-09-892-864A-26
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US-09-884-948-27
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Fatent No. US20020133021A1
GENERAL INFORMATION:
APPLICANT: YOKOWAMA, KELICHI
APPLICANT: WAKAWURA, NAMI
APPLICANT: MIWA, TETSUYA
TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
FILE REPERENCE: 0010-0937-0
CURRENT APPLICATION NUMBER: US/09/884,948
CURRENT APPLICATION NUMBER: US/09/884,948
CURRENT APPLICATION NUMBER: 090-11-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH 45
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                                                                                     ) OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA US-09-996-561-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA US-09-884-948-26
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| Sequence 26, Application US/09892864A
| Patent No. US20020090675A1
| GENERAL INFORMATION:
| APPLICANT: YOKOYAMA, Keiichi
| APPLICANT: ONO, Kunio
| APPLICANT: EJIMA, Dalsuke
| TITLE OF INVENTION: PROBUCING TRANSGLUTAMINASE
| FILE REFERENCE: Z00524U50CONT
| CURRENT APPLICATION NUMBER: US/09/892,864A
| CURRENT FILING DATE: 2001-06-28
| PRIOR APPLICATION NUMBER: PCT/JP99/07250
| PRIOR APPLICATION NUMBER: JP 10-373131
| PRIOR APPLICATION NUMBER: JP 10-373131
| PRIOR FILING DATE: 1998-12-28
| NUMBER OF SEQ ID NOS: 58
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 26
                                                                                                                                                                Query Match 52.0%; Score 15.6; DB 9; Length 45; Best Local Similarity 81.8%; Pred. No. 7.2e+03; Matches 18; Conservative 0; Mismatches 4; Indels
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                  TYPE: DNA ORGANISM: Artificial Sequence
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Matches
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US-10-719-900-258355
Sequence 258355, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11.20
PRIOR FILING DATE: 2002 11.20
PRIOR FILING DATE: 2002 11.20
NUMBER: OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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CURRENT XUE ME TO INVENTION: METHODS OF GENETIC Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002 11 20

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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51.3%; Score 15.4; DB 24; Length 25;
Best Local Similarity 94.1%; Pred. No. 9.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels
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  Length 50;
                                                4; Indels
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Score 15.6; DB 9;
Pred. No. 7.1e+03;
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Query Match 52.0%; Score 15.6; D
Best Local Similarity 81.8%; Pred. No. 7.1e
Matches 18; Conservative 0; Mismatches
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APPLICANT: Xue Mei Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 ATCCAGGTAGGCAGACTTGTCAGCC 29
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                                                                                                                           13 ATCCAGGTAAGCAGATTCATCA 34
                                                                                          5 ATCCAGGTAGGCAGACTTGTCA 26
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Best Local Similarity 76.03
Matches 19; Conservative
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CORGANISM: Mus musculus
US-10-719-900-258355
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US-10-719-956-463637/c
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A0 bp DNA linear ROD 15-FEB-2001 (rlst-1) gene, exon 1.
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Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                      Unclassified.

1 (bases 1 to 24)
Seidman, T., Watkins, H. and Rosenzweig, A.
Method for detecting hypertrophic cardiomyophathy associated
                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Length 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="unassigned DNA"
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Location/Qualifiers
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Sequence 3 from patent US 5429923.
AX651216
CQ840251
CQ857597
AX518421
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AX175458
AX442928
AX442928
AX651213
AX651213
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AX098266
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/organism="unknown"
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AX51027 Sequence
CQ664052 Sequence
AX116342 Sequence
AX411254 Sequence
AX411254 Sequence
AX451311 Sequence
AX65115 Sequence
AX651259 Sequence
BD250383 BD294805
CQ008720 Sequence
CQ008720 Sequence
CQ008720 Sequence
CQ008721 Sequence
A84013 Sequence
A84013 Sequence
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A84013 Sequence
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                                                     November 18, 2005, 11:12:34 ; Search time 665.886 Seconds (without alignments) 1746.433 Million cell updates/sec
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       GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                4708233 seqs, 24227607955 residues
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AX515479
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Maximum Match 100%
Listing first 45 summaries
                                      - nucleic search, using sw model
                                                                                       US-10-788-779-3
24
1 ATGCCAACCCTGCTCTGGAGGCCT
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AX284760
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seq length: 50
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Match 1
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PAT 26-JUL-1995

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /i
Patent: WO 2004072265-A 2685 26-AUG-2004,
Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);
Dorner, Andrew J. (US); Trepicchio, William L. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.8%; Score 15.8; DB 6; Length 41; Best Local Similarity 81.0%; Pred. No. 6.5e+03; Matches 17; Conservative 1; Mismatches 3; Indels
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Patent: WO 02052044-A 7225 04-JUJ-2002;
Riken (JP)
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Sequence 7225 from Patent WO02052044.
AX521027
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    .41
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AX521027/c
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                                                                                                                                                                                                                                                 Submitted (26-MAY-2000) Pharmacology, University of Kansas Medical Center, 3901 Rainbow Blvd., Kansas City, KS 66160, USA
Center, 3901 Rainbow Blvd., Kansas City, KS 66160, USA
Choudhuri,S., Ogura,K. and Klaassen,C.D.
Direct Submission
Submitted (15-FEB-2001) Pharmacology, University of Kansas Medical Center, 3901 Rainbow Blvd., Kansas City, KS 66160, USA
Sequence update by submitter
On Feb 15, 2001 this sequence version replaced gi:9624341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                    The state of the full-length coding sequence of rat liver-specific Clouduri, S., Ogura, K. and Klaassen, C.D.
Clouding of the full-length coding sequence of rat liver-specific organic anion transporter-1 (rlst-1) and a splice variant and partial characterization of the rat lst-1 gene
Biochem. Biophys. Res. Commun. 274 (1), 79-86 (2000)
10903899
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Patent: WO 02052044-A 1677 04-JUL-2002;
                                                                                                                                                                                          2 (bases 1 to 40)
Choudhuri, S., Ogura, K. and Klaassen, C.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Rattus norvegicus"
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Sequence 1677 from Patent WO02052044.
AX515479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol type="genomic DNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/number=1
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Best Local Similarity 79.2
Matches 19; Conservative
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Best Local Similarity
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AX515479/c
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PAT 10-SEP-2004

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linear

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PAT 27-MAR-2003

SOURCE ORGANISM

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AUTHORS TITLE

REFERENCE

AX316342/c

LOCUS

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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

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Byckerman,S., Tavernier,J. and Vandekerckhove,J.
Reversed mammalian protein_protein interaction trap
Patent: WO 03004643-A 18 16-JAN-2003;
Vlaams Interniversitair Instituut voor Biotechnologie vzw. (BE)
Location/Qualifiers
/mol_type="unassigned_DNA"
/db_xref="taxon:32630"
/note="reverse_primer for murine CIS amplicication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood, K.V., Wood, M.G., Zhuang, Y. and Paguio, A. Synthetic nucleic acid molecule compositions and methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/note="reverse primer; MBU-O-678; mcIS primer"
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81.0%; Pred. No. 2.7e+04;
ive 0; Mismatches 4; Indels
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                                                                                         Query Match 60.8%; Score 14.6; DB 6; Best Local Similarity 81.0%; Pred. No. 2.7e+04; Matches 17; Conservative 0; Mismatches 4;
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other sequences; artificial sequences.
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Patent: WO 0216944-A 169 28-FEB-2002;
PROMEGA CORPORATION (US)
Location/Qualifiers
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Sequence 18 from Patent WO03004643.
AX671506
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/organism="synthetic const
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Matches 17; Conserv
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Tavernier,J.
Receptor-based interaction trap
Receptor-based interaction trap
Patent: WO 0190188-A 30 29-NOV-2001;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
Location/Qualifiers
                                                1 (bases 1 to 47)
Blumenfeld, M., Chumakov, I., Bougueleret, L. and Cohen, A.
Blallelic markers related to genes involved in drug metabolism
Patent: US 6528260-A 812 04-MAR-2003;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.8%; Score 14.6; DB 6; Best Local Similarity 81.0%; Pred. No. 2.7e+04; Matches 17; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                            61.7%; Score 14.8; DB 6; 80.0%; Pred. No. 2.2e+04;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:22630"
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/organism="synthetic construct"
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Sequence 30 from Patent WO0190188.
AX316342
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Sequence 18 from Patent WO0240543.
                                                                                                                                                              /organism="unknown"
/wol_type="genomic DNA"
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               Unknown.
Unclassified.
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 8

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DEFINITION ACCESSION VERSION KEYWORDS

RESULT 11

AR291259

ORGANISM

AUTHORS TITLE REFERENCE

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NAL. Patent: JP 2002541794-A 28 10-DEC-2002;

OUEEN MARY AND WESTFIELD COLLEGE

OUEEN MARY AND WESTFIELD COLLEGE

PN JP 2002541794-A/28

PN JP 2002541794-A/28

PP 12-APR-2000 JP 2000611653

PR 13-APR-1999 GB 9906458.4

PI ULVI GERST TALAS, JOHN DUNLOP, DAVID PETER KELSELL PC
C12N15/09, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N15/10, C12N9/ PC
50, C12Q1/68,

PC C12Q1/68,

PC C12Q1/68,

CC Primer

Location/Qualifiers

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Patent: WO 0061728-A 28 19-OCT-2000;
DUNLOP JOHN (ES) ; KELSELL DAVID PETER (GB) ; GERST TALAS ULVI (GB)
; QUEEN MARY & WESTFIELD COLLEGE (GB)
Location/Qualifiers
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ilarity 93.8%; Pred. No. 3.4e+04;
Conservative 0; Mismatches 1;
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llarity 93.8%; Pred. No. 3.4e+04;
Conservative 0; Mismatches 1;
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/organism="synthetic construct"
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synthetic construct
other sequences, artificial sequences.
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Talas, U.G., Dunlop, J. and Kelsell, D.P.
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Sequence 28 from Patent W00061728.
AX038772
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/db_xref="taxon:32630"
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/db_xref="taxon:32644"
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A61K37/02,
(CI2N5/00,CI2R1:91)
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PD 10-DEC-2002
PF 11-APR-2000 DF 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC CIZN15/09,AG1K38/00,AG1K48/00,AG1P43/00,AG1K38/10, PC
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 2598 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 47)
Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallellic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 2994 25-WAR-2003;
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Location/Qualifiers
                                                                                                                                                                                                               AR291259 47 bp DNA Sequence 2994 from patent US 6537751.
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DEFINITION

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RESULT 12 BD254805 LOCUS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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bp DNA linear PAT 27-AUG-2002
r the construction of recombinant
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unidentified
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1 (bases 1 to 24)
Bovenberg, R.A. and Selten, G.C.
GENE CONVERSION AS A TOOL FOR THE CONSTRUCTION OF RECOMBINANT
INDUSTRIAL FILAMENTOUS FUNGI
PATENT: WO 9846772-A 24 22-OCT-1998;
BOVENBERG ROELOF ARY LANS (NL); GIST BROCADES BV (NL)
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unclassified.
1 (bases 1 to 24)
Selten,G.C.M., Swinkels,B.W. and Bovenberg,R.A.L.
Gene conversion as a tool for the construction of recombinant industrial organisms
Patent: JP 2001518798-A 24 16-OCT-2001;
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PN JP 200118198-A/24

PD 16-OCT-2001

PF 09-APR-1998 JP 1998543456

PR 11-APR-1997 EP 97201091.2

PI GERARDUS CORNEILS MARIA SELTEN, BART WILLEM SWINKELS, PI ROLLOF ANY LANS BOVENBERG

PC C12N15/80,C12N15/65,C12N15/87
              25.7.26
/note="Nucleotide deleted between bases 25 and
Accession number cg43966585"
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                                                                                               Score 14.4; DB 6;
Pred. No. 3.5e+04;
0; Mismatches 6;
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Sequence 24 from Patent WO9846772.
A84037
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db_xref="taxon:9606"
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Gene conversion as a tool
industrial organisms.
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JP 2001518798-A/24.
                                                                                               Query Match 60.0%;
Best Local Similarity 75.0%;
Matches 18; Conservative (
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof Patent: WO 0147944-A 2576 05-JUL-2001;
Curagen Corporation (US)
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

Datent: WO 014794A 7360 05-JUL-2001;

Curagen Corporation (US)

Location/Qualifiers
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/note="Nucleotide deleted between bases 25 and 26
Accession number cg43985274"
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                                                                                                                Length 20;
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llarity 93.8%; Pred. No. 3.4e+04;
Conservative 0; Mismatches 1;
         /organism="synthetic construct"
/mol_type="unassigned DNA"
/mol xref="taxon:32630"
/nofe="primer"
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Sequence 7360 from Patent WO0147944.
CQ008720. GI:41015434
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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Cimadevilla,J.C. and Villahermosa,J.M.

Nucleic acid probes for the detection of small exons and methods of designing the same
Patent: WO 20040/70060-A 7 19-AUG-2004;

GENOMICA S.A.U. (ES)
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Location/Qualifiers
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|mol_type="unassigned DNA"
|db_xref="taxon:32630"
|nofe="primer INSP105- exon4R"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide probe"
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other sequences; artificial sequences.
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Sequence 18 from Patent WO2004056863.
CQ840251
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Sequence 7 from Patent WO2004070060.
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       /db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: EP 1273560-A 3055 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1273660-A 3056 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
                                                                    /organism='Unidentified'.
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Pred. No. 5.5e+04;
0; Mismatches 5;
                                      Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/mol_type="genomic DNA"
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Popology: Linear;
desc = 'oligonucleotide'
                                                         1. .24
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Best Local Similarity 77.3%;
Matches 17; Conservative
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 0140521-A 612 07-JUN-2001;
Curagen Corporation (US)
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/db.traxon:9606"
25...26
/note="Nucleotide deleted between bases 25 and
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Patent: US 6309826-A 15 30-OCT-2001;
Location/Qualifiers
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Sequence 15 from patent US 6309826.
AR175455
AR175455.1 GI:17916754
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/organism="unknown"
/mol_type="unassigned DNA"
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AX157284.1 GI:14538615
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                                                      Homo sapiens (human)
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Nucleic acid probes for the detection of small exons and methods of designing the same
Patent: WO 20040/70060-A 8 19-AUG-2004;
GENOMICA S.A.U. (ES)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Detection of genetic polymorphisms
Petent: WO 02052044-A 4619 04-JUL-2002;
Riken (JP)
                                                                                                                                                                                                                                                                                                                                             1. 40
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/db_xref="caxon:32630"
/note="oligonucleotide probe"
                                                                                                   DNA
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                                                                                                                                                                                                                other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX518421 41 bp DN. Sequence 4619 from Patent WO02052044.
                                                                                        CQ857598 . 40 bp Dl
Sequence 8 from Patent WO2004070060.
CQ857598
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                    5 ATCCAAACGCTGATGTGGAGGC 26
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CQ857598.1 GI:51851748
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AX518421.1 GI:23568007
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synthetic construct
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CQ857598
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AX518421
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PAT 22-MAR-2003
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human sodium-hydrogen exchanger like protein 1
Patent: BP 1273660-A 3053 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1273560-A 3054 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 3054 from Patent EP1273660.
AX651214
AX651214.1 GI:29154032
                                                                                                                                    25 bp DP Sequence 3053 from Patent EP1273660. AX551213 AX651213.1 GI:29154031

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    0; Mismatches
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                                  CCAACCCTGCTCTGGAGGCC 23
                                                              ccaeccrecrerraagecc 24
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Best Local Similarity 80.0°
Matches 16; Conservative
    16; Conservative
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BD170870/c
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Patent: Bp 1356824-A 15 29-OCT-2003;
Serrero, Ginette (US)
Location/Qualifiers
             Servero, G.
88kDa tumorigenic growth factor and antagonists
Patent: US 6670183-A 15 30-DEC-2003;
Location/Qualifiers
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Patent: US 6720159-A 15 13-APR-2004;
Location/Qualifiers
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AR494164
AR494164.1 GI:47267029
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Sequence 15 from Patent EP1356824.
AX934355
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                                                                                 1. .24
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Serrero, G.
   (bases 1 to 24)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Unclassified.
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AR494164
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BD172240 50 bp DNA linear PAT 18-FEB-2003 Secreted and transmembrane polypeptides and nucleic acids encoding
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C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
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60/059263
60/062125
60/062285
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60/063127
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60/063327
60/063541
60/063542
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60/063738
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60/065186
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60/066840

    .36
    /organism='Artificial Sequence'.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IS 60/059115,17-SEP-1997
60/059122,17-SEP-1997 US
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Pred. No. 8.9e+04;
); Mismatches 4;
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60/063329, 27-0CT-1997 U
60/063549, 28-0CT-1997 U
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                   Location/Qualifiers
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60/062814, 24-0CT-1997
60/063120, 24-0CT-1997
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60/063732,31-OCT-1997
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60/066453,25-NOV-1997
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60/059266,15-OCT-1997
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60/063704, 29-OCT-1997
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60/064809,12-NOV-1997
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1 (bases 1 to 50)
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JP 200223786-A/13
13-ANG-2002
18-DEC-2001 UP 2001385135
17-SEP-1997 US 60/059115
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1 Similarity 80.0%;
16; Conservative (
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BD172240/c
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HIROSHI WATARAI, YASUNORI YAMAGUCHI
C12N15/02, C07K16/18, C12N15/09, C12P21/08, C12Q1/02, G01N33/53, PC
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Antibody against dendritic cell (DC) membrane moleucle, Siglec-9, and DC detection method and DC separation method using it.
BD095049
                 PAT 17-JAN-2003
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synthetic construct
construct
cher sequences, artificial sequences.

1 (bases 1 to 36)
Watarai,H. and Yamaguchi,Y.
Matibody against dendritic cell (DC) membrane moleucle, Siglec-9,
and DC detection method and DC separation method using it
Patent: JP 201352977-A 2 25-DEC-2001;
KIRIN BREWERY CO LTD
OS Artificial Sequence
PN JP 201352977-A/2
PD 25-DEC-2001
                                                                                                                                                                                                                                              OS Arrificial Sequence
PN W0 0205744-A/25
PD 25-JUL-2002
PF 22-JAN-2002 W 2002JP000413
PR 22-JAN-2001 JP 01P 013217,11-MAY-2001 JP 01P 141490 PI
SHINAE KONDO, NOBUTAKE AKIYAMA
PC CI2NIS/09,CO7K14/47,CO7K16/18,CI2NS/10,A61K38/00,A61K48/00,
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Description of Artificial Sequence: a sense primer specific for 5'-leader
sequence of Siglec-9 gene
                                                                                                                                                                               Human apoptosis-associated gene and human apoptosis-associated protein produced by the gene Patent: WO 02057444-A 25 25-ULL-2002; SHINAE KONDO, NOBUTAKE AKIYAWA OS Artificial Sequence PN WO 02057444-A/25
Human apoptosis-associated gene and human apoptosis-associated protein produced by the gene.
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Description of Artificial Sequence: Synthesized CC
oligonucleotide
FH Key
Location/Qualifiers
1. .34
/organism='Artificial Sequence',
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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                        other sequences; artificial sequences.
1 (bases 1 to 34)
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                                                                          BD170870.1 GI:27876682
WO 02057444-A/25.
                                                                                                                                                                       Kondo, S. and Akiyama, N.
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synthetic construct
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Best Local Similarity
Matches 16; Conserv
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Secreted and transmembrane polypeptides and nucleic acids encoding
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C12N5/10,
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60/066840 PI
), DIANE PENNICA,
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1 (bases 1 to 50)
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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(C12P21/02,C12R1:645),C12N15/00,C12N5/00
C Description of Artificial Sequence: Synthetic FH Location/Qualifiers
T source
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                                                                           6; Length 50;
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60/063045,24-OCT-1997 U
60/063329,27-OCT-1997 U
60/063549,28-OCT-1997 U
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60/062287,17-OCT-1997
60/063486,24-OCT-1997
60/062814,24-OCT-1997
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60/059113,17-SEP-1997
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GENENTECH INC
OS Artificial Sequence
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Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches
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DIANE PENNICA,
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60/059117
                                                                                                                                                     Description of Artificial Sequence: Synthetic FH Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 50;
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Pred. No. 9e+04;
); Mismatches 4; Indels
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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GENENTECH INC
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27-AUG-2002
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Best Local Similarity 80.0°
Matches 16; Conservative
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Secretory and transmembrane polypeptide and nucleic acid encoding the same.

BD175231
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C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
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C12PS/102/C12PS/08,(C12NI/J9,C12R1.645),(C12NI/21,C12R1.19),
PC (C12PS/10,C12R1:91),C12NI/S/00,C12NS/00,(C12NS/00,C12R1:91) CC
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            24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
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80.0%; Pred. No. 9e+04;
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GENENTECH INC
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18-DEC-2001 JP 2001385319
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PC 12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC C12N15/02,C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC C12P21/02,C12P21/02,C12P21/02,C12R1:645),C12P21/02,C12R1:645),C12N15/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,
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17-SEP-1997 US 60/0591:
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PC C12N15/09, A61K45/00, A61P1/00, A61P13/12, A61P17/00, A61P17/06, PC
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Ashkenazi, A., Botsein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,
Filvaroff, E., Fong, S., Gao, W.-O., Gerber, H., Gerritsen, M.E.,
Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,
Kijavin, I.J., Mather, J.P., Pani, J., Paoni, N.F., Roy, M.A.,
Stewart, T.A., Tunas, D., Williams, P.M. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
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C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395,
A61P43/00,
C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10,
                                                                                                            A61P25/00,
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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066840 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA,
                                                                                                                          PC 76125/16, A61P25/28, A61P31/12, A61P35/00, CO7X14/47, CO7X11
PC CO7X19/00,
PC C12N1/19, C12N1/21, C12N5/10//A61X38/00, A61X39/395, A61X39
PC A61P43/00,
PC C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19), (C12PC C12N1/21), C12R1:645), (C12N15/00, C12R1:91), PC C12N15/00, A61X37/02, (C12N15/00, C12R1:91) CC Description of Artificial Sequence: Synthetic FH Key Location/Qualifiers
FF source /organism='Artificial Sequence'.
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/organism='Artificial Sequence'
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/organism="synthetic construct"
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Location/Qualifiers
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Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding the same
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Aav68288 Penicilli Adco6568 Human Na/ Adc06569 Human Na/ Aaq70259 T. gondii Aag71324 Human INS Adg99501 Flanked e Adg99500 Flanked e

Abz19539 Human glu Abz45912 Human glu Abc6436 Sense PCR Abz84928 Human oli Abd21158 Human Kra Ado31281 Human Kra Aax05223 Murine IC Abx5568 CAMP depe Abx11966 Human TIM Abx11967 Human TIM Abx11967 Human Bil

Adp22838 Human BUB Adp22760 Human BUB

Abk88718 Human YB-Aav82832 Human GP8 Aat35560 Beta-HCG

Run on:

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AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-invasive method for diagnosis of hypertrophic cardio-myopathy useful for testing asymptomatic individual(s).
                                                                                                                                                                                                                                                                                                                                                                                  chain; non-invasive; hypertrophic cardiomyopathy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARD ) HARVARD COLLEGE.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
(GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA.
                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; primer; mutation; detection; ss.
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                                                       ADQ99501
ADQ99500
ABZ49539
ABZ45912
ACH66436
ABZ84928
                                                                                                              ABD21158
ADO31281
AAXO5223
ABS5568
ABK11966
ABK11967
AAI73671
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ADP22760
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ABK88718
AAV82832
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 Seidman J, Seidman C,
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Myosin; heavy
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                                                                                            Synthetic.
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Abz4893 Human cyt
Adm97521 CD1d-1gG-
Adm9783 CD1d-1gG-
Adm9783 CD1d-1gG-
Adm7483 CD1d-1gG-
Abz5334 Drug ther
Abz5324 Drug ther
Abz160842 Murine C
Abz162021 Recombina
Abs192021 Recombina
Abs2020 Green/red
Aa152036 Human SNP
Aa129368 Human SNP
Aa13152 Human SNP
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Adr05299 Human bet
Adp10021 50-mer ol
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Adg86349 Human SMR
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                                                             November 18, 2005, 05:29:23 ; Search time 165.262 Seconds (without alignments) 859.686 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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seq length: 50
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Result No. υ υ

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oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain

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asymptomatic individuals suspected of having the disease. The method has a broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease and phenylketonuria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC; familial hypertrophic cardiomyopathy; SHC; Gaucher's disease; sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia; buchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease; phenylketonuria; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting a presence or absence of a mutation associated with hypertrophic cardiomypathy, useful for diagnosing cystic fibrosis or hemophila, by detecting a mutation in an amplified product of a beta cardiac myosin heavy-chain DNA.
                                                                                                                                                                                                 Gaps
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                                                                                                                                                      100.0%; Score 24; DB 2; Length 24; 100.0%; Pred. No. 0.57; o; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human beta cardiac myosin heavy chain PCR primer A'.
                                                                                                                 Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                            ACA63113 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                               24; Conservative
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(ROSE/) ROSENZWEIG A.
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(SEID/) SEIDMAN J.
(WATK/) WATKINS H.
                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                ACA63113;
                                                                                                                                                          Query Match
Best Local &
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             DNA. The method is useful for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. This method is sepecially useful for diagnosing SHC and FHC, as well as for determining the estimated the life expectancy of a person with familial hypertrophic cardiomyopathy. In particular, the method is useful for determining an individual's genetic information, and diagnosing e.g. Gaucher's disease, haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease, phenylketonuria or cystic fibrosis. The present sequence is a nested PCR primer used to amplify a region of the beta cardiac myosin heavy chain cDNA containing an FHC-associated mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting mutations associated with hypertrophic cardiomyopathy to diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac myosin heavy-chain DNA and detecting the mutation in the amplified
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, beta cardiac myosin, heavy chain, PCR, primer, ss, PHC, SHC, familial hypertrophic cardiomyopathy, sporadic hypertrophic cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta cardiac myosin heavy chain mutation detection primer A'.
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                                                                                                                                                                                                                                                    100.0%; Score 24; DB 9; Length 24; 100.0%; Pred. No. 0.57; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                  Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watkins H, Rosenzweig A;
                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                             1 ATGCCAACCCTGCTCTGGAGGCCT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2004; 2004US-00788779.
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95US-00469172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADR05299 standard; DNA; 24
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                                                                                                                                                                                                                                                                                         24; Conservative
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SEIDMAN J.
WATKINS H.
                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
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Best Local S
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88666666666688888
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2; SEQ ID NO 30; 1762pp; English.

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cc which amplify beta-cardiac myosin heavy-chain DNA (the set of oligonucleotide primers being useful for facilitating the diagnosis of hypertrophic cardiomyopathy by being capable of detecting a hypertrophic cardiomyopathy and with for facilitating the diagnosis of hypertrophic cardiomyopathy (comprising a first container heavy chain DNA, where the RNA probe is capable of detecting a first container completely hybridisable to the beta-cardiac myosin heavy chain DNA, where the RNA probe is capable of detecting a hypertrophic cardiomyopathy-associated mutation, a second container container for amplifying beta-cardiac myosin heavy-chain DNA and instructions for using the components of the kit to detect the presence or absence of a hypertrophic cardiomyopathy-associated mutation in amplified beta-cardiac myosin heavy-chain DNA). The method is used for detecting the presence or absence of a mutation associated with chypertrophic cardiomyopathy for facilitating the diagnosis of individuals hypertrophic cardiomyopathy for facilitating the diagnosis of the theorem of clinical symptoms and the demonstration of unexplained ventricular cardiomyopathy relies on the presence of typical cardiomyopathy relies on the presence of typical clinical symptoms and the demonstration of unexplained ventricular contained by the present invention is non-invasive and based, at least in hypertrophy established that there are no extensive studies involving a large number of families which mutations in the beta cardiac myosin heavy-chain gene. Prior and contained by nother mutations in the beta cardiac myosin heavy-chain gene. Prior and contained by nother mutations in the beta cardiac myosin heavy-chain gene or dispersed the mutations in the beta cardiac myosin heavy-chain gene or dispersed the method of the presence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caused by point mutations in the beta cardiac myosin heavy-chain gene. The present sequence is a PCR primer used to amplify a region of the beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain having a disease-related point mutation.
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100.0%; Score 24; DB 13; Length 24;
 Score 24; ...
Pred. No. 0.57;
Pred. no. 0.57;
                Similarity 100.0%; Pred. No. 0.5 24; Conservative 0; Mismatches
                                                              1 ATGCCAACCCTGCTCTGGAGGCCT 24
                                                                                 ATGCCAACCCTGCTCTGGAGGCCT 24
                Local Similarity
 Query Match
                  Best Loca
Matches
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Gaps

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transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS; 88. 50-mer oligonucleotide marker probe of the invention #30. BP ADP10021 standard; DNA; 50 (first entry) 12-AUG-2004 ADP10021; ADP10021/c

24-APR-2003; 2003WO-US012946. 24-APR-2002; 2002US-00131831. 20-DEC-2002; 2002US-00325899. WO2004042346-A2. Homo sapiens, 21-MAY-2004,

Prentice J, Morris M; Ly N, (EXPR-) EXPRESSION DIAGNOSTICS INC. Woodward R, Fry K, Wohlgemuth J, Rosenberg S;

WPI; 2004-400724/37.

Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of genes

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                                            rejection, e.g. cardiac or kidney transplant rejection, in an individual rejection, e.g. cardiac or kidney transplant rejection, in an individual methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a 50 mer oligonucleotide marker for diagnosis and monitoring of allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
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/standard_name= "Single nucleotide polymorphism (SNP)"
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                                 present invention relates to diagnosing or monitoring transplant
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                                                                                                                                                                                                                                                                                                                                  Score 16.8; DB 12; Length 50;
Pred. No. 9.8e+02;
0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cytochrome P450 CYP4F3 gene polymorphic site, #7225.
                                                                                                                                                                                                                                                                                                  Sequence 50 BP; 9 A; 13 C; 18 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                           4 CCAACCCTGCTCTGGAGGCC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                            37 ccaccccrcrcrcadaccc 18
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                                                                                                                                                                                                                                                                 rejection and other disorders.
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Matches 18; Conservative
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27-DEC-2000; 2000JP-00399443.

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Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ4317-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of arrays and screening drugs using genetic polymorphism data. Genetic polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to that cause or exacerbate certain diseases. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur.
                                                                                                                                                                                                                                                                                                                                                                        Frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients.

This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and periods of the invention are also useful in the drug discovery and such of the invention are also useful in the drug discovery and capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patient are on medication and the number of different may medications a patient needs to take before finding an effective therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytochrome P450 CYP4F3 gene polymorphic site, #1677.
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replace(21,A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.5
Best Local Similarity 85.7
Matches 18; Conservative
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Conceining enzymes associated with drug metabolism. The invention relates encoding enzymes associated with drug metabolism. The invention relates conceining and compositions for identifying individuals who have at least to methods and compositions for identifying individuals who have at least cone polymorphisms may be identified in a mucleic acid sample using probes or primers specific for a sequence selected from ABZ4317-ABZ50887 using a variety of detection assays, including hybridisation assays, mucleic acid sample using probes or primers specific for a sequence selected from ABZ4317-ABZ50887 using a variety of detection assays, including hybridisation assays, mucleic acceptable drugs using genetic polymorphism data. Genetic polymorphism and screening drugs using genetic polymorphism data, particularly that relating the relationship between polymorphism (SMPS), may be used in studying the relationship between polymorphisms (SMPS), may be used in studying the relationship between polymorphisms (SMPS), may be used in studying the relationship between polymorphisms (SMPS), may be used in studying the relationship between the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genesic profile of individual patients.

This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety.

This would not only if thair genetic profiles indicate that they are clinical trials only if thair genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previouely familed drug tradstes and decreases in the number of adverse educe the liment populations. The embrance of adverse reactions, thereby individuals could be revived if they were matched or the particular and 
                                                                                                                                                                                                                      Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD1d complex; cytostatic; antiinflammatory; cancer; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.5%; Score 16.2; DB 6; Length 41; 85.7%; Pred. No. 1.8e+03; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 41 BP; 12 A; 6 C; 16 G; 7 T; 0 U; 0 Other;
                                                                                                                                    ŝ
                                                                                                                                      Saito
                                                                                                                                                                                                                                                                                                                                          Claim 23; Page 92; 2785pp; English.
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                                                                                                                                 Iida A,
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                02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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ID ADM97503 standard; DNA; 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                 Sekine A,
                                                                                                                                                                              WPI; 2002-583571/62.
                                                                                    (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                               nucleic acid.
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                                                                                                                                 Nakamura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM97503;
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Unidentified.

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The present invention relates to a compound comprising one or more CDId complexes and an antibody or its fragment specific for a cell surface marker. The CDId complexes comprise a CDId and a beta2-microglobulin molecule, and are linked to the antibody or its fragment. The composition and methods are useful for preventing or treating tumours and autoimmune/inflammatory or infectious diseases, such as multiple sclerosis, type I diabetes, ankylosing spondylitis, acute anterior uveitis, atrophic gastritis, ankylosing spondylitis, acute anterior uveitis, atrophic gastritis, ankylosing spondylitis, psoriatic arthitis, rheumatodiarthitis, systemic lupus erythematosus, systemic sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary cirrhosis, ulcerative colitis or autoimmune hepatitis. The present sequence is a PCR primer used in the exemplification of the invention.
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 inflammatory disease; immunosuppressive; antimicrobial; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compound comprising CDId complexes and an antibody specific for a cell surface marker, useful for preventing or treating tumors and autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
              antidiabetic; antiarthritic; antirheumatic; ophthalmological; gastrointestinal; nephrotropic; dermatological; hepatotropic; beta2-microglobulin; ss; primer; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.0%; Score 15.6; DB 12; Length 45; 81.8%; Pred. No. 3.3e+03; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD1d-IgG complex F(ab'2) fragment PCR primer SEQ ID NO: 44.
                                                                                                                                                                                                                                                                                                                                                                               Cesson V, Mach J, Zauderer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45 BP; 5 A; 15 C; 17 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 10; Page 85; 152pp; English.
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                                                                                                                                                                                                                                 27-SEP-2002; 2002EP-00405838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.00,
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ADM97521 standard; DNA; 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetes or psoriasis
                                                                                                                                                                                                                                                                   (VACC-) VACCINEX INC.
                                                                                                                                                                                                                                                                                                                                                                               Robert B, Donda A,
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-316095/29
                                                                                                                                                                                                                                                                                  ROBERT B.
DONDA A.
CESSON V.
                                                                                                                                                                                                                                                                                                       (DOND/) DONDA A.
(CESS/) CESSON V
(MACH/) MACH J.
                                                                                                                         WO2004029206-A2
                                                                                       Unidentified
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                                                                                                                                                            08-APR-2004.
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                                                                                                                                                                                                                                                                                    ROBE/)
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The present invention relates to a compound comprising one or more CDId complexes and an antibody or its fragment specific for a cell surface marker. The CDId complexes comprise a CDId and a beta2-microglobulin molecule, and are linked to the antibody or its fragment. The composition and methods are useful for preventing or treating tumours and autoimmune/inflammatory or infectious disease, such as multiple sclerosis, type I diabetees, ankylosing spondylitis, acute anterior uveitis, atrophic gastritis, Goodpasture's syndrome, Grave's disease, Hashimoto's thyroiditis, myasthenia gravis, psoriasis, psoriatic arthritis, rheumatoid arthritis, systemic lupus erythematosus, systemic sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary cirrhosis, ulcerative colitis or autoimmune hepatitis. The present sequence is a PCR primer used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDId complex, cytostatic, antiinflammatory, cancer; autoimmune disease, inflammatory disease; immunosuppressive; antimicrobial; neuroprotective; antidiabetic; antiarthritic; antirheumatic; ophthalmological; gastrointestinal; nephrotropic; dermatological; hepatotropic; beta2-microglobulin; ss; primer; PCR.
                                                                                                                                                                                                                                                                                                                                           New compound comprising CD1d complexes and an antibody specific for a cell surface marker, useful for preventing or treating tumors and autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.0%; Score 15.6; DB 12; Length 45; 81.8%; Pred. No. 3.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                         Cesson V, Mach J, Zauderer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45 BP; 5 A; 15 C; 17 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 3.3e+03;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 15; Page 95; 152pp; English.
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                                                                                                26-SEP-2003; 2003WO-US030238
                                                                                                                                  27-SEP-2002; 2002EP-00405838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 81.8 es 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 diabetes or psoriasis.
                                                                                                                                                                     VACCINEX INC
                                                                                                                                                                                                                                                                         Donda A,
                                                                                                                                                                                                                                                                                                       WPI; 2004-316095/29.
                                                                                                                                                                                                     DONDA A.
CESSON V.
                                                                                                                                                                                      ROBERT B.
                                WO2004029206-A2
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                                                                                                                                                                                                                                       MACH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                  08-APR-2004.
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                                                                                                                                                                                                                                                                         Robert B,
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                                                                                                                                                                                                                       (CESS/)
(MACH/)
                                                                                                                                                                     (VACC-)
                                                                                                                                                                                      (ROBE/)
                                                                                                                                                                                                        (DOND)
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ADM97483/c
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WO200240543-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2002
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                                                                                                                       (DORN/) I
(TREP/) 1
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                                (AMHP)
                                                       (BURC/)
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a compound comprising one or more CDId complexes and an antibody or its fragment specific for a cell surface marker. The CDId complexes comprise a CDId and a beta2-microglobulin molecule, and are linked to the antibody or its fragment. The composition and methods are useful for preventing or treating tumours and autoimmunef/inflammatory or infectious diseases, such as multiple sclerosis, type I diabetes, anklylosing spondylitis, acute anterior uveitis, atrophic gastritis, Goodpasture's syndrome, Grave's disease, Hashimoto's thyroiditis, myasthenia gravis, psoriasis, psoriatic arthritis, systemic lupus erythematosus, systemic sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary cirrhosis, ulcerative colltis or autoimmune hepatitis. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              New compound comprising CDId complexes and an antibody specific for a cell surface marker, useful for preventing or treating tumors and autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence is a PCR primer used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                             Zauderer M;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                          Cesson V, Mach J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 74; 152pp; English.
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03-APR-2003; 2003US-0459782P.
23-JAN-2004; 2004US-0538246P.
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                             26-SEP-2003; 2003WO-US030238
                                                                                          27-SEP-2002; 2002EP-00405838
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                                                                                                                                                 VACCINEX INC.
ROBERT B.
DONDA A.
CESSON V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes or psoriasis.
                                                                                                                                                                                                                                                                                                                                             Robert B, Donda A,
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-316095/29
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Best Local Similarity
                                                                                                                                                                                                               (DOND/) DONDA A.
(CESS/) CESSON V
(MACH/) MACH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004072265-A2
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                                                                                                                                                 (VACC-)
(ROBE/)
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ADR55334/c
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The invention relates to a method of monitoring drug activities in vivo by comparing an expression profile of at least one gene in a peripheral blood sample of a patient to a reference expression profile of the at least one gene is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients who have a non-blood disease and are subjected to a drug therapy as compared to PBMCs isolated from the patient before the drug therapy, and where the patient has the non-blood disease and is being treated by the drug therapy. The method, kit, and nucleic acid array are useful for monitoring drug cutivities in vivo. The drug is especially CCI-779, an ester analogue of the immunosuppressant rapamycin which is a potent inhibitor of the mammalian target of rapamycin (mTOR). This sequence represents a gene mammalian target of rapamycin (mTOR). This sequence represents a gene corporate in PBMC altered by the drug therapy. (Note: this sequence does no form part of the printed specification but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences/).
                                                                                                                                                                                                                                                                                                                                                               Monitoring drug activities in vivo comprises comparing an expression profile of a gene in a peripheral blood sample of a patient before and after drug therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                    Trepicchio WL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine CIS DNA fragment amplifying reverse primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 7 A; 7 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 2685; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tavernier J, Zabeau L;
                                                                                                                                                                                                        Dorner AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TGCCAACCCTGCTCTGGAGGCCT 24
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15-NOV-2000; 2000US-0248970P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-2001; 2001WO-EP012569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; PCR; primer; ss
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                                                                                                                                                                                                        Twine N,
                                                                               DORNER A J.
TREPICCHIO W L.
BURCZYNSKI M.
TWINE N.
                                                                                                                                                                                                                                                                                WPI; 2004-642301/62
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RESULT 13
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                                                                                              The invention relates to functional fragments of a leptin receptor, involved in suppressor of cytokine signalling 3 (SOCS3), cytokine-inducible SRL-Contraining protein (CIS) and/or Vav signalling. The leptin receptor functional fragments are useful for modulating ligand (e.g. leptin) induced signalling, and to screen compounds that interfere with the binding of the functional fragment with a signalling molecule e.g. Vav, SOCS3 or CIS. Modulators of leptin may be useful in food intake disorders and regulation of weight, angiogenesis, wound healing and susceptibility to digestive cancers. The present sequence represents a PCR primer for amplifying the murine CIS DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a novel recombinant transmembrane receptor comprising an extracellular ligand binding domain and a cytoplasmic domain that contains a heterologous bait polypeptide. The receptor is activated by binding of a ligand to the ligand binding domain and by binding of a prey polypeptide to the heterologous bait peptide. The receptor or the prey polypeptide is useful for detection of compound-compound binding, where the binding is modification state dependent and
                     New functional fragment of leptin receptor, involved in suppressor of cytokine signaling 3, cytokine-inducible SH2-containing protein and/or Vav signaling, useful for modulating ligand induced signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant transmembrane receptor, useful for detecting compound-compound binding, comprises extracellular ligand binding domain and cytoplasmic domain containing heterologous bait polypeptide,.
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                        60.8%; Score 14.6; DB 6; Length 30; 81.0%; Pred. No. 9.1e+03;
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                                                                                                                                                                                                                                             Sequence 30 BP; 7 A; 5 C; 11 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant transmembrane receptor; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Ostade X, Vandekerckhove J,
                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                           2 TGCCAACCCTGCTCTGGAGGC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 9; Page 41; 74pp; English.
                                                                                                                                                                                                                                                                                                                                           21 TTCCAACTCTGATCTAGAGGC 1
                                                                          Example; Page 9; 35pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-2000; 2000EP-00201771
                                                                                                                                                                                                                                                                                                                                                                                                                   ABK16712 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                   Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIS primer MBU-0-678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-097646/13.
WPI; 2002-500206/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200190188-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eyckerman S,
Tavernier J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK16712;
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the modification is phosphorylation, acetylation, acylation, methylation, ubiquitinilation or glycosylation. The binding is mediated by three or more partners, where one or more of the partners is not or not completely of proteinaceous nature. This sequence is one of 47 PCR primers (see ABK16683-ABK16729) associated with the construction of the recombinant transmembrane receptor, described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant receptor comprising a ligand binding domain and a domain that comprises a heterologous bait polypeptide, useful for screening compounds that disrupt compound-compound binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR; primer, ss; recombinant receptor; ligand binding domain; heterologous bait polypeptide; protein-protein interaction; screening.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                     / Match 60.8%; Score 14.6; DB 6; Length 30; Local Similarity 81.0%; Pred. No. 9.1e+03; Nes 17; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.6; DB 8; Length 30;
Pred. No. 9.1e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant receptor-related construction PCR primer #18.
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                          Sequence 30 BP; 7 A; 5 C; 11 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tavernier J, Vandekerckhove J;
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TGCCAACCCTGCTCTGGAGGC 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2001; 2001EP-00202569.
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Best Local Similarity 81.0%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL52021 standard; DNA; 30
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                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                        Matches
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Mcswiggen J;

Pavco P,

us-10-788-779-3.rng

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Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                          Claim 37; Page 76; 164pp; English
                                                            11-APR-2000; 2000WO-US009721
                                                                                  99US-0129390P
                                                                                                         (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                     WPI; 2000-647423/62.
                                                                                                                               Zwick M,
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 15; Conserv
             WO200061729-A2.
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                                                                                   12-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                    19-OCT-2000
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                                                                                                                               Blatt L,
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the preparation of synthetic nucleic acid molecules which have altered transcriptional regulatory sequences compared to the wild-type. These sequences are then transcribed with less frequency compared to the wild-type. In particular, the invention relates to altered luciferase sequences. This can be used to detect weak promoter activity, to express fusion proteins, to detect and/or measure levels of gene expression, subcellular localisation or targeting, in life science research, agrogenetics, gene therapy, developmental science and pharmaceutical development. The present sequence is an oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                  transcriptional characteristics when expressed in a cell, for e.g making fusion proteins, by altering a wild type or another synthetic nucleic
                                                                                                                                                                                                                                                                                                                                                     a synthetic nucleic acid molecule with reduced inappropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical development. The present sequence is an oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                  Luciferase, synthetic nucleic acid; transcriptional characteristic;
transcription; codon usage; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribozyme; erythropoietin; granulocyte colony stimulating factor;
                                                                                           Green/red click beetle luciferase preparing oligo SEQ ID NO:169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.6; DB 6; Length 40;
Pred. No. 9.3e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40 BP; 4 A; 10 C; 16 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                           Paguio A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hammerhead ribozyme substrate #902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
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                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 6; 294pp; English.
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                                                                                                                                                                                                                                                                                                           Zhuang Y,
                                                                                                                                                                                                                                     24-AUG-2001; 2001WO-US026566.
                                                                                                                                                                                                                                                            24-AUG-2000; 2000US-00645706.
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Best Local Similarity 81.0%;
Matches 17; Conservative
                       ABL99201 standard; DNA; 40
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                                                                     (first entry)
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                                                                                                                                                                                                                                                                                   (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                WPI; 2002-304140/34.
                                                                                                                                                                                                                                                                                                           Wood MG,
                                                                                                                                                                                      WO200216944-A2
                                                                                                                                                                                                                                                                                                                                                                                           acid sequence.
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                                                                     28-JUN-2002
                                                                                                                                                                                                               28-FEB-2002
                                                                                                                                                      Coleoptera.
                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                       Preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF02607;
                                              ABL99201;
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RESULT 14
           AAF02607
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consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha
The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRR-2 and/or the CAAT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant polynucleotide encoding human elastase I mutant useful for determining the predisposition of a subject to cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; elastase I; chromosome 12q13; mutant; serine protease; eczema; hyperproliferative skin condition; psoriasis; lupus erythmatosis; erythema; cancer; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reverse primer used to amplify a human elastase I gene exon 8.
                                                                                                                                                                                                                                                                                                                                                                                               60.0%; Score 14.4; DB 3; Length 17; llarity 93.8%; Pred. No. 1.1e+04; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 2 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ACCCTGCTCTGGAGGC
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us-10-788-779-3.rng

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PCR primers AAC62091-92 were used to amplify a human elastase I gene fragment. The elastase I gene maps to chromosome 12q13. Elastase is a serine protease, and is localised in the basal layer of the mammalian skin. The specification describes a mutant elastase I, with a frame shift mutation in any one of the codons 207-225. The mutation results in the disruption of the carboxy terminal of the protein, and possibly affects substrate binding. An allele encoding a mutant elastase I can be detected to determine the predisposition of a subject to a hyperproliferative skin condition (e.g. psoriasis, eczema, lupus erythmatosis and erythema) or
hyperproliferative skin condition such as psoriasis, eczema,
                                                                           Disclosure; Page 20; 35pp; English.
                             erythematosis.
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Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

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Gaps
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60.0%; Score 14.4; DB 3; Length 20; 93.8%; Pred. No. 1.1e+04; ive 0; Mismatches 1; Indels
                    .93.88;
                  Best Local Similarity 93.8
Matches 15; Conservative
Query Match
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21 ACCCTGCTCTGGAGG 20 6 AACCCTGCTCTGGAGG ò

AAL29368 standard; DNA; 50 RESULT 17 AAL29368

AAL29368;

(first entry)

24 - JAN - 2002

Human SNP oligonucleotide #2576.

Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; euroropicetive; antiinficrobial; gene therapy; vaccine; amylase; cancer; amylode protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioseterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.

Homo sapiens.

WO200147944-A2

05-JUL-2001

28-DEC-2000; 2000WO-US035498

nervous system disease; ss.

WO200147944-A2.

05-JUL-2001.

Homo sapiens

99US-0173419P

28-DEC-1999;

27-DEC-2000; 2000US-00173419

(CURA-) CURAGEN CORP.

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WPI; 2001-465210/50. Shimkets RA, Leach

28-DEC-2000; 2000WO-US035498

99US-0173419P. 28-DEC-1999;

27-DEC-2000; 2000US-00173419.

(CURA-) CURAGEN CORP.

Leach M; Shimkets RA,

WPI; 2001-465210/50.

cyclins, polymerases, treating, e.g. cancer, Polymorphic nucleic acids encoding e.g. amylases, oncogenes and histones, useful for diagnosing and autoimmune diseases and infections.

Claim 1; Page 2121; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, anglopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, Gpotein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.

Claim 1; Page 3504; 4143pp; English.

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proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotides and the peptides encoded by them oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lugus erythromatosus and Grave's disease), inflammation, cancer leugamin, diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; euroropotective; antimicrobial; gene therapy; vaccine; amqlase; cancer; amyloid protein; angiopotetin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; cyclin; polymerased protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thiosesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                    60.0%; Score 14.4; DB 4; Length 50;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                       Sequence 50 BP; 6 A; 21 C; 15 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                  Pred. No. 1.2e+04; ; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                  2 TGCCAACCCTGCTCTG 17
                                                                                                                                                                                                                                                    93.88;
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                                                                                                                                                                                                                                                                                                                         22 TGCCAGCCCTGCTCTG
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                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                  Local Similarity
Les 15; Conserv
                                                                                                                                                                          organisms
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                                                                                                                                                                                                                                                                    Matches
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AAL34152/
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rheumatoid arthritis.
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                  associated with inappropriate expression of the proteins listed above. Bisorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's 6 disease, inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel antisense compound targeted to nucleic acid encoding SMRT (silencing mediator for retinoid and thyroid hormone action), useful for treating animal having disease associated with SMRT such as cancer,
be used in the prevention, diagnosis and treatment of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMRT; silencing mediator for retinoid and thyroid hormone action; SMRT inhibitor; cytostatic; antiinflammatory; antiarthritic; antirheumatic; antirheumatic; antirheumatic; autienses therapy; inflammatory disorder; rheumatoid arthritis; hyperproliferative disorder; cancer; leukaemia; breast cancer; human; phosphorothioate; ss; chimeric.
                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                     Score 14.4; DB 4; Length 50;
Pred. No. 1.2e+04;
0; Mismatches 6; Indels
                                                                                                                                                                                                   Sequence 50 BP; 10 A; 21 C; 10 G; 9 T; 0 U; 0 Other;
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16..20
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                                                                                                                                                                                                                                                                                                                         1 ATGCCAACCCTGCTCTGGAGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG86318 standard; DNA; 20 BP
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                                                                                                                                                                                                                                           60.0%;
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2004
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                                                                                                                                                                 organisms
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  them may
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                                                                                                                                                                                                                                           Query Match
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The present invention describes a compound (1) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding SMRT (silencing mediator for retinoid and thyroid hormone action), where (1) specifically hybridises with the nucleic acid molecule encoding SMRT and inhibits expression of SMRT. (1) specifically hybridises with at least 8-nucleobase portion of a preferred target region on nucleic acid molecule encoding SMRT. Also caecribed is a composition (11) comprising (1) and a carrier or diluent. (1) and (11) have cytostatic, antiinflammatory, antiarthritic and antirheumatic activities, and can be used in antisense therapy, and as SMRT expression inhibitors. (1) is also useful for inhibiting the expression inhibitors. (1) is also useful for inhibiting an animal having a disease or condition associated with SMRT, e.g., inflammatory disorder such as rheumatoid arthritis, or a hyperproliferative disorder such as rheumatoid arthritis, or a hyperproliferative disorder such as research reagents and breast cancer, by inhibiting the expression of SMRT. (1) is useful for diagnostics, therapeutics, cypophylaxis and as research reagents and kits. The present sequence compliance is designated as SEQ ID NO:30 in cinhibits human SMRT, which is used in an example from the present cinvention. N. B. The present sequence is designated as SEQ ID NO:30 in example 15 but corresponds to SEQ ID NO:32 in the Sequence Listing.
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Example 15; SEQ ID NO 32; 260pp; English.
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Best Local Similarity
Local 16; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-2003.
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The present invention describes a compound (I) 8-50 nucleobases Renal cell carcinoma differentially expressed gene probe #3906. Sequence 20 BP; 4 A; 5 C; 9 G; 2 T; 0 U; 0 Other; Example 15; SEQ ID NO 63; 260pp; English. 3 GCCAACCCTGCTCTGGAGG 21 19 ścóckácciráchicháchia 1 BP. Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative (21-NOV-2003; 2003WO-US037481. 21-NOV-2002; 2002US-0427982P. 03-APR-2003; 2003US-0459782P. ADP17501/c ID ADP17501 standard; DNA; 25 (first entry) in the Sequence Listing TWINE N C. BURCZYNSKI M H TREPICCHIO W I (DORN/) DORNER A. (STOV/) STOVER J A. (SLON/) SLONI D K. WO2004048933-A2. (AMHP) WYETH 26-AUG-2004 Homo sapiens 10-JUN-2004. ADP17501; TWIN/) (BURC/) TREP/) RESULT 21 ઠે g

The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood ample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from compared to PBMCs of normal humans. The solid tumor is chosen from compared to ample comprises enriched PBMCs. The peripheral blood sample (claimed). (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples is also another solid tumors. This sequence corresponds to a probe to detect a gene that is differentially expressed and detected by the method Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes. PCR; amplification; primer; filamentous fungus; recombinant DNA; Recombinant filamentous fungus produced by gene conversion - has integrated into two or more mostly homologous DNA domains of its chromosomes, used in the fermentation industry. Length 25; Indels Sequence 25 BP; 6 A; 6 C; 8 G; 5 T; 0 U; 0 Other; Score 14.2; DB 12; Pred. No. 1.4e+04; 0; Mismatches 3; Disclosure; SEQ ID NO 4237; 350pp; English Bovenberg RAL; Penicillium chrysogenum primer 24. . 1 ATGCCAACCCTGCTCTGGA 19 19 Argécharcachica 1 AAV68288 standard; DNA; 24 BP 59.2%; 98WO-EP002070 97EP-00201091 01-MAR-1999 (first entry) Swinkels BW, (KONN) GIST-BROCADES BV. 16; Conservative DNA domain; fermentation. Penicillium chrysogenum. WPI; 1998-609917/51. Query Match Best Local Similarity of the invention. 09-APR-1998; 11-APR-1997; WO9846772-A2 22-OCT-1998. Selten GCM, Synthetic. AAV68288; Matches RESULT 22 AAV68288 à g targeted to a nucleic acid molecule encoding SMRT (silencing mediator for retinoid and thyroid hormone action), where (1) specifically hybridises with the nucleic acid molecule encoding SMRT and inhibits expression of SMRT. (1) specifically hybridises with at least 8-nucleobase portion of a preferred target region on nucleic acid molecule encoding SMRT. Also described is a composition (11) comprising (1) and acarrier or diluent. (1) and (11) have cytostatic, antiinflammatory, antiarthritic and antirheumatic activities, and can be used in antisense therapy, and as SMRT activities, and can be used in antisense therapy, and as SMRT in cells or tissues. (1) is useful for treating an animal cof SMRT in cells or tissues. (1) is useful for treating an animal having a disease or condition associated with SMRT, e.g., inflammatory composition as rheumatoid arthritis, or a hyperproliferative disorder such as rheumatoid arthritis, or a hyperproliferative disorder such as rheumatoid arthritis, or a hyperproliferative disorder such as research reagents and breast cancer, by inhibiting the expression of SMRT. (1) is useful for diagnostics, therapeutics, represente a human SMRT target region sequence is prophylaxis and as research reagents and kits. The present sequence represents a human SMRT target region sequence which is used in an example from the present invention. N. B. The present sequence is ö ss; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression; probe. Gaps ö Score 14.2; DB 12; Length 20; Pred. No. 1.3e+04; 0; Mismatches 3; Indels (

The primers AAV68265-V68314 are used in examples of the construction of new filamentous fungus with a recombinant DNA molecule integrated into at least 2 substantially homologous DNA domains of its chromosome(s), and

Example, Page 33; 171pp; English.

Stover JA;

Dorner A,

Trepicchio WL,

Burczynski ME,

ÖĶ;

Sloni

Twine NC,

WPI; 2004-460799/43

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Gaps

; 0

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where the DNA domains are not the ribosomal DNA repeats. The recombinant fungus is used in the fermentation industry, and the DNA domains can be further multiplied with integrated recombinant DNA through gene conversion or amplification. The new fungi provide greater versatility compared with available systems, because the fungus is not confined to the use of deficient selectable marker genes for transformation, and is not confined to the use of only ribosomal DNA as target sequences for integration. Also, the fungi provide greater genetic stability of the integrated multiple copies compared with conventional recombinant fungilin which recombinant DNA are randomly integrated in tandem arrays. The genotype of the fungi can be completely defined, facilitating regulatory
                                                                                                                                                                                                                                                                                                                                                               approval, and the phenotype will be more predictable
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Query Match 58.3%; Score 14; DB 2; Length 24; Best Local Similarity 77.3%; Pred. No. 1.7e+04; Matches 17; Conservative 0; Mismatches 5; Indels

Sequence 24 BP; 3 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

ö

Gaps

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3 GCCAACCCTGCTCTGGAGGCCT 24 1 GCCTACTCTGTTCTGGAGGCT 22 ò 셤

ADC06568 standard; DNA; 25 BP (first entry) 18-DEC-2003 ADC06568; RESULT 23

Human Na/H exchanger-like protein 1 gene oligonucleotide #3015.

ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein; NHELP1; passive replacement therapy; vaccine; diagnosis.

Homo sapiens

EP1273660-A2.

08-JAN-2003.

25-JAN-2002; 2002EP-00001160

30-JAN-2001; 2001WO-US000666

23-MAY-2001; 2001US-00864761. 21-DEC-2001; 2001US-0343331P.

(AEOM-) AEOMICA INC

WPI; 2003-302724/30.

៧ New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as passive replacement therapy or as a vaccine for treating or preventing disorders associated with aberrant expression or activity of human NHELP1.

Example 2; SEQ ID NO 3055; 468pp; English.

The invention relates to a nucleic acid molecule which encodes a Na+/H+ exchanger like protein (NHELP1). The NHELP1 nucleic acid molecule, NHELP1 polypeptide, an antibody against the protein or its antigen-binding fragment is useful in therapy. The NHELP1 nucleic acid molecule, NHELP1 polypeptide and an agonist are particularly useful for manufacturing a medicament for treating or preventing a disorder associated with decreased expression or activity of human NHELP1. The antibody or its antigen-binding fragment, and an antagonist, are useful for manufacturing a medicament for treating or preventing a disorder associated with increased expression or activity of human NHELP1. The NHELP1 nucleic acid or protein is useful as passive replacement therapy, as a vaccine, or in

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The invention relates to a nucleic acid molecule which encodes a Na+/H+
exchanger like protein (NHELP1). The NHELP1 nucleic acid molecule, NHELP1
polypeptide, an antibody against the protein or its antigen-binding
fragment is useful in therapy. The NHELP1 nucleic acid molecule, NHELP1
polypeptide and an agonist are particularly useful for manufacturing a
medicament for treating or preventing a disorder associated with
acreased expression or activity of human NHELP1. The antibody or its
antigen-binding fragment, and an antagonist, are useful for manufacturing
a medicament for treating or preventing a disorder associated with
increased expression or activity of human NHELP1. The NHELP1 nucleic acid
or protein is useful as passive replacement therapy, as a vaccine, or in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as passive replacement therapy or as a vaccine for treating or preventing disorders associated with aberrant expression or activity of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
NHBLP1; passive replacement therapy; vaccine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                      Human Na/H exchanger-like protein 1 gene oligonucleotide #3016.
diagnostic methods. This sequence corresponds to a 256-mer oligonucleotide spanning the sequence of the human NHELP1 gene (ADC03514).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the sequence of the human NHELP1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.3%; Score 14; DB 10; Length 25; Best Local Similarity 77.3%; Pred. No. 1.7e+04; Matches 17; Conservative 0; Mismatches 5; Indels
                                                                                                               Score 14; DB 10; Length 25;
Pred. No. 1.7e+04;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence corresponds to a
                                                                            Sequence 25 BP; 4 A; 5 C; 8 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 4 A; 4 C; 9 G; 8 T; 0 U; 0 Other;
                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 3056; 468pp; English.
                                                                                                                                                                                     22
                                                                                                                                                                                                            25 ACGCCAACTCTGATCTGAAGCC 4
                                                                                                                                                                                       1 ATGCCAACCCTGCTCTGGAGGC
                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US000666.
23-MAY-2001; 2001US-00864761.
21-DEC-2001; 2001US-0343331P.
                                                                                                                 58.3%;
ilarity 77.3%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2002; 2002EP-00001160
                                                                                                                                                                                                                                                                                                              ADC06569 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic methods. This oligonucleotide spanning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-302724/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AEOM-) AEOMICA INC
                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1273660-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JAN-2003.
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                                                                                                                                                                                                                                                                                                                                                   ADC06569;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gu Y;
                                                                                                                                                                                                                                                                                               ADC06569,
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cytostatic;

human; INSP105; growth hormone; antiinflammatory;

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for the T. gondii tachyzoite major surface antigen P30 (AAR57065). DNA fragment np30.873 encoding T. gondii antigen P30.291 was obtained by PCR amplification of a clone encoding the P30 gene using the primers given in AAQ70259-60. P30.291 comprises amino acids 46.336 of P30, but is functionally equivalent to the natural protein. Deletion of the Neterninal hydropholic region of P30 allows improved secretion from producer cells, for use in toxollasmosis vaccine production. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of packaging defective alpha-virus expression vectors - for prodn. of protective cpds. for protecting animals from disease, partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence is provided (AAQ70254) that contains the entire coding region
                                                                                                                                                                                                                   Toxoplasma gondii; toxoplasmosis; P30; P30.291; nP30.873; trachyzoite;
                                                                                                                                                                                                                                surface antigen; vaccine; alpha-virus; vector; PCR;
polymerase chain reaction; amplification; primer; secretion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.3%; Score 14; DB 2; Length 35; Best Local Similarity 77.3%; Pred. No. 1.7e+04; Matches 17; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35 BP; 6 A; 13 C; 10 G; 6 T; 0 U; 0 Other;
          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 81; 128pp; English.
          1 ATGCCAACCCTGCTCTGGAGGC
                                24 Acecchacrerearcreadece
                                                                                                    BP.
                                                                                                                                                                                          T. gondii P30.291 PCR primer.
                                                                                                                                                                                                                                                                                                                                                   94WO-US001398.
                                                                                                                                                                                                                                                                                                                                                                             93US-00015414
                                                                                                 AAQ70259 standard; DNA; 35
                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Grieve RB, Xiong C;
                                                                                                                                                                                                                                                                                                                                                                                                       (PARA-) PARAVAX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-279381/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxoplasmosis.
                                                                                                                                                                                                                                                                                                                                                     08-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                             08-FEB-1993;
                                                                                                                                                                                                                                                                                                 WO9417813-A1
                                                                                                                                                    25-MAR-2003
15-MAR-1995
                                                                                                                                                                                                                                                                                                                           18-AUG-1994.
                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                           AAQ70259;
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The present invention describes an INSP105 polypeptide comprising: (a) a composition acid sequence given in SEQ ID NO:8 (ADP71313); (b) a fragment common with (1); or (c) a functional equivalent of (1) or determinant in common with (1); or (c) a functional equivalent of (1) or (2). Also described: (1) a purified nucleic acid molecule which encodes the polypeptide; (2) a vector comprising the nucleic acid molecule; (3) a certifically to the growth hormone polypeptide; (5) a compound that specifically to the growth hormone polypeptide; (5) a compound that composition comprising the polypeptide; (7) a patient; (7) a pharmaceutical composition comprising the polypeptide; (8) a vaccine of composition comprising the polypeptide or nucleic acid molecule; (9) a composition comprising the polypeptide or nucleic acid molecule; (9) a composition comprising the polypeptide or nucleic acid molecule; (9) a composition comprising the polypeptide or nucleic acid molecule; (9) a composition comprising the polypeptide or nucleic acid molecule; (9) a composition comprising the polypeptide or nucleic acid molecule; (9) a composition disease in a patient; (11) a method for treating a disease; (13) a transgenic or knockout non-human comprisition and disease; (13) a transgenic or knockout non-human comprisition and disease; (13) a transgenic or knockout non-human comprotective, virucide, osteopathic, antibacterial, fungicide, conceptive, virucide, osteopathic, antibacterial, fungicide, anorectic, nephrotropic and cardiant activities. The INSP105 polypeptide or activity. The polypeptide, nucleic acid molecule, vector, host cell, is useful as a growth hormone or as a modulator of growth hormone or as a modulator of growth hormone or as a modulator of growth hormone or expression as a silver Russian expression and sector, disorders; preponenting a disease associated with growth and associated with 
neuroprotective; virucides osteopathic; antibacterial; fungicide; anorectic; nephrotropic; cardiant; reproductive disorder; pregnancy disorder; gestational trophoblastic disease; pregnancy disorder; gestational trophoblastic disease; growth disorder; gevel profiterative disorder; sliver-Russeals syndrome; growth disorder; growth hormone deficiency; Cushing's disease; endocrine disorder; cell proliferative disorder; neoplasm; carcinoma; tumour; melanoma; adenocarcinoma; choriocarcinoma; osteosarcoma; angiogenesis; myeloproliferative disorder; autoimmune disorder; inflammatory disorder; cardiovascular disorder; neurological disorder; pain; metabolic disorder; diabetes mellitus; osteoporosis; obesity; cachexia; AIDS; renal disease; lung injury; agging; infection; PCR; primer; ss; chromosome 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New INSP105 polypeptides, useful in preparing a composition for treating or preventing a disease associated with growth hormone proteins, e.g. cell proliferative, inflammatory or neurological disorders or infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carcinoma, pituitary tumour, ovary tumour, melanoma, lung, colorectal, breate, pancreata, head and neck, placental site trophoblastic tumour, adenocarcinoma, orboriocarcinoma, osteosarcoma and other solid tumours; angiogenesis; myeloproliferative disorders; autoimmune/inflammatory disorders; cardiovascular disorders; neurological disorders; pain, metabolic disorders including diabetes mellitus; osteoporosis; obesity cachexia; AIDS; renal disease; lung injury; ageing; or infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syndrome; growth disorders; growth hormone deficiency; Cushing's disecendocrine disorders; cell proliferative disorders, including neoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Tiani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Power C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fagan RJ, Phelps CB, Rodrigues TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 55; 84pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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Gaps

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1 ATGCCAACCCTGCTCTGGAGGC 22 Areccarcceegreragagre 4

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25

Human INSP105 PCR primer INSP105-exon4R.

(first entry)

23-SEP-2004

ADP71324;

BXXXXX

ADP71324 standard; DNA; 36

ADP71324/c RESULT 26

Sequence 40 BP; 12 A; 7 C; 15 G; 6 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for designing polymeric nucleic acid probes whose sequence is complementary to naturally occurring polymeric nucleic acids. The naturally occurring nucleic acids are composed of an alternative exon surrounded by seamlessly preceding and/or following nucleic acid sequences. The invention also claims an oligonucleotide probe for an alternatively splicing exon, the probe being complementary to a sequence comprising the exon sequence and flanking nucleic acids; and a series of probes, designed for a flanked exon nucleic acids; and a series of probes, designed for a flanked exon plognucleotide (FEO) array. The method is useful for designing of polymeric probes. The method is useful for obtaining detectable hybridisation levels between FEOs and alternative exons imbedded in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Designing of polymeric nucleic acid probes, useful for developing flanked exon oligonuclectide arrays used in expression profiling or for detecting the presence or expression levels of segments within genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcripts, when those alternative exons are of a length that does not ensure a reliable hybridisation, i.e. small exons. The method is especially designed for the detection of so-called small exons, i.e. fragments less than 70 base pair long and especially less than 40 base pair long. The method is useful for developing arrays of FEO used in expression profiling or other techniques aimed at detecting the presence or expression levels of segments within genes. The present sequence represents a symmetric FEO, a three exon oligonucleotide (THEO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; flanked exon oligonucleotide; FEO; three exon oligonucleotide; THEO;
including viral infection, bacterial infection, fungal infection or parastic infection. The present sequence respresents a PCR primer for human INSP105, which is used in an example from the present invention. The human growth hormone-related gene family is located on chromosome
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                        ö
                                                                                                                                                                           Length 36;
                                                                                                                                                                                                                    5; Indels
                                                                                                                              Sequence 36 BP; 6 A; 13 C; 7 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                      ch 58.3%; Score 14; DB 12; 1 Similarity 77.3%; Pred. No. 1.7e+04; 17; Conservative 0; Mismatches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flanked exon oligonucleotide THEO Hgh4-V-4-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Villahermosa JML;
                                                                                                                                                                                                                                                                                         34 ATCCAAACGCTGATGTGGAGGC 13
                                                                                                                                                                                                                                                              1 ATGCCAACCCTGCTCTGGAGGC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 9; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ99501 standard; DNA; 40 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-604470/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hybridisation; array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RUFFLES G K.
                                                                                                                                                                                               Local Similarity
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                                                                                          17g22-24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD099501;
                                                                                                                                                                           Query Match
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Matches
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ADQ99501
    88888888
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The invention relates to a novel method for designing polymeric nucleic acid probes whose sequence is complementary to naturally occurring to polymeric nucleic acids. The naturally occurring nucleic acids are composed of an alternative exon surrounded by seamlessly preceding and/or following nucleic acid sequences. The invention also claims and/or composed for an alternatively splicing exon, the probe being complementary to a sequence comprising the exon sequence and flanking nucleic acids; and a series of probes, designed for a flanked exon componentary to a sequence comprising the exon sequence and flanking nucleic acids; and a series of probes, designed for a flanked exon conjonucleotide (FEO) array. The method is useful for obtaining detectable hybridisation levels between FEOs and alternative exons imbedded in cranscripts, when those alternative exons are of a length that does not ensure a reliable hybridisation, i.e. small exons. The method is useful for developing and especially less than 40 base pair long. The method is useful for developing arrays of FEO used in expression profiling or other techniques aimed at detecting the presence or expression profiling or stream arrays of respectable for the designed and a fragments within genes. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Designing of polymeric nucleic acid probes, useful for developing flanked exon oligonucleotide arrays used in expression profiling or for detecting the presence or expression levels of segments within genes.
                                                                                                                                                                                                                                                                                                                                                                            ss; flanked exon oligonucleotide; FEO; three exon oligonucleotide; THEO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represents a symmetric FEO, a three exon oligonucleotide (THEO).
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  Length 40;
Score 14; DB 13; Length 40
Pred. No. 1.7e+04;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40 BP; 11 A; 8 C; 15 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        Flanked exon oligonucleotide THEO Hgh4-V-3-s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cimadevilla JCR, Villahermosa JML;
                                                                                                      1 ATGCCAACCCTGCTCTGGAGGC 22
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                                                                                                                                                                                                                     BP
Query Match
Best Local Similarity 77.3%;
Matches 17; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-2004; 2004WO-GB000522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-FEB-2003; 2003GB-00003006
                                                                                                                                                                                                                   ADQ99500 standard; DNA; 40
                                                                                                                                                                                                                                                                                            04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   hybridisation; array
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004070060-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                          ADQ99500;
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To mercinous and compositions for identifying individuals who have at least one polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ0887 using a craisety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of arrays and PCR-based methods. The invention also encompasses methods of callating and screening drugs using genetic polymorphism data, genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between the superposed of arrays are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful to frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms to grud therapies based upon the genetic profile of individual patients. This would not only take the genetic loreling the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying individuals having a polymorphism, useful for determining th effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                                                         Human; drug metabolising enzyme; gene; drug metabolism; chromosome 12; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; ds.
                                                                                                                                                                                                                                                                   Human glutathione-S-transferase MGST1 gene polymorphic site, #6322.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
replace(20. .23,CT)
/*tag= a
  22
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  1 ATGCCAACCCTGCTCTGGAGGC
                                    Arccaacgercarcrecaege
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                                                                                                                                           BP.
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02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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                                                                                                                                         ABZ49539 standard; DNA; 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variation
                                                                                                                                                                                 ABZ49539;
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                                                                                                  RESULT 29
                                                                                                                       ABZ49539
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clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time time for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers appecific for a sequence selected from ABZ43217-ABZ50897 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying individuals having a polymorphism, useful for determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug metabolism; chromosome 12;
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          effectiveness or side effect of a drug or treatment protocol, compridetecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human glutathione-S-transferase MGST1 gene polymorphic site, #2696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; drug metabolising enzyme; gene; drug metabolism; chromos
polymorphic site, drug evaluation; drug screening; genotyping;
genetic profiling; therapeutic customisation; adverse reaction;
clinical trial; drug approval; ds.
                                                                                                                                                                                                                             6; Length 42;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                        Sequence 42 BP; 13 A; 16 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                             58.3%; Score 14; DB 6; Le
100.0%; Pred. No. 1.7e+04;
ive 0; Mismatches 0;
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replace(20. .23,CT)
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ45912 standard; DNA; 42 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-2000; 2000JP-00399443.
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27-AUG-2001; 2001JP-00256862.
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                                                                                                                                                                                                                             58.3%;
                                                                                                                                                                                                                                                                                                       7 ACCCTGCTCTGGAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; drug
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                                                                                                                                                                                                                             Query Match
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constraining and screening drugs using genetic polymorphism data. Genetic polymorphisms data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur in the above respects as they are stable in populations, occur in the above respects as they are stable in populations occur in genes encoding drug metabolising enzymes allows the customisation of frequently, and have lower mutation rates than other genome variations in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients.

This would not only take the guesswork out of selecting the drug with the companies therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and suppropriate patient populations. The methods, data and compositions of the invention may therefore lead to a mincrease in the range of the invention may therefore lead to a mincrease in the range of the invention may therefore lead to a mincrease in the range of the invention may therefore lead to a mincrease in the range of the invention may therefore lead to a mincrease in the approved, the length of time patients are on medication and the number of adverse drug creactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different constraints a patient needs to take before finding an effective therapy

58.3%; Score 14; DB 6; Length 42; 100.0%; Pred. No. 1.7e+04; Sequence 42 BP; 13 A; 16 C; 7 G; 6 T; 0 U; 0 Other; Query Match Best Local Similarity 100. Matches 14; Conservative

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Gaps ö

0; Indels

100.0%; Prea. ... 7 ACCCTGCTCTGGAG 20 19 Accerdenciadas 32 ò g

ACH66436 standard; DNA; 20 BP. (first entry) 16-OCT-2003 ACH66436; ACH66436/C
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AC
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ACH66
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BDB Sense
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BC Se RESULT 31

Sense PCR primer used to amplify AOC3.

Promoter; ss, genomic DNA; gDNA; untranslated region; UTR; DNA high-density microarray; biosite; large scale production; gDNA probe; microarray; Type I primer; PCR; primer.

sapiens Synthetic Ношо

Location/Qualifiers modified base

note= "OTHER= linked to the bacteriophage T7 promoter ACH66426)" /*tag= a /label= OTHER

US2003073085-A1.

17-APR-2003.

05-OCT-2001; 2001US-00972469

05-OCT-2001; 2001US-00972469

(LAIF/) LAI F. (ZHOU/) ZHOU D.

Zhou D; Œ,

WPI; 2003-555942/52

Amplifying expressed genetic sequences from genomic DNA of mammalian or higher order plant species for printing on DNA microarrays, involves using the 3' untranslated region of the gene sequence.

Disclosure; Page 6; 15pp; English.

The invention discloses a method for amplifying expressed genetic
sequences from genomic DNA (gDNA) from mammalian or higher order plant
species. The method involves identifying a 3' untranslated region (UTR)
of a gDNA sequence, designing probe, performing PCR, separating the
product by size differentiation and performing a second PCR to amplify
the predetermined sequence. Also claimed is a biological analysis device,
comprising a substrate and an array of a set of expressed genetic
sequences, located on the substrate, which are generated by the method
above and a DNA high-density microarray comprising a substrate upon which
cs are deposited an array of blosites of genomic DNA fragments having the
sequence of at least one exon, and absent polyadanine and vector
sequences, where the genomic DNA fragments have a sequence length of from
about 75-2000 nucleotides. The method is efficient for amplifying gene
sequences, enables large-scale production of DNA sequences, generates
crapped quantities of gDNA probes, which enables greater efficiency for
printing in microarray formats, fabricates high-density DNA arrays of
enhanced, widely varying genetic content and abstains from using RNAderived sequences by simple PCR amplifications without cloning. The
method produces amplified sequences that have greater specificity and
size consistency than that observed with cDNA fragments, and allows for
greater signal sensitivity than oligonoucloades. The sequence of
sa Type I gene specific primer which is linked at its 5' termini to the
construction producer.

Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Gaps ö 57.5%; Score 13.8; DB 9; Length 20; 88.2%; Pred. No. 2e+04; tive 0; Mismatches 2; Indels Best Local Similarity 88.2 Matches 15, Conservative Query Match

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18 2 TGCCAACCCTGCTCTGG 17 reschacechaereres ò 요

ABZ84928 standard; DNA; 20 BP RESULT 32 ABZ84928

17-OCT-2003 (first entry) ABZ84928;

Human oligonucleotide sequence.

Human; antisense; lung dysfunction, nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodiation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

(EPIG-) EPIGENESIS PHARM INC.

us-10-788-779-3.rng

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intitation codon, coding regain, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal alrawy dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an preventing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, for reacting bronchoconstriction, lung allammation, lung allargies, or a respiratory disease or condition. Note: The sequence date for this patent is not represented in the printed a specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                      Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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  Katz E, Pabalan J, Aguilar D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.5%; Score 13.8; DB 10; Length 20; 88.2%; Pred. No. 2e+04; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 1 A; 10 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human transglutaminase-derived oligo SEQ ID 170.
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                                                                                                                                                                                                           Claim 15; SEQ ID NO 170; 872pp; English.
Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                                                              WPI; 2003-229219/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200285309-A2
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                                                                                                                                                                     ubiquinone.
                 Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABD21158;
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ABD21158
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This invention describes a novel composition (a) a first active agent, comprising oligomucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and bronchoconstriction, respiratory tract inflammation, allergies and bronchoconstriction, respiratory tract inflammation, allergies and creducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligomucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA.

The invention also describes a kit, that comprises: (a) adelivery device, in separate containers, (b) the oligomucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a consosition comprises oligo and is administered to reduce the production or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The cultural disease or conditions and/or bronchoconstriction and/or lung with a disease or conditions and/or bronchoconstriction, and/or bronchoconstriction and associated with a disease or conditions used and activity and an analymonary disease, pulmonary contransion, emphysema, chronic obstructions, and or surfactant hypoproduction, are associated with a disease or conditions present in the target RNA serves to prevent the breakdown of the range oligos corresponding to the infinite present in the target RNA serves to prevent the breakdown of the bronchiles or condens the prevent of prevent or prevent or introduced adenosine content of the reduced activity pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human XT-II gene fragment for glucosaminoglycan reduction in glial scars.
                                                                                                                                                                                                                                                                                                                                 invention describes a novel composition (a) a first active agent
                                                                                                                                                                Pharmaceutical composition for treating asthma, has antisense oligonuclectide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss; vulnerary; cell therapy; glial scar; primary proteoglycan; chain initiation enzyme; elongation enzyme; neuronal regeneration;
                                               Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 2e+04;
0; Mismatches 2; Indels (
                                               Pabalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 1 A; 10 C; 6 G; 3 T; 0 U; 0 Other;
                                               Katz E,
                                                                                                                                                                                                                                                                                    Claim 15; SEQ ID NO 170; 763pp; English.
                                             Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
                                                                                                                                                                                                                                            bronchodilating agent.
                                                                                                                      WPI; 2003-093058/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucosaminoglycan.
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                                             Nyce JW, 1
Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO31281;
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The invention relates to methods of treating amyotrophic lateral sclerosis (ALS) or ALS-like symptoms that comprises inhibiting interleukin-1 converting enzyme (ICE) by gene therapy. A mutant ICE gene product can also be used for modulating programmed cell death accompanying ALS. Transgenic non-human animal (including progeny) containing a mutant ICE and SOD (ALS phenotype) gene are used to screen compounds for treating ALS. Inhibitors of an ICE-like caspase are used to cremate or prevent apoptosis resulting from traumatic brain injury (TBI), and to reduce the formation of reactive oxygen species following TBI. Diseases caused by acute and chronic disregulation of cell death, which are treated by the ICE gene product, include malignant and premalignant conditions, neurological, neurodegenerative disorders, heart disease, immune system disorders, intestinal disorders, kidney disease, disease, immune system disorders, intestinal disorders, kidney disease, aging, viral infections and acquired immune deficiency syndrome (AIDS). The methods, mutant genes and inhibitors of ICE enable a better understanding of the role of cell death and what triggers cell death in of the pathways mediating post traumatic apoptosis, which lead to novel pharmacotherapy of TBI. Sequences AMSOS223-27 represent PCR mutant property primers of mouse ICE cDNA used for constructing vectors containing mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; CAMP dependent kinase regulation subunit 8.8; cyclic AMP;
malignant tumour; inflammation; antagonist; reverse transcriptase PCR;
RT-PCR; primer; ss.
Treating amyotrophic lateral sclerosis (ALS) or ALS-like symptoms comprises inhibiting interleukin-1 converting enzyme (ICE) by gene therapy, useful for treating central nervous system damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human CAMP dependent protein kinase regulation subunit 8.8 polypeptide for treating diseases, such as, malignant tumors and inflammations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.5%; Score 13.8; DB 2; Length 25; 88.2%; Pred. No. 2e+04; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAMP dependent kinase regulation subunit 8.8 PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25 BP; 9 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                  Example 1; Page 29; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 CCCTGCTCTGGAGGCCT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS55668 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 88.2
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-733428/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CN1352179-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS55668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of reducing glucosaminoglycan (GAG) content in a gilal scar by inhibiting the expression of primary proteoglycans or the expression and/or activity of a chain initiation or elongation enzyme. The method is useful in reducing GAG content in a gilal scar and promoting neuronal regeneration. This sequence corresponds to a fragment of the human X-II gene used to identify sequences to which antisense oligos, ribozymes, RNAi constructs can designed.
                                                                                                                                                                                                                                                                                                                                           expression
a chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICE; ALS; SOD gene; interleukin-1 converting enzyme; mutant; cell death; amyotrophic lateral sclerosis; transgenic; ICE-like caspase; apoptosis; transmatic brain injury; TBI; neurological; neurodegenerative; kidney; heart disease; immune system; intestinal; aging; viral infection; AIDS; acquired immune deficiency syndrome; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                      Reducing GAG content in a glial scar comprises inhibiting the of primary proteoglycans or the expression and/or activity of initiation or elongation enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.5%; Score 13.8; DB 12; Length 20; 88.2%; Pred. No. 2e+04; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 2 A; 8 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 12; SEQ ID NO 103; 265pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine ICE mutagenic PCR primer m8p/s.
                                                                                                                                                                                               (UYCA-) UNIV CASE WESTERN RESERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CCCTGCTCTGGAGGCCT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cccrecerreadecer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX05223 standard; DNA; 25 BP
                                                                        31-OCT-2003; 2003WO-US034806.
                                                                                                                      01-NOV-2002; 2002US-0423082P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Friedlander RM;
                                                                                                                                                                                                                                            Silver J;
                                                                                                                                                                                                                                                                                         WPI; 2004-400518/37.
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Matches 15; Conserv
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                         21-MAY-2004
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                                                                                                                                                                                                                                              Grimpe B,
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Pred. No.

88.2%;

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Best Local Similarity 88.2
Matches 15; Conservative
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Matches
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                                                                                                                                ABK11967,
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                        The present invention discloses a new kind of polypeptide, human cAMP dependent kinase regulation subunit 8.8, polymorlectides encoding the polypeptide and a DNA recombination process to produce the polypeptide. The present invention also discloses applying the polypeptide in treating various diseases, such as malignant tumours, and inflammations. The present invention also discloses the antagonist resisting the polypeptide and its treatment effect. This sequence represents a PCR primer used to amplify DNA encoding the human cAMP dependent kinase regulation subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel isolated polypeptide of human mitochondrial endomembrane transferase TIM 23 11.66, the polynucleotide encoding the protein and a method for producing the procedinant protein. The protein of the invention and the nucleic acid encoding the protein may be used in diagnosis and treatment of mitochondrial disease, tumours, developmental disorders, inflammation, and immune disorders by gene therapy. The invention also discloses an antagonist of the TIM23 protein and therapeutic uses thereof. The present sequence represents the human mitochondrial endomembrane transferase specific oligonucleotide probe #1. This probe is used to probe the mitochondrial endomembrane transferase.
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mitochondrial endomembrane transferase; TIM 23 11.66; mitochondrial disease; tumour; developmental disorder; inflammation; immune disorder; gene therapy; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human mitochondrial endomembrane transferase TIM 23 11.66 for diagnosing and treating tumors, inflammation, and immune disorders.
                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                            Match 57.5%; Score 13.8; DB 6; Length 33; Local Similarity 88.2%; Pred. No. 2.1e+04; les 15; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                 Sequence 33 BP; 8 A; 8 C; 11 G; 6 T; 0 U; 0 Other;
Example 4; Page 19 (Disclosure); Opp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TIM23 specific oligonucleotide probe #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 22; 37pp; Chinese.
                                                                                                                                                                                                                                                   6 AACCCTGCTCTGGAGGC 22
                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                    ABK11966 standard; DNA; 41 BP.
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                                                                                                                                                                                                                                                                     ATCCCTACTCTGGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xie Y;
                                                                                                                                       .8 protein
                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                              ABK11966;
                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                     ABK11966/c
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Matches
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8

DB 6; Length 41;

57.5%; Score 13.8;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel isolated polypeptide of human mitochondrial endomembrane transferase TIM 23 11.66, the polynucleotide encoding the protein and a method for producing the recombinant protein. The protein of the invention and the nucleic acid encoding the protein may be used in diagnosis and treatment of mitochondrial disease, tumours, developmental disorders, inflammation, and immune disorders by gene therapy. The invention also discloses an antagonist of the TIM23 protein and therapeutic uses thereof. The present sequence represents the human mitochondrial endomembrane transferase specific oligonucleotide probe #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This probe is used to probe the mitochondrial endomembrane transferase cDNA of the invention
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; mitochondrial endomembrane transferase; TIM 23 11.66;
mitochondrial disease; tumour; developmental disorder; inflammation;
immune disorder; gene therapy; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human mitochondrial endomembrane transferase TIM 23 11.66 for diagnosing and treating tumors, inflammation, and immune disorders.
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Pred. No. 2.1e+04;
0; Mismatches 2; Indels
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41 BP; 12 A; 11 C; 15 G; 3 T; 0 U; 0 Other;
. 2.1e+04;
2;
                                                                                                                                                                                                                                                                                                                                                                                              Human TIM23 specific oligonucleoide probe #2.
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000CN-00116939
                                                                                                                                   41 ccagcccrccrccad
                                                                                                                                                                                                                                                        ABK11967 standard; DNA; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CCAACCCTGCTCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ccagcccrecrecrecas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI73671 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-241621/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
Les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200210397-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                               05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-2001
                                                                                                                                                                                                                                                                                                    ABK11967;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AA173060 to AA179867 represent isolated human polymorphic polymucleotide sequences (I), which contain single mucleotide polymorphisms (SNBs).

AAM53114 to AAM53329 represent peptides related to human polymorphic polymocleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polymeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polymeptides. For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polymeptides by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polymorphic polypeptides. The antibodies may also be used as uniques. The antibodies may also be used as uniques. The antibodies may also be used acond the production of antibodies may also be used acond the production of antibodies may also be used acond the production of antibodies may also be used to down regulate expression and activity. The antibodies may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used as diagnostic agents for detecting the presence of polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                       Human, single nucleotide polymorphism; SNP; genome; gene therapy; protein therapy; vaccine; probe; diagnostic assay; detection; quantitation; restorative therapy; polymorphic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic nucleic acid sequences, useful in genetic testing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%; Score 13.8; DB 4; Length 50; 88.2%; Pred. No. 2.1e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; BUB1-beta; hyperproliferative disorder; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50 BP; 8 A; 16 C; 17 G; 9 T; 0 U; 0 Other;
                 Human silent SNP containing nucleic acid SEQ:612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human BUBl-beta target sequence ISIS 196160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 241; 2653pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 ccardcrcrddagcccr 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP22838 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                       30-NOV-1999; 99US-0168138P.
29-NOV-2000; 2000US-00726173.
                                                                                                                                                                                                                                                                 30-NOV-2000; 2000WO-US032758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                July Match Barity 88.43, Best Local Similarity 88.43, The Best Local 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CCCTGCTCTGGAGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides in samples
                                                                                                                                                                                                                                                                                                                                                                                                             Leach M;
                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-356160/37.
                                                                                                                                                                                  WO200140521-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA,
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be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy
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1D ADP228:

XX ADP228:

XX 26-AUG

XX BE HUMAN

XX SS; BU

XX SS; BU

XX OS HOMO S
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Search completed: November 18, 2005, 11:52:22

Job time : 167.262 secs

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The invention relates to a new compound, having a sequence targeted to a nucleic acid encoding BUBI-beta, which specifically hybridises with the nucleic acid encoding BUBI-beta and inhibits expression of BUBI-beta. The oligomucleotide compound is useful for preparing a composition for treating a hyperproliferative disorder, e.g. cancer. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                           New oligonucleotide compound that inhibits expression of BUB1-beta, useful for preparing a composition for treating hyperproliferative disorder, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 56.7%; Score 13.6; DB 12; Length 20; Best Local Similarity 80.0%; Pred. No. 2.5e+04; Matches 16; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      represents a human BUB1-beta target sequence.
                                                                                                                                                                                                                                                                                                                  Example 15; SEQ ID NO 104; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 CAACCCTGCTCTGGAGGCCT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-2002; 2002US-00316459
                                                                               10-DEC-2002; 2002US-00316459
                                                                                                                                                 (ISIS-) ISIS PHARM INC
                                                                                                                                                                                  Jain R;
                                                                                                                                                                                                                 WPI; 2004-440338/41.
             US2004110149-A1
                                              10-JUN-2004
                                                                                                                                                                                  Bennett CF,
셤
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AG191198

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Database

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High gality sequence starts: 1 High gality sequence stops: 1 Source: INAGE Consortium, LLNL This clone is available royalty-free through LLNL, contact the INAGE Consortium (info@image.llnl.gov) For further information. Trace considered overall poor quality Possible reversed clone: polyT not found Insert Length: 965 Std Error: 0.00 Seg primer: -21ml3 High quality sequence stop: 1.
             AU102722 AU102722
AU102724 AU102724
AU1021601 ubb09f01.r
AZ474035 IM0296F18
AZ475952 IM0294121
AU103032 AU103032
AU397039 Eb25602.y
AU255522 AU255522
AZ75757 ZM0068E24
NB341 KK317F Hum
AZ7566605 IM0564L13
CG724386 1119081A0
CL528330 ASV5801.f
BIS21426 AC03081524
AA482116 ZV43c12.s
R48775 yj69c01.s1
AZ621187 IM0454F18
AZ827187 ZM0464F18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 35)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 bp mRNA linear EST 02-MAR-1: yc54a06.sl Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:84466 3' similar to gb:X02162 APOLIPOPROTEIN A-I PRECURSOR (HDMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 35
/organism="Homo sapiens"
/mol_type="mRNN"
/db_xref="GDB:501523"
/db_xref="taxon:9606"
/clone="IMAGB:84466"
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                 AU102722
AU102724
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Location/Qualifiers
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RESULT 1
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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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 1
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BH865457 SALK 0985
AZ809714 2M0073P16
T73421 Ye53808.81
AZ768397 1M056BD23
BM034402 BM034402
BX209982 Danio rer
T69149 Ye532008.81
AA917511 0152c07.8
BJ039939 BJ039939
AU103163 AU103164
AU103164 AU103166
AZ762084 1119062H0
CG72084 1119062H0
CG72084 1119062H0
CG72084 1119062H0
CG869098 AC0059 Sa
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AI323319 mh78a09.x
AU102721 AU102721
                                                                                                                      November 18, 2005, 11:22:09 ; Search time 1147.98 Seconds (without alignments) 795.779 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                            34239544 segs, 19032134700 residues
                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                   1 ATGCCAACCCTGCTCTGGAGGCCT 24
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Maximum Match 100%
Listing first 45 summaries
                                                                                     nucleic search, using sw model
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AA917511
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CG720584
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AU103164
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Gapop 10.0 , Gapext 1.0
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gb_htc:*;
gb_est4::*;
gb_est4::*;
gb_est6::*;
gb_gss1::*;
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seq length: 50
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Match
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14.6 14.4 14.4 14.4

Score

Result è 02-MAR-1995

Gaps

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45 bp mRNA linear EST 01-MAR-1995 yc62e05.81 Stratagene liver (#937224) Homo sapiens CDNA clone IMAGE:85280 3' similar to gb:X02162 APOLIPOPROTEIN A-I PRECURSOR (HUMAD);, mRNA sequence.
                    T 3/1; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Econed into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Smail: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzukit,Y., Yoshitcom-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU102721 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                             60.0%; Score 14.4; DB 1; Length 31; 93.8%; Pred. No. 1.1e+05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.0%; Score 14.4; DB 1; Length 50; 75.0%; Pred. No. 1.1e+05; ive 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                27 AAACCTGCTCTGGAGG 12
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                                                                                                                                                                                                                                                                                                 6 AACCCTGCTCTGGAGG
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                                                                                                                                                                        Homo sapiens
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T71655.1
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DEFINITION
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T71655/c
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AU102721
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases I to 31)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/note="Organ: placenta; Vector: pT7730-Pac (Pharmacia)
with a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
lst strand cDNA was primed with a Not I - oligo[dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI323319
31 bp mRNA linear EST 23-DEC-1998 mh78a09.x1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus CDNA clone IMAGE:457048 3' similar to TR:Q64366 Q64366 SYNAPTOTAGMIN
                                                                                                                                                                                                                                                                                                                                                   ó
               /dev stage="49 years old"
/lab host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Prīmer:
Dijdo dr. Hepatectomy from normal male caucasian. Average insert size: l. l. kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATICGGCACGAG 3' ~3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:273936
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                            60.8%; Score 14.6; DB 7; Length 35; larity 73.9%; Pred. No. 8.7e+04; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                         CTCGAGTTTTTTTTTTTTT 3'"
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/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="taxon:10090"
'clone="IMAGE:457048"
                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGCCAACCCTGCTCTGGAGGCC 23
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIII ;, mRNA sequence. AI323319
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                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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COMMENT
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KEYWORDS
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Gaps

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/ Mod_type="genomic DNA"

/ mod_type="genomic DNA"

/ ecotype="Col-0"

/ db_xref="texon:3702"

/ db_xref="texon:3702"

/ clone="shik 03858"

/ clone="shik 03858"

/ clone="shik 03858"

/ clone="shik 03858"

/ clone lib="Arabidopsis thaliana TDNA insertion lines"

/ note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
  Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., dadatinab, C., Jeske, A., Karnes, M., Kin, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R. A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (basea 1 to 31)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niegelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ809714 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0073P16 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                        This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                     Contact: Joseph R. Bcker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Fear: 958 958 6400 x1752 Fear: 958 958 6400 km.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
58.3%; Score 14; DB 8; Length 48;
Best Local Similarity 77.3%; Pred. No. 1.6e+05;
Matches 17; Conservative 0; Mismatches 5; Indels
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/organism="Arabidopsis thaliana"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: P column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Mus musculus
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                                                                                                        Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                        Class: TDNA tagged
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84112, USA
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: estGwatSon.wustl.edu
Insert Size: 33
High qality sequence starts: 1 High qality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL; contact the IMAGE Consortium (infc@image.llnl.gov)
for further information. Trace considered overall poor quality
Possible reversed clone: polyT not found
                                          Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 45)
Hillier L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
Trevaskis, L., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 48)
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                                                                                                                                                                                                                                                                                                                                   Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 58.3%; Score 14; DB 7; Length 45; 1 Similarity 73.9%; Pred. No. 1.6e+05; 17; Conservative 0; Mismatches 6; Indels
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="GDB:502337"
/db_xref="taxon:9606"
/clone="IMAGE:85280"
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High quality sequence stop: 1.
Location/Qualifiers
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BH865457.1 GI:22101355
                          sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 17; Conserv
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JOURNAL
                                                                                                                          REFERENCE
                                                                                                                                                     AUTHORS
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KEYWORDS
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BH865457
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 45)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nise, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Dunse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ768397
1M0568D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0568D23 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S6.7%; Score 13.6; DB 7; Length 33; Similarity 76.2%; Pred. No. 2.4e+05; 6; Conservative 0; Mismatches 5; Indels
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/63"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0568 row: D column: 23
                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="GDB:499703"
                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:82646"
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                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
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Best Local Simi
Matches 16;
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                                                                                                                                                                                                                                             /done lib="Mouse lobb plasmid UUGCIM library"
/clone lib="Wouse lobb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel-
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 bp mRNA linear EST 02-MAR-1995 yc35a08.sl Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82646 3' similar to gb:X02162 APOLIPOPROTEIN A-I PRECURSOR (HUMAN);, mRNA sequence.
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1 (bases 1 to 33)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Travaskis, E., Underwood, K., Wohldmann, P., Materston, R., Wilson, R., Marsis, M.
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Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 1800
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.7%; Score 13.6; DB 8; Length 31; 80.0%; Pred. No. 2.4e+05; live 0; Mismatches 4; Indels
                                                                          'organism="Mus musculus"
                                                                                                mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                  db_xref="taxon:10090"
clone="UUGC2M0073P16"
High quality sequence stop: 31.
Location/Qualifiers
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Insert Size: 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGCCAACCCTGCTCTGGAG 20
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local S
                                                        source
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COMMENT
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                        FEATURES
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ORIGIN

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bX209782 41 bp DNA linear GSS 29-JAN-2003
Danic rerio genomic clone DKEY-250L15, genomic survey sequence.
BX209782
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Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campung, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 250L15. 250L15
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 23-FEB-1995
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., iacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Trevaskis, E., Underwood, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (Dases 1 to 41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 bp mRNA linear EST 23-FEB-1: yc32e08.sl Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82406 3' similar to gb:X02162 APOLIPOPROTEIN A-I PRECURSOR (HDMAN);, mRNA sequence.
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
                                                Length 37;
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                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                             Score 13.4; DB 4;
Pred. No. 3e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3e+05;
0; Mismatches
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/tissue_type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .41
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
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                         55.8%; Scur.
93.3%; Pred
0; h
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio (zebrafish)
                                                                                                                                     TGCCAACCCTGCTCT 16
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EST.
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                                                                                                Conservative
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Best Local Similarity
Matches 14; Conser
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T69149/c
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                                                                                                                                                     Laboratory Mouse DNR Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gil 4732114 [gb] APL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BJ034402 37 bp mRNA linear EST 26-SEP-2003 BJ034402 NIBB Mochii normalized Kenopus neurula library Kenopus laevis cDNA clone XL028h05 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus.
                                                            /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone_lib="Mouse_lokb plasmid UnGIM library."
/note="Wector: PWD4Zhry, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           il: tshini@genes.nig.ac.jp
information of this clone is available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/dev_stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 37)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 56.7%; Score 13.6; DB 8; Length 45; Best Local Similarity 80.0%; Pred. No. 2.5e+05; Matches 16; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
17El: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed genes in X. laevis embryo Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
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               /clone="UUGC1M0568D23"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL028h05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://xenopus.nibb.ac.jp.
Location/Qualifiers
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/clone lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Patima Bonaldo. "
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( Dases 1 to 40)

Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 bp mRNA linear EST 26-SEP-2
B#0139939 NIBB Mochii normalized Xenopus neurula library Xenopus
Beris CDNA clone XL038p16 5', mRNA sequence.
B#039939
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/dev stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library:
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Pred. No. 3.7e+05;
0; Mismatches 4; Indels
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                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                   /clone="IMAGE:1527084"
/lab_host="DH108"
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/db_xref="taxon:8355"
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Location/Qualifiers
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ilarity 78.9%;
Conservative
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Best Local Similarity
Matches 15; Conserv
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                          High gality sequence starts: 1 High gality sequence stops: 1 Source: IMAGE Consortium, LIML This clone is available royalty-free through LIML; context the IMAGE Consortium (info@image.llnl.gov) For further information. Trace considered overall poor quality Possible reversed clone: polyT not found Seq primer: -21ml3 stop: 1. High quality sequence stop: 1. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Hepatectcomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGGG3' 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTTTTTTT" 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ol52c07.sl Soares NFL T GBC_S1 Homo sapiens cDNA clone IMAGE:1527084 3' similar to SW:HFC1_HUMAN P51610 HOST CELL FACTOR C1 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Trace consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1437 Std Brror: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequences stop: 1.
Location/Qualifiers
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                                                                                                Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/db_xref="GDB:499463"
/db_xref="taxon:9606"
/clone="IMAGE:82406"
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                                                                                                                                                                                                                           Email: est@watson.wustl.edu
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Unpublished (1997)
                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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AA917511/c
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Department of Virology Institute of Medical Science, University of Tokyo Institute of Medical Science, University of Tokyo Edical Science, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                          Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shizokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Bata,H., Otca,T., 18ogai,T., Tanaka,T., Morishita,S., Okubo,K.,

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library'
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Pred. No. 3.7e+05;
0; Mismatches 3;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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AU103168.1 GI:13552689
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                                          Contact: Yutaka Suzuki
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ilarity 83.3%;
Conservative 0
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
Inength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
                                                                                                                                                                  AU103163 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone COLF1812, mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                    GCCAACCCTGCTCTGGAGG 21
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AU103164.1 GI:13552685
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWBA12 (gil #4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG720584 42 bp DNA linear GSS 20-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
hote="Vector: PWD42ny; Purified genomic DNA from M.
musculus C578L/6J (feanle) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                            University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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76.2%; Pred. No. 4.5e+05;
Live 0; Mismatches 5; Indels
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0230 row: H column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0230H05"
          University of Utah Genome Center
                                                                                                                                                                                                                                                                              High quality sequence stop: 38.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Female"
/lab_host="E.
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Contact: Walbot V
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CG720584
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Best Local Similarity
Matches 16; Conserv
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TITLE
JOURNAL
COMMENT
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CG720584
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Brail: Suzukielims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full
Inength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                              AUI03176 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone AUI03176 wRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, K., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/clone_lib="Sugano Homo sapiens cDNA library"
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
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Unpublished (2000)
Contact: Robert B. Weiss
28 ACCCAGCTCTGGCGTCCT 11
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AZ961550.1 GI:13832777
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                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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Best Local Similarity 83.3
Matches 15; Conservative
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//db xref="textor.4577"
//db xref="textor.4577"
//db xref="textor.4577"
//db xref="textor.4577"
//db bost="DH10B"
//done_lib="l119 - RescueMu Grid AA"
//done_lib="l119 - RescueMu Site = 1: BamHl; Site_2: BglII;
//done="lib="lib" Ab, modified maize Mu transposon
//designed to allow plasmid rescue from total genomic DNA.
//dw insert preferentially into transcription
//done insert preferentially into transcription
//designed to allow ab grown at UC San Diego in 2002. DNA
//designed from leaf strips, double digested using
//designed to allow lighted to form circular plasmids.
//designed to allow grown at UC San Diego in 2002. DNA
//designed from leaf strips, double digested using
//designed to allow greater plasmids.
//designed from leaf strips, double digested using
//designed from circular plasmids.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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2M0029P14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0029P14 R, genomic survey sequence.
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119062 row: 26
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                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13; DB 9; Length 42; Pred. No. 4.5e+05; Mismatches 5; Indels
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20
84112, USA
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Fax: 801 585 7177
Fail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 43.
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                                                                                                                                                                                                                                                  organism="Zea mays"
                                                                                                                                                             Class: transposon-tagged.
Location/Qualifiers
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Best Local Similarity
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                                                                                                                                                                                                                           source
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AZ785692/c
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwapto (giffa732114[ph] PRI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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AC0059 Sanger Institute Gene Trap Library pGT0lxr Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 43)
http://www.sanger.ac.uk/PostGenomics/genetrap/
http://www.sanger.ac.uk/PostGenomics/genetrap/
Unpublished (2003)
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Bmail: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
Gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
                                                                                                                                                                                                                                                                     /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.2%; Score 13; DB 8; Length 43; 76.2%; Pred. No. 4.5e+05; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.ganger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.
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/cell_type="Embryonic Stem Cell"
                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
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/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
                                                            organism="Mus musculus"
                                                                                                                                               db_xref="taxon:10090"
clone="UUGC2M0029P14"
Location/Qualifiers
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                                                                                                                     strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 cchrccrrcrcrrcccccr 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG869098.1 GI:38532778
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                                                                                                                                                                                                               sex="Male"
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ORIGIN

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/mol type="genomic DNA"
/mol type="mixed background W23/A188/B73"
/db_xref="texton:4577"
/tissue type="leaf"
/dev stage="leaf"
/dev stage=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          рквыдзт 35 bp DNA linear GSS 27-NOV-2002
Danio rerio genomic clone DKEY-8L23, genomic survey sequence.
AL747763
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Cypriniformes; Cyprinidae; Danio.

1 (Dases 1 to 35)

Humphray, S. J., Huckle, E. and Hunt, S. E.

Direct Submission

Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
                                                                                                                                                                                                                                                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 49)

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Flat: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008093 row: 18
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Pred. No. 4.6e+05;
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Stanford University
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Location/Qualifiers
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                                                             GI:20304939
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76.2%;
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Matches 16;
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DEFINITION
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DR8L23T
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1008093E10.2EL_yl 1008 - RescueMu Grid I Zea mays genomic, genomic
survey sequence.
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db xref="taxon:8296"

/tissue_type="Tail Blastema"

/cell type="Tail Blastema"

/clone_lib="6-Day Axolot| Tail Blastema (6DAXBL)"

/clone_lib
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Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
/clone_lib="Sanger Institute Gene Trap Library pGT0lxr"
/note="Vector: pGT0lxr"
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                                                                                                                                                                                                              Length 43;
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Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Alate: BL282B row: 08 column: A
Seg primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
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Pred. No. 4.5e+05;
0; Mismatches 8
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Contact: Elly M. Tanaka
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CO784990.1 GI:51000970
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ilarity 66.7%;
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Bail: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
Inength-enriched and s'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                    AU102722 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS02544, mRNA sequence.
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1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA stark sites
BEBO Rep. 2 (5), 388-393 (2001)
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1 (bases 1 to 50).

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
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Pred. No. 5.6e+05;
0; Mismatches 7;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                             6 ACCTGCTCTACAGGC
                                 7 ACCCTGCTCTGGAGGC
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Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Bun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-qu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:s82-42-866-181, Fax:82-44-860-4409)
clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG191198 49 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-067A16.T7, genomic survey
sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 8L23. 8L23 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
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                                                                                       Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
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'clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                    Length 35;
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                                                                                                                                                                                                                               /clone="DKEY-8L23"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
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                                                                                                                                                            /organism="Danio rerio"
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/db_xref="taxon:7955"
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/db_xref="taxon:9598"
/clone="RP43-067A16.T7"
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R.Site 1 : ECORI
R.Site 2 : ECORI.
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AG191198.1 GI:45223374
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Query Match 52.5. Best Local Similarity 78.9 Matches 15; Conservative
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Fax: 801 585 7177
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                                                            Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 40)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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40 bp mRNA linear EST 16-JUN-1998
ub050510.r1 Soares mammary gland NbWMG Mus musculus cDNA clone
IMAGE:1366489 5' similar to SW:CTSY PIG 900889 CITRATE SYNTHASE,
MITCCHONDRIAL PRECURSOR ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                      53.3%; Score 12.8; DB 1; Length 50; 70.8%; Pred. No. 5.6e+05; Live 0; Mismatches 7; Indels
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Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/organism="Homo sapiens"
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The WashU-HHMI Mouse EST Project
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/strain="C57BL/6J"
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                    11375929
Contact: Yutaka Suzuki
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AI021601.1 GI:3235937
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Best Local Similarity 70.8'
...rhes 17; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1M0290F18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 43)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Pred. No. 6.8e+05;
0; Mismatches 4; Indels
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Insert Length: 10000 Std Error:
Plate: 0290 row: F column: 18
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 43.
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/strain="C57BL/6J"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|RP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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S Unun,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
C Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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MO294I21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0294I21 F, genomic survey sequence.
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/clome_lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (Male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0294 row: I column: 21
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db xref="taxon:10090"
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AZ475962.1 GI:10634087
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Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 30

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ORIGIN

AZ475962

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1-length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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1 (basea 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.5%; Score 12.6; DB 8; Length 48; 78.9%; Pred. No. 6.8e+05; ive 0; Mismatches 4; Indels
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 caaccerecrecercasec
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Best Local Similarity 78.9
Matches 15; Conservative
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KEYWORDS

COMMENT

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Score 12.4; DB 1; Length 25;
Pred. No. 8.1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                       BED0005649 3', mRNA sequence.
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  Query Match 51.7%;
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72...
Local 16; Conservative
                                                                                                                    7 ACCCTGCTCTGGAG 20
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                                                                                                                                                                                                                                                                                                                                               DEFINITION
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TITLE
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CA796933
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: 2brafishWatson.wustl.edu

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact:
Info@genomesystems.com) (email contact:
Matthew Contact:
Matthe
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (bases 1 to 25)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Riter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish dison, R.

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                  AI397039

Eb25e02.yl Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE:3712922 5' similar to SW:IQGA HUMAN P46940 RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP! ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
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/organism="Danio rerio"
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/db_xref="taxon:7955"
/clone="IMAGE:3712922"
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POLYA=No.
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                                                                                                                                                                                                                                                           Danio rerio (zebrafish)
                                                                                                                                                                                                  AI397039.1 GI:4226932
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                                                                                                                                                                                                                                                                                         Danio rerio
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RESULT 32
AI397039/c
                                                     LOCUS
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                                                                                                                                                                    ACCESSION
VERSION
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AUTHORS
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JOURNAL
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FEATURES

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CA796933 37 bp mRNA linear EST 05-DEC-2002 Cac_BL_3999 Cac_BL (Bean and Leaf from Amelonardo type Cacao) Theobroma cacao cDNA clone Cac_BL_3999 5', mRNA sequence.
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                                                                                                                                                                                                                                                                    AU255522 3'-directed mouse cDNA library Mus musculus cDNA clone
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Maukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 34) and Macba,R. Generation of expressed sequence tags from mouse brain Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 37)
Sones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Planta 216 (2), 255-264 (2002) 22337596
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished (1996)
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Brigham and Women's Hospital
Harvard Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GCCAACCCTGCTCTGGAGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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AUTHORS
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84112, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ775757 40 bp DNA linear GSS 16-FEB-200
2M0008B24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                         db_xref="taxon:3641"
| clone="cac_BL" 1999"
| clone="taxon:3641"
| clone="taxon:3641"
| cell_type="Whole organ"
| dev_stage="maturity"
| lab_host="XL-1 Blue MRP'"
| clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBK-CMV; Bean and leaf tissue from an Amelonado type Cacao tree."
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0
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               Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
11: +44 1664 41664 41664 Bmail: Paul.Jones@eu.effem.com
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone UUGC2M0008B24 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.4; DB 6;
Pred. No. 8.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ddunn@genetics.utah.edu
Length: 10000 Std Error: 0.00
                                                                                                                                                                'organism="Theobroma cacao"
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.
                                                                                                                                                                                    /mol_type="mRNA"
/strain="Amelonado type"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC2M0008B24"
                                                                                                                               Location/Qualifiers
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| Similarity 69.6%; Pro
| 16; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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indectatory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N83841 Linear EST 01-APR-1996 KK3617F Human fetal heart, Lambda ZAP Express Homo sapiens CDNA Clone KK3617 5' similar to STAT4, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. coli XL1-Blue"
/clone lib="Human fetal heart, Lambda ZAP Express"
/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
XhoI; mRNA was purified from human fetal hearts (8-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
                                    /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
Seq primer: GAAATTAACCCTCATTAAAGGG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Gaps

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GSS 20-OCT-2003

DEFINITION ACCESSION VERSION

KEYWORDS

AZ766605

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REFERENCE AUTHORS.

JOURNAL COMMENT

TITLE

FEATURES

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/clone lib="1119 - RescueMu Grid AA"
/clone lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone), Site 1: BamHI; Site 2: BqIII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. NNA was extracted from leaf strips, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CL528330 50 bp DNA linear GSS 17-MAY-2004 ASV5B01.fwd ASLV-vector integration sites in human 293T-TVA cells Homo sapiens genomic clone ASV5B01.fwd, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Papermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
                                                                                                                                                                                                                                                                                       1119081A01.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
/tissue_type="leaf"
/leav_stage="alleaf"
/lab_nost="DH108"
        Length 50;
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                                                              Indels
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Fax: 650 725 8221
Email: walbotestanford.edu
Elae: 1119081 row: A column: 01
Class: transposon-tagged.
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72.7%; Pred. No. 8.4e+05;
iive 0; Mismatches 6;
     Score 12.4; DB 8;
Pred. No. 8.4e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Walbot V
Department of Biological Sciences
Stanford University
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     51.7%;
92.9%;
                                                                                                                  8 CCCTGCTCTGGAGG 21
                                                                                                                                                                     26 cccricricricarde 39
  Query Match
Best Local Similarity 92.9
Matches 13; Conservative
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated baseage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated for a state
igated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil | 4732114 | gb | AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                        AZ766605 16-FEB-200
1M0564L13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0564L13 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 50)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                           Gaps
                                                           ö
ch 51.7%; Score 12.4; DB 7; Length 46; 
1 Similarity 72.7%; Pred. No. 8.4e+05; 
16; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: CGTTCTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 50.
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organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref="taxon:10090"
'clone="UUGC1M0564L13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 0564 row: L column: 13
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                                                                                                      2 TGCCAACCTGCTCTGGAGGCC 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                           AZ766605.1 GI:12883846
                                                                                                                                                                                                                                                                                                                                                              clone UUGC1M0564L13 F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
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Gaps

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ORIGIN

column: 05

row: o

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Search completed: November 18, 2005, 21:12:40 Job time : 1150.98 secs
    Plate: LLAM11555
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                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 50).
Mitchell, R.S., Beitzel, B.F., Schroder, A.R.W., Shinn, P., Chen, H., Berry, C.C., Ecker, J.R. and Bushman, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 31)
NIH-WGC http://mgc.nci.nih.gov/.
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Contact: Robert Strausberg, Ph.D.

Email: Gapbs-romail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salk Institute Infectious Disease Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
TH: 858 453 4100 x1630
Fax: 858 554 0341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/organism="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bushman@salk.edu
Class: PCR with specific primers.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="ASV5B01.fwd"
                                                                                                                                                                                                                                                                                                                                                                                                                               Site Preferences
Unpublished (2004)
Contact: Frederic Bushman
                                    CL528330.1 GI:47421526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence. _ _ BI522142
BI522142.1 GI:15346934
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Homo sapiens
                                                                                                                Homo sapiens (human)
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                         Homo sapiens
    CL528330
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
ACCESSION:
                                    VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                              AUTHORS
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/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1: 5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                         /organism="Homo sapiens"
High quality sequence start: 7
High quality sequence stop: 31.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GCCAACCCTGCTCTGGA 19
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Sequence 72981, A Sequence 10, Appl Sequence 3461, Ap Sequence 72, Appl Sequence 4320, Ap

Sequence 2169, Ap Sequence 3026, Ap Sequence 3027, Ap

2169,

Sequence

Sequence 3027, A Sequence 15020,

Appl Appl Appl Appl Appl Appl

Sequence 16, 1 Sequence 16, 1 Sequence 24, 1

Sequence 3

Sequence

Sequence

72, Appl 4320, Ap

OM nucleic

Run on:

Sequence:

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Query Match 100.0%; Score 24; DB 1; Length Best Local Similarity 100.0%; Pred. No. 0.094; Matches 24; Conservative 0; Mismatches 0; Indel
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCORMATION:
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: WATKINS, HUGH
APPLICANT: WATKINS, HUGH
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
          US-09-906-700-16
US-09-906-700-16
US-09-904-920A-16
US-09-904-920A-16
US-09-906-618-16
US-09-906-618-16
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US-09-396-1960-3026
US-09-396-1960-3027
US-09-396-1960-3021
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US-09-396-1960-3021
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US-09-396-1960-3021
US-09-396-1960-3021
                                                                                                                                                                                                                                                                                              ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/07989160; Patent No. 5429923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOSTON
                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-07-989-160-3
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Sequence 54586, A
Sequence 54585, A
Sequence 63266, A
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2325, Ap
8574, Ap
124901,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2994, Ap
57276, A
70618, A
76806, A
24, Appl
6, Appli
58955, A
                                                                                             November 18, 2005, 00:26:13 ; Search time 46.6312 Seconds (without alignments) 842.154 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-396-196G-54586

US-09-396-196G-63266

US-09-396-196G-63266

US-09-396-196G-127234

US-09-396-196G-127234

US-09-396-196G-127234

US-09-396-196G-124901

US-09-396-196G-124901

US-09-396-196G-124901

US-09-396-196G-70618

US-09-396-196G-505

US-09-991-862-15

US-09-991-862-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-396-196G-71340
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US-09-905-125A-16
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                     1 ATGCCAACCCTGCTCTGGAGGCCT 24
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                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                     US-10-788-779-3
24
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Match Length
                         Copyright
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seg length: 50
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                                                                                                                                                                                                                  Scoring table:
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Perfect score:
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Minimum DB Maximum DB

Searched:

Database :

Result

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Gaps

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Indels

24;

Gaps

; 0

us-10-788-779-3.rni

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62.5%; Score 15; DB 4; Length 25; 78.3%; Pred. No. 1.2e+03; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                            62.5%; Score 15; DB 4; Length 25; 78.3%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PELING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: AFFymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58956, Application US/09396196G Patent No. 6821724
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Best Local Similarity 78.39
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 78.35
Matches 18; Conservative
   David Mack
David Lockhart
                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-63266
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; ORGANISM: mus musculus
US-09-396-196G-127234
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US-09-396-196G-58956
                     APPLICANT:
APPLICANT:
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Pred. No. 5.2e+02;
0; Mismatches 2; Indels
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GENERAL NO. 05211/24;
GENERAL David Mack
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FasteseQ for Windows Version 4.0
SSOFTWARE: 25
                                                                                                                                                APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PELING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FasteSEQ for Windows Version 4.0
SSOFTWARE: 25
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US-09-396-196G-63266
; Sequence 63266, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
                                                                                           Sequence 54586, Application US/09396196G Patent No. 6821724 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-396-196G-54585
; Sequence 54585, Application US/09396196G
; Patent No. 6821724
1 ATGCCAACCCTGCTCTGGAGGCCT 24
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
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ORGANISM: mus musculus
US-09-396-196G-54586
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ORGANISM: mus musculus
US-09-396-196G-54585
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Best Local Similarity
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Sequence 8574, Application US/09396196G
Sequence 8574, Application US/09396196G
Sequence 8574, Application US/09396196G
PAPELICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NOS: 127806
SEQ ID NOS: 127806
SEQ ID NO 8574
LINGUAR: FastSEQ for Windows Version 4.0
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; Patent No. 6821724
; GRNERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Mack
; APPLICANT: Affwertix, Inc.
; APPLICANT: Affwertix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 310.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT PILING DATE: 1999-09-15
; PRIOR PELING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 60.8%; Score 14.6; DB 4; Best Local Similarity 81.0%; Pred. No. 1.8e+03; Matches 17; Conservative 0; Mismatches 4;
                                NUMBER OF SEQ ID NOS: 127806
SOFTHARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2325
LENGTH: 25
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         PRIOR FILING DATE: 1998-09-17
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CRGANISM: Mus musculus
US-09-396-196G-8574
                                                                                                                            TYPE: DNA
CORGANISM: Mus musculus
US-09-396-196G-2325
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; ORGANISM: mus musculus
US-09-396-196G-124901
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APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REFRENCE: 62.US3.CIP
CURRENT APPLICATION NUMBER: US 09/671,317
CURRENT APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-03-23
PRIOR PLILING DATE: 1099-03-25
PRIOR PLILING DATE: 1999-03-25
PRIOR PLILING DATE: 1999-04-30
NUMBER: US 60/131,961
PRIOR FILING DATE: 1999-04-30
NUMBER: PREQUIN NUMBER: US 60/131,961
SOFTWARE: Patent.pm
SEQ ID NO 812
LENGTH: 47
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                                                                                                                                                                                               Score 14.8; DB 4; Length 25; Pred. No. 1.5e+03;
                                                                                                                                                                                                                                               2; Indels
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; OTHER INFORMATION: 12-138-141 : polymorphic base G or A
US-09-671-317-812
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Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Bavid Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
                                                                                                                                                                           61.7%; Scor.
88.3%; Pred. No. ...
0; Mismatches
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58956
LENGTH: 25
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                            TYPE: DNA; ORGANISM: mus musculus
US-09-396-196G-58956
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Best Local Similarity
Matches 16; Conserve
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US-09-396-196G-2325
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US-09-671-317-812
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US-09-396-76806/C
iSequence 76806, Application US/09396196G
iPatent No. 6821724
iGENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: APFLICANT: APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: APPLICANT: MATHORS OF Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE FRAESEQ for Windows Version 4.0
SEQ ID NO 76806
TABLICANT: 25
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84.2%; Pred. No. 2.8e+03;
tive 0; Mismatches 3;
                                                                                                                                                                                                                          Sequence 70618, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: APFLICANT: AFFYmetrix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FASTERQ FOR Windows Version 4.0
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US-09-402-631A-24
; Sequence 24, Application US/09402631A
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Best Local Similarity 84.27
These 16; Conservative
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; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-70618
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US-09-396-196G-76806
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Best Local Similarity
Matches 16; Conserv
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US-09-396-196G-70618
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LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                  ## APPLICANT: Cohen, Daniel
## APPLICANT: Chen, Daniel
## APPLICANT: Blumenfeld, Marta
## APPLICANT: Blumenfeld, Marta
## APPLICANT: Blumenfeld, Marta
## APPLICANT: Chunakov, IJya
## TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
## TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
## CURRENT APPLICATION NUMBER: US/09/422,978
## CURRENT FILING DATE: 1999-10-20
## EARLIER PELING DATE: 1999-10-20
## EARLIER PELING DATE: 1998-11-23
## EARLIER PELING DATE: 1998-11-23
## EARLIER PELING DATE: 1998-11-23
## EARLIER FILING DATE: 1998-14-21
## CONTINUABER OF SEQ ID NOS: 11796
## CENTRAL OF SEQ ID NOS: 11796
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        60.8%; Score 14.6; DB 4; Length 25; 81.0%; Pred. No. 1.8e+03; ive 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.8%; Score 14.6; DB 4; Length 47; Best Local Similarity 73.9%; Pred. No. 2e+03; Matches 17; Conservative 1; Mismatches 5; Indels
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; OTHER INFORMATION: 99-21492-310 : polymorphic base C or T
US-09-422-978-2994
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Sequence 5724,6
Sequence 5724
Sequence 5724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: DAVID LOCKHART
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57276
LENGTH: 25
                                                                                                                                                                                                                                                                                                          Sequence 2994, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
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                                                                                                                     2 TGCCAACCCTGCTCTGGAGGC 22
                                                                                                                                                        21 TGCCCACACAGATCTGGAGGC 1
Query Match
Best Local Similarity 81.0°
Matches 17; Conservative
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Matches 16; Conservative
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-396-196G-57276
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                                                                                                                                                                                                                                                                                   US-09-422-978-2994
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Gaps
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Sequence 13, Application US/08987326
Sequence 13, Application US/08987326
Sequence 13, Application US/08987326
GENERAL INFORMATION:
TITLE OF INVENTION: Detection of Melanoma or Breast Metastasis with a TITLE OF INVENTION: Multiple Marker Assay
TITLE REFERENCE: NGI 20823-701 COURENT APPLICATION NUMBER: US/08/987,326
CURRENT FILING DATE: 1997-12-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.3%; Score 14; DB 1; Length 35; Best Local Similarity 77.3%; Pred. No. 3.6e+03; Matches 17; Conservative 0; Mismatches 5; Indels
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Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymerix, Inc.
APPLICANT: Affymerix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT PILING DATE: 1999-09-15
FRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 58955
LENGTH: 25
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                                                                                                                                                                                                                                   P30 antigen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGCCAACCCTGCTCTGGAGGC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 Argcchrcccggrcragagrc 4
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INDIVIDUAL ISOLATE: P30 ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CCAACCCTGCTCTGGAG 20
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SEQUENCE CHARACTERISTICS:
                     : 35 base pairs
nucleic acid
EDNESS: single
                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / ORGANISM: mus musculus
US-09-396-196G-58955
                                                                                                                                                                                                                                                                               Primer #5
                                                                                                                                                                                                                                                    IMMEDIATE SOURCE
CLONE: Primer
                                              TYPE: nucleic STRANDEDNESS:
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US-09-396-196G-58955
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; LOCATION:
US-08-375-235-6
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       GENERAL INPORMATION:
APPLICANT: Gist-Brocades B. V.
APPLICANT: Seleen, Gerardus
APPLICANT: Seleen, Gerardus
APPLICANT: Seleen, Gerardus
APPLICANT: Seleen, Gerardus
TITLE OF INVENTION: Gene Conversion as a Tool for the Construction of Recombinant I
TITLE OF INVENTION: Organisms
TITLE OF INVENTION WUMBER: US/09/402,631A
CURRENT APPLICATION NUMBER: P00-12-4
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
LENGTH: 24
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APPLICANT: Xiong Ph.D., Cheng
APPLICANT: Aiong Ph.D., Robert B.
TITLE OF INVENTION: "RECOMBINANT VIRAL PARTICLE VACCINES"
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSED: SHERIDAN ROSS & MCINTOSH
STREET: 1700 Lincoln St., #3500
CITY: Denver
STREET: USA
STREET: USA
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.3%; Score 14; DB 3; Length 24; 77.3%; Pred. No. 3.46+03; Live 0; Mismatches 5; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US/08/015,414
FILING DATE: 08-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOVATIK ESQ., JOSEPH E.
REGISTATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2618-3
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: oligonucleotide;
NAME/KEY: misc feature
COTHER INFORMATION: PCR primer
US-09-402-631A-24
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US-08-375-235-6/c
; Sequence 6, Application US/08375235
; Patent No. 5766602
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TELEFAX: (303) 863-0223
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Best Local Similarity 77.34
Matches 17; Conservative
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INFORMATION FOR SEQ ID NO:
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TYPE: DNA
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Patent No. 6670183

GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: Z9996.488/P001-A
CURRENT FILING DATE: 2001-03-1
PRIOR APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOUTHARE: PatentIN Ver. 2.0
SEQ ID NO 15
LENGTH: 24
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APPLICANT: Serrero, Ginette
APPLICANT: Serrero, Ginette
TITLE OF INVENTON: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE OF INVENTON: 25996.488/PD011-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER PILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 24
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                                                                                                                                                                                                                                                                                                    Query Match 56.7%; Score 13.6; DB 3; Length 22; Best Local Similarity 80.0%; Pred. No. 5.2e+03; Matches 16; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.7%; Score 13.6; DB 3; Length 24; 80.0%; Pred. No. 5.2e+03; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: primer | 10.CATION: (1)..(24) | 10.CATION: (1)..(24) | 10.CHER INFORMATION: Antisense oligonucleotide to human GP88 US-08-991-862-15
EARLIER APPLICATION NUMBER: 08/406,307
EARLIER FILING DATE: 1995-03-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 19
US-08-991-862-15
Sequence 15, Application US/08991862
; Patent No. 6309826
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                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.7
Best Local Similarity 80.0
Matches 16; Conservative
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ORGANISM: mammalian
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                                                                                                                                                                                                                                                       US-08-987-326-13
                                                                                                                                           TYPE: DNA
                                                                                                                                                                                     FEATURE:
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| Sequence 15. Application US/09824647
| Patent No. 6824775
| Patent No. 6824775
| Patent No. 6824775
| Patent No. 6824775
| GENERAL INFORMATION:
| APPLICANT: Serrero, Ginette
| TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
| TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
| FILE REFRENCE: 29996-488/P001-A
| CURRENT APPLICATION NUMBER: US/09/824,647
| PRIOR PILING DATE: EARLIER FILING DATE: 1998-08-17
| PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
| NUMBER OF SEQ ID NOS: 17
| SEQ ID NO 15
| LENGTH: 24
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TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPRENEUE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/456,886
CURRENT FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US/08/991,862
PRIOR FILING DATE: 1999-08-17
PRIOR PLING DATE: 1999-08-17
PRIOR PLING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 24
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                                                                                                                                                                                             Query Match 56.7%; Score 13.6; DB 4; Length 24; Best Local Similarity 80.0%; Pred. No. 5.2e+03; Matches 16; Conservative 0; Mismatches 4; Indels
ORGANISM: mammalian
FEATURE:
NAME/KEY: primer
LOCATION: (1)..(24)
OTHER INFORMATION: Antisense oligonucleotide to human GP88
US-09-813-156-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: primer; LOCATION: (1)..(24); OTHER INFORMATION: Antisense oligonucleotide to human GP88; OS-09-456-886-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-456-886-15; Application US/09456886; Patent No. 6720159; GENERAL INFORMATION:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/USO0/04414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.6; DB 4; Length 25;
Pred. No. 5.3e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                      APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
ITLE OF INVENTION: Methods of Genetic Analysis
ITLE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 124900
                                                                                                                                         US-09-396-196G-124900/c
; Sequence 124900, Application US/09396196G
; Patent No. 6821724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-907-794A-16/c
; Sequence 16, Application US/09907794A
; Patent No. 6635468
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Grimaldi, Christopher J.
                                                     ccagrccrecrcrecarecc 24
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Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
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Gerber, Hanspeter
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0°
Matches 16; Conservative
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Ashkenazi, Avi
Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: mus musculus US-09-396-196G-124900
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                                                                                                                Query Match 56.7%; Score 13.6; DB 4; Length 24; Best Local Similarity 80.0%; Pred. No. 5.2e+03; Matches 16; Conservative 0; Mismatches 4; Indels
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                       ; LOCATION: [1)..(24)
; OTHER INFORMATION: Antisense oligonucleotide to human GP88
US-09-824-647-15
                                                                                                                                                                                                                                                                                                                                                     Sequence 71340, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Mathods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: 1899-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
MINMED OF COLUMBER: 1998-09-17
MINMED OF COLUMBER: 1998-09-17
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APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NO 74893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71340
LENGTH: 25
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; Sequence 74893, Application US/09396196G
; Patent No. 6821724
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                                                                                                                                                                                                         4 CCAACCCTGCTCTGGAGGCC 23
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Best Local Similarity 80.0
Matches 16; Conservative
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NAME/KEY: primer
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APPLICANT: ROY, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/005,125A
CURRENT APPLICATION NUMBER: PCT/US00/0414
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-07
PRIOR PRIOR DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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PRIOR PILLING DATE: 1999-10-05
PRIOR PILLING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR PILLING DATE: 1999-11-29
PRIOR PILLING DATE: 1999-11-30
PRIOR PILLING DATE: 1999-11-30
PRIOR PILLING DATE: 1999-12-02
PRIOR PILLING DATE: 1999-12-03
PRIOR PILLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PELICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
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; Sequence 16, Application US/09902775A
; Patent No. 6686451
; RENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGCCAACCCTGCTCTGGAG 20
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                                                                                                      Paoni, Nicholas F.
                                          Mather, Jennie P.
Pan, James
                   Kljavin, Ivar J.
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PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-06

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-18

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423
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Sequence 16, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Query Match
Best Local Similarity
Matches 16; Conserv
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21647

PRIOR APPLICATION NUMBER: PCT/US99/21647

PRIOR PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21891

PRIOR PILING DATE: 1999-10-10

PRIOR PILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR PILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PR
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                       Ferrara, Napoleone
Filvaroff, Ellen
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ORGANISM: Artificial Sequence
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Gao, Wei-Qiang
Gerber, Hanspeter
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                                                                       Desnoyers, Luc
Saton, Dan L.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
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56.7%; Score 13.6; DB 4; Length 50; 80.0%; Pred. No. 5.7e+03; ive 0; Mismatches 4; Indels
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CURRENT FILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR PLILOGATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
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REIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1900-10 AT
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PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR FILING DATE: 1999-11-29
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Grimaldi, Christopher J.
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; Sequence 16, Application US/09906700
; Patent No. 6723535
                                                                                                        1 ATGCCAACCCTGCTCTGGAG 20
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Mather, Jennie P.
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Ashkenazi, Avi
Botstein, David
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                                                     16; Conservative
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Sao, Wei-Qiang
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Eaton, Dan L.
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APPLICANT:
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/903,603A

CURRENT PILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR PILING DATE: 1909-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; NUMBER OF SEQ ID NOS: 423
; LENGTH: 50
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APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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; Sequence 16, Application US/09903603A
; Patent No. 6767995
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Gerritsen, Mary E.
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Paoni, Nicholas F.
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Best Local Similarity 80.0°
Matches 16; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
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                                                                    PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
PCT/US99/21547
                         FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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; Sequence 16, Application US/09904920A
; Patent No. 6806352
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
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Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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Transmembrane Polypeptides and Nucleic
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/909,064

CURRENT FILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-03

PRIOR PLIN
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Stewart, Timothy A.
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                                                                        Kljavin, Ivar J.
Mather, Jennie P.
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Tumas, Daniel
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Best Local Similarity
Matches 16; Conserv
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       CURRENT FILING DATE: 2001-0/-15

PRIOR APPLICATION NUMBER: PCT/USOO/04414

PRIOR FILING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-13-03

PRIOR PILING DATE: 1999-13-03

PRIOR PILING DATE: 1999-13-03
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Grimaldi, Christopher J.
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Patent No. 6818449
GENERAL INFORMATION:
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Filvaroff, Ellen
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Gerritsen, Mary E
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wei-Qiang
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CURRENT FILING DATE:
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APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                  Score 13.6; DB 4; Length 50;
Pred. No. 5.7e+03;
0; Mismatches 4; Indels
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FULE REFERENCE: 10466-14

FULE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906,618

CURRENT FILING DATE: 2001-07-16

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PG 60/146,222

PRIOR FILING DATE: 1999-00-28
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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FILING DATE: 1999-09-15
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Grimaldi, Christopher J.
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Patent No. 6828146
                                                                                                                                                                                1 ATGCCAACCCTGCTCTGGAG 20
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Stewart, Timothy A.
Tumas, Daniel
                                                        56.7%;
80.0%;
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Mather, Jennie P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                     Query Match
Best Local Similarity 80.0°
Matches 16; Conservative
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Eaton, Dan L.
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Sao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                     RESULT 34
US-09-906-618-16/c
US-09-905-381A-16
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APPLICANT: Wood, William, I.
TITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe
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CURRENT APPLICATION NUMBER: US/09/905,381A

CURRENT FILING DATE: 2001-07-13

FRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

FRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-13

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-00-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-20

PRIOR FILING DATE: 1999-11-20

PRIOR PLING DATE: 1999-11-20

PRIOR PLING DATE: 1999-11-20

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-03

PRIOR PRIOR DATE: 1999-12-03

PRIOR PRIOR DATE: 1999-12-03

PRIOR PRIOR DATE: 1999-12-03

PRIOR PRIOR DATE: 1999-12-0
                                                                                                                                                                                                                                                                                                                                                                                    Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                  Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy, Margaret Ann
                      Genentech, Inc.
Ashkenazi, Avi
Botstein, David
                                                                                                                    Desnoyers, Luc
Eaton, Dan L.
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Gao, Wei-Qiang
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FILING DATE
        PCT-US95-04075-24
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                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; COTHER INFORMATION: oligonucleotide probe US-09-906-618-16
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                                                                                                                                                                                                                                                                                                                                                  56.7%; Score 13.6; DB 4; Length 50;
80.0%; Pred. No. 5.7e+03;
tive 0; Mismatches 4; Indels
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Pred. No. 6.2e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lichenstein, Henri
APPLICANT: Lichenstein, Henri
APPLICANT: Wurfel, Mark
APPLICANT: Wright, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
TITLE OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Amgen Center, Patent Operations/RRC 1840 DeHavilland Drive
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR PILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 2090-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 16
; LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 13120-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/08222619
Patent No. 5652352
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGCCAACCCTGCTCTGGAG 20
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93.3%;
                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity 80.0°
Matches 16; Conservative
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CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                            TYPE: DNA
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RESULT 36

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GENERAL INFORMATION:

APPLICANT: LANGER, STIC S.

APPLICANT: Treland, James S.

APPLICANT: Treland, James S.

APPLICANT: Daley, George Q.

APPLICANT: Baley, George Q.

APPLICANT: McCarthy, Jeanette J.

TILLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES FILE REFERENCE: 2825.1027-001

CURRENT FILING DATE: 2000-09-07.

FRIOR FILING DATE: 2000-09-07.

PRIOR PLICATION NUMBER: US 60/153,357

PRIOR PLICATION NUMBER: US 60/153,357

PRIOR PLING DATE: 2000-09-10

PRIOR PLING DATE: 2000-09-16

PRIOR PLING DATE: 2000-09-16

PRIOR PLING DATE: 2000-09-16

PRIOR PLING DATE: 2000-07-26

PRIOR PLING DATE: 2000-09-16

PRIOR DATE: 2000-07-26

PRIOR DATE: 2000-07-26
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Pred. No. 6.3e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Sequence 24, Application PC/TUS9504075
GENERAL INFORMATION:
APPLICANT: ANGENI INC.
TITLE OF INVENTION:
FITLE OF INVENTION:
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
                                                                                                                                                                                                                                     ADDRESSEE: Amgen Center, Patent Operations/RRC STREET: 1840 DeHavilland Drive CITY: Thousand Oaks CITY: Thousand Oaks STATE: California COUNTRY: U.S. ZIP: 91320-1789 COMPUTER READABLE FORM: MEDIUM TYPE: Flogby disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: PCT/US95/04075 APPLICATION NUMBER: PCT/US95/04075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.8%; Score 13.4; DB 5; Best Local Similarity 93.3%; Pred. No. 6.2e+03; Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2169, Application US/09657472
Patent No. 6727063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Best Local Similarity 93.3%;
Matches 14; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: unkno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Homo sapiens
US-09-657-472-2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.8%; Score 13.4; DB 4; Length 25; Best Local Similarity 73.9%; Pred. No. 6.5e+03; Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                 Sequence 3026, Application US/09396196G
; Sequence 3026, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT FILING DATE: 1998-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3027, Application US/09396196G; Patent No. 6821724; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR PELLONG DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FRALESQ for Windows Version 4.0
; SEQ ID NO 3027
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US-09-396-196G-15020
Sequence 15020, Application US/09396196G
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  23
                                            18 ccrecrcrecaeccc 4
9 CCTGCTCTGGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-3026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-3027
                                                                                                                                          US-09-396-196G-3026
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US-09-396-196G-3027
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54586, *1* 188380,

Sequence Sequence Sequence Sequence Sequence 26759, A 95487, A 671714, 52603, A 194782,

Sequence Sequence Sequence Sequence

513335, 796279, 196604,

Sequence Sequence Sequence Sequence

21, Appl 327390,

Sequence Sequence Sequence

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Sequence Sequence Sequence

2, Appli 2685, Ap 13488, A 408446,

Sequence

Sequence

322925, 443709,

Sequence Sequence Sequence

256216,

Sequence

311815,

294807, 305597, 257640,

Sequence Sequence Sequence

63266, A 127234, 188382,

Sequence

Sequence

833110, 924759,

Sequence Sequence Sequence

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US-10-719-900-833111

US-10-719-900-833111

US-10-719-905-189-54586

US-10-719-905-174561

US-11-01-719-900-174561

US-11-060-756-77825

US-10-015-813A-1677

US-10-119-900-17847

US-10-119-956-26759

US-10-119-956-26759

US-10-119-956-26759

US-10-119-956-26759

US-10-119-956-26759

US-10-119-956-26759

US-11-018-317-257640

US-11-018-317-257640

US-11-018-317-257640

US-11-018-317-257640

US-11-018-317-31815

US-11-018-317-31815

US-11-018-317-31816

US-11-018-317-31816

US-11-018-317-31816

US-11-018-317-31816

US-11-018-317-31816

US-10-719-900-913110

US-10-719-900-913110

US-10-719-900-913110

US-10-719-900-913110

US-10-719-900-913110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: WATKINS, HIGH
APPLICANT: WATKINS, HIGH
APPLICANT: WATKINS, HIGH
APPLICANT: NOSENZWEIG, ANTHONY
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: LAHIVE & COCKFIELD STREET, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/08469172; Publication No. US20030054343A1
     Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 60 STATE CITY: BOSTON STATE: Massachuse COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-08-469-172-3
     Sequence 3, Appli
Sequence 3035, Ap
Sequence 8035, Ap
Sequence 18356, A
                                                                                                                     ; ; Search time 322.586 Seconds (without alignments) 615.265 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          runished Applications Na;

(9GDZ 6/ptodata1/pubpna/USO7 PUBCOMB.seq:*
(9GDZ 6/ptodata1/pubpna/USO7 PUBCOMB.seq:*
(9GDZ 6/ptodata1/pubpna/USO6 FUBF PUB.seq:*
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(9GDZ 6/ptodata1/pubpna/USO9 FUBF PUBF Seq:*
(9GDZ 6/ptodata1/pubpna/USO9 FUBFOOMB.seq:*
(9GDZ 6/ptodata1/pubpna/USO9 FUBFOOMB.seq:*
(9GDZ 6/ptodata1/pubpna/USO9 NEW PUB.seq:*
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(9GDZ 6/ptodata1/pubpna/USO9 PUBCOMB.seq:*
(9GDZ 6/ptodata1/pubpna/USO0 NEW PUB.seq:*
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                  GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-110-788-779-3

S US-11-036-317-8035

S US-11-036-317-18356

S US-11-036-317-584705
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     9794790 seqs, 4134909567 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                             1 ATGCCAACCCTGCTCTGGAGGCCT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:*
                                                                                                                       November 18, 2005, 06:36:48
                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-788-779-3
24
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Match Length
                                                                                                                                                                                                                                                                 IDENTITY NUC
                                   Copyright
                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0 Maximum DB seq length: 50
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100.0
80.0
74.2
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17.8
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Result Š.

Gaps

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APPLICANT: Williams, Alan APPLICANT: Williams, John TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
                                                                                                            DB 20; Length 24;
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CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 8035
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 26;
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                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 19.2; 187.5%; Pred. No. 60;
                                                                                                            Score 24;
Pred. No. 0
                             MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                    1 ATGCCAACCCTGCTCTGGAGGCCT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGCCAACCCTGCTCTGGAGGCCT 24
                                                                                                                                                                                                                                                                                                                     US-11-036-317-8035
. Sequence 8035, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGGCTAACCCGCTCTGGAGGCCT
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                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 24; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.2%;
90.5%;
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Best Local Similarity 87.59
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Best Local Similarity 90.5<sup>3</sup>
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Mus musculus
US-11-036-317-8035
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US-11-036-317-18356
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US-11-036-317-18356
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US-10-788-779-3
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Publication No. US20040152121A1
GENERAL INFORMATION:
APPLICANT: SEIDWAN, CHRISTINE
SEIDWAN, JOHN
WATKINS, HIGH
ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
DISEASE-ASSOCIATED MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/788,779
FILING DATE: 27-Feb-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/469,172
FILING DATE: «Unknown»

APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.

REGISTRATION NUMBER: 33,505
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS.
ADDRESSEE: LAHIVE &:
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGCCAACCCTGCTCTGGAGGCCT 24
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                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: CDNA
US-08-469-172-3
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                                                                                                                                                                                                                                               Sequence 18356, Application US/11036317
; Sequence 18356, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; RICH RING DATE: 2004-01-13
; NUMBER OF EX ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18356
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Length 25;
                                            Indels
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Gaps
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Pred. No. 9.6e+02;
0; Mismatches 4; Indels (
                                                                                                                                                                                                        Length 25;
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPRENCE: 3527.
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOTTWARE: Microarray Probe Sequence Listing Generator V 1.1
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 924760
LENGTH: 25
                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 54586, Application US/10809189; Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT APPLICATION NUMBER: US/09/396,196
FRIOR APPLICATION NUMBER: 60/100,678
                                                                                                                                                                                                     69.2%; Score 16.6; DB 22; 82.6%; Pred. No. 9.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.6; DB 22;
Pred. No. 9.6e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                   Pred. No. 9.6e
0; Mismatches
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, Publication No. US20040146910A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                3 ATACCAACCTGCTGTGGTGACC 25
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82.6%;
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82.6%;
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; ORGANISM: Rattus norvegicus
US-10-719-956-188380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.6°
Matches 19; Conservative
                                                                                                                                                                                                                                                                  19; Conservative
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Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                ; ORGANISM: Mus musculus
US-10-719-900-924760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: mus musculus
US-10-809-189-54586
                                                                                                                                                                                                                                   Sest Local Similarity
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                                             Sequence 584705, Application US/11036317

Sequence 584705, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPERENCE: 3654.1

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR PILING DATE: 2004-01-13

NUMBER: OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 584705

LENGTH: 25
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Sequence 833111, Application US/10719900
Publication No. US20550026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
ITTLE OF INVERNION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT PILING DATE: 2003-11-20
PRIOR FILING DATE: 2002 11 20
PRIOR FILING DATE: 2002 11 20
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 833111

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 74.2%; Score 17.8; DB 26; Length 25; Local Similarity 90.5%; Pred. No. 2.7e+02; nes 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.2%; Score 16.6; DB 22; Length 25; larity 82.6%; Pred. No. 9.6e+02; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-719-900-924760
; Sequence 924760, Application US/10719900
; Publication No. US200S0026164A1
; GENERAL INFORMATION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR PILING DATE: 2003-11.20
; PRIOR FILING DATE: 2002-11.20
; NUMBER OF SEQ ID NOS: 982914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-584705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-833111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                           RESULT 5
US-11-036-317-584705
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Best Local S
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RESULT 7

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US-10-719-900-53167

Sequence 53167, Application US/10719900

Publication No. US20550026164A1

GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou

TITLE OF INVERTION: Methods of Genetic Analysis of Mouse
FILE REPERBUGE 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT APPLICATION NUMBER: 60/427,808

PRIOR PILING DATE: 2002-11.20

PRIOR FILING DATE: 2002-11.20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 53167

LENGTH: 2567
                                                                                                                                                                                                                                                                    Length 25;
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; Sequence 54585, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Mack
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT APPLICATION NUMBER: US/09/396,196
; PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1999-09-15
; WINCR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FRSEEQ for Windows Version 4.0
; SEQ ID NO 54585
                                                                                                                                                                                                                                                             Score 16.2; DB 26;
Pred. No. 1.5e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.8%; Score 15.8; DB 22;
89.5%; Pred. No. 2.2e+03;
vative 0; Mismatches 2;
      FILE REFERENCE: AMI01083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 77825
LENGTH: 25
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TITLE OF INVENTION: Target Genes
                                                                                                                                                                                                                                                               Query Match 67.5%;
Best Local Similarity 85.7%;
Matches 18; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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US-10-719-900-53167
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                                                                                                                                                                                                ORGANISM: probe US-11-060-756-77825
                                                                                                                                                                           TYPE: DNA
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Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
ITILE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
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US-11-036-317-584704

US-11-036-317-584704

Sequence 584704, Application US/11036317

PUBLICACTOR NO. US2000214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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                                                                                                                             Sequence 174561/c

Sequence 174561, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002 11 20

WUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                    23
                                                            1 Argaciaccardereregaace 23
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85.7%;
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Best Local Similarity 85.7'
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Best Local Similarity 85.77
Marches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-174561
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CRGANISM: Mus musculus
US-11-036-317-584704
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US-11-060-756-77825/c
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Gaps

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Sequence 327390, Application US/11036317
Sequence 327390, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Williams, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US/6536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                                                                               Peptide-Antibody Conjugates with Modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Primer used in Production of VH Cassette/CH1/hinge US-10-887-230-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT PEPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.0%; Score 15.6; DB 22;
81.8%; Pred. No. 2.6e+03;
iive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.2%; Score 15.4; DB 26; 94.1%; Pred. No. 3.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                 TITLE OF INVENTION: MACCIass I - Peptide-An:
TITLE OF INVENTION: MECCIass I - Peptide-An:
TITLE OF INVENTION: MECCIass I - Peptide-An:
TITLE OF INVENTION: MEANING TO COUR.
CURRENT APPLICATION NUMBER: US/10/887,230
CURRENT FILING DATE: 2004-07-09
PRIOR FILING DATE: 2003-7-10
PRIOR FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.2
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 170847, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 ATGCCCACCGTGCCCAGGAGGC 19
  Sequence 21, Application US/10887230 Publication No. US20050042218A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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1es 18; Conservative
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US-11-036-317-327390
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Best Local Similarity
The 16; Conserv?
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US-11-036-317-327390/c
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                                                Length 25;
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                                                                                        Indels
                                                                                                                                                                                                                                                US-10-035-833A-1677/c

US-10-035-833A-1677/c

Sequence 1677, Application US/10035833A

Publication No. US20040072156A1

GENERAL INFORMATION:

APPLICANT: Nakamura Yuho

APPLICANT: Setine, Akiniro

APPLICANT: Saito, Osamu

TITLE REFERENCE: FORS-06904

CURRENT APPLICATION NUMBER: US/10/035,833A

CURRENT APPLICATION NUMBER: US/10/035,833A

WUMBER OF SEQ ID NOS: 7669

SOFTWARE: Patentin Version 3.2

SEQ ID NO 1677
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APPLICANT: 11da, Aritoshi
APPLICANT: Saito, Osamu
TITLE OF INVENTION: Detection of Genetic Polymorphisms
FILE REPERENCE: FORS-06904
                                            Query Match 65.8%; Score 15.8; DB 22; Best Local Similarity 89.5%; Pred. No. 2.2e+03; Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 65.8%; Score 15.8; DB 19;
1. Similarity 81.0%; Pred. No. 2.1e+03;
17; Conservative 1; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7225, Application US/10035833A Publication No. US20040072156A1 GENERAL INFORMATION:
APPLICANT: Nakamura, Yuho
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                                                                                                                                    2 TGCCAACCCTGCTCTGGAG 20
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US-10-035-833A-7225
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Best Local Similarity
US-10-809-189-54585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-035-833A-1677
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US-10-887-230-21/c
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TILLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT PLING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SQTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 170848
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FUBLICALINFORMATION:
FUBLICALINFORMATION:
FILE REFERENCE: 3520.1
FURRENT FILING DATE: 2003-11-20
FRIOR APPLICATION NUMBER: 60/427,808
FRIOR FILING DATE: 2003-11-20
FRIOR PFLING DATE: 2002-11-20
FRIOR FILING DATE: 2002-11-20
FRIOR SEQ ID NOS: 982914
FRIOR FILING DATE: 2002-11-20
FRIOR FILING DAT
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85.0%; Pred. No. 4.3e+03;
iive 0; Mismatches 3; Indels (
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                                                                                                                                                                                                                                                                                                                                                               63.3%; Score 15.2; DB 22; Length 25; 85.0%; Pred. No. 4.3e+03; ive 0; Mismatches 3; Indels
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 170847
LENGTH: 25
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Best Local Similarity 85.0°
Matches 17; Conservative
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Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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; ORGANISM: Mus musculus
US-10-719-900-352179
                                                                                                                                                                                                              TYPE: DNA ORGANISM: Mus musculus
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; ORGANISM: Mus musculus
US-10-719-900-170848
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US-10-719-900-352179/c
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US-10-719-900-170848
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Sequence 196604, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERBERS: 031896-043000 (AM 101081)
FILE REPERBERS: 031896-043000 (AM 101081)
CURRENT APPLICATION HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION: UNDERS: US/10/956,157

CURRENT PILING DATE: 2004-10-04
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US-10-719-900-513335

US-10-719-900-513335

Sequence 51335, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVERNION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT APPLICATION NUMBER: 05/427,808

PRIOR PILING DATE: 2002-11.20

PRIOR FILING DATE: 2002-11.20

NUMBER: OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 51335

LENGTH: 25
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse; TILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR PILING DATE: 2003-11-20
; PRIOR PILING DATE: 2003-11-20
; PRIOR PILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 796279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Best Local Similarity 85.0°
Matches 17; Conservative
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Best Local Similarity 85.0°
Matches 17; Conservative
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US-10-719-900-513335
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US-10-719-900-796279
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US-10-719-900-796279
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NUMBER OF SEQ ID NOS: 319805

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; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-671714
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US-11-036-317-52603
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Best Local Similarity
Matches 17; Conserv
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US-11-036-317-52603
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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US-10-719-956-95487/Application US/10719956
; Sequence 95487, Application US/10719956
; Publication No. US20040146910A1
; GRENEAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; ERNGTH: 25
                                                                                                                                                                                                                                                                                                                                                                        Sequence 26759, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT APPLICATION NUMBER: 00/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
                                                                                                                                                       Length 25;
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                                                                                                                                                 Query Match 63.3%; Score 15.2; DB 22; Best Local Similarity 85.0%; Pred. No. 4.3e+03; Matches 17; Conservative 0; Mismatches 3;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 196604
LENGTH: 25
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; ORGANISM: Rattus norvegicus
US-10-719-956-26759
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; ORGANISM: Rattus norvegicus
US-10-719-956-95487
                                                               ; TYPE: DNA; ORGANISM: Probe Sequence US-10-956-157-196604
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RESULT 34
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Sequence 294807, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US/11/036,317
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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; Sequence 25/640, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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                                                                                                                                                                                  Length 25;
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 194782
LENGTH: 25
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85.0%; Pred. No. 4.3e+03;
iive 0; Mismatches 3;
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85.0%; Pred. No. 4.3e+03;
tive 0; Mismatches 3;
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Matches 17; Conservative
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Matches 17; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-294807
                                                                                                   TYPE: DNA ORGANISM: Mus musculus
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US-11-036-317-257640
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les 17; Conserv
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US-11-036-317-257640/c
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Sequence 305597, Application US/11036317
Sequence 305597, Application US/11036317
Sublication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPRENCE: 36540.
FILE REPRENCE: 36540.
CURRENT PILING DATE: 2005-01-13
FRIOR APPLICATION NUMBER: US 60/536,639
FRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 305597
ILBROAD 305597
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Sequence 311815, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Williams, John
TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1

CURRENT PILING DATE: 2005-01-13

PRIOR PILING DATE: 2004-01-13

PRIOR FILING DATE: 2004-01-13

NUMBER: OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
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Pred. No. 4.3e+03;
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3 GCCAACCCTGCTCTGGAGGC 22
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85.0%;
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Best Local Similarity 85.0°
Matches 17; Conservative
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Best Local Similarity 85.03
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-305597
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US-11-036-317-305597/c
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) OTHER INFORMATION: Human oxidosqualene synthase nucleotide probe with XbaI site inse
) OTHER INFORMATION: (TCTAGA).
US-10-885-190B-2
                                    Gaps
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APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Tronect, Andrew
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REPERENCE: AM101080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
LENGTH: 25
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85.0%; Pred. No. 4.2e+03;
iive 0; Mismatches 3;
         Best Local Similarity 85.0%; Pred. No. 4.3e+03; Matches 17; Conservative 0; Mismatches 3;
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Pred. No. 5.3e+03;
0; Mismatches 5;
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Sequence 2, Application US/10885190B

Publication No. US20050202548A1

GENERAL INFORMATION:

APPLICANT: Hoffmann-La Roche Inc.

TITLE OF INVENTION: Crystal structure of OSC

FILE REFERENCE: Case 21/97

CURRENT APPLICATION NUMBER: US/10/885,190B

CURRENT APPLICATION NUMBER: US/10/885,190B

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1
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; Publication No. US20050026164A1
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Matches 17; Conservative
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Best Local Similarity
Matches 18; Conserv
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US-10-775-169-2685/c
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CRGANISM: probe
US-10-775-169-2685
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LENGTH: 29
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Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Woults, William Martin
APPLICANT: Woults, William Martin
APPLICANT: Woults, William Martin
APPLICANT: Woults, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SSOFTWARE: Parentin version 3.2
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blume, John TITLE OF INTERNITON: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.1 CURRENT APPLICATION NUMBER: US/11/036,317 CURRENT PILING DATE: 2005-01-13 PRIOR APPLICATION NUMBER: US 60/536,639
                                                                                                                                                                                                                                                                                                                                            Gaps
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FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 322925
LENGTH: 25
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SOFTHARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 443709
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                          Indels
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85.0%; Pred. No. 4.3e+03;
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               3 GCCAACCCTGCTCTGGAGGC 22
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Best Local Similarity 85.0%
Matches 17; Conservative
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Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                    ; ORGANISM: Mus musculus
US-11-036-317-322925
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CORGANISM: Mus musculus
US-11-036-317-443709
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US-11-036-317-443709
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; ORGANISM: probe
US-11-060-756-256216
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US-10-719-900-408446

is Sequence 408446, Application US/10719900

is Publication No. US20050026164A1

is GENERAL INFORMATION:

if APPLICANT: Xue Mei Zhou

if TILLE OP INVENTION:

if CURRENT APPLICATION NUMBER: US/10/719,900

if CURRENT FILING DATE: 2003-11-20

if PRIOR FILING DATE: 2003-11-20

if REPRINGED INVENTION NUMBER: 60/427,808

if RICHARD APPLICATION NUMBER: 60/427,808
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT PILIGE DATE: 2003-11-20

PRIOR PILICATION NUMBER: 60/427,808

PRIOR PILICATION NUMBER: 60/427,808

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.5%; Score 15; DB 22; Length 25; Best Local Similarity 78.3%; Pred. No. 5.38+03; Matches 18; Conservative 0; Mismatches 5; Indels
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CORGANISM: Mus musculus
US-10-719-900-13488
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CORGANISM: Mus musculus
US-10-719-900-408446
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Search completed: November 18, 2005, 15:41:04 Job time : 323.586 Becs

Sequence

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Run on:

Sequence:

Searched:

Database

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AK697195 Sequence
AR53746 Sequence
AR53326 Sequence
AK53326 Sequence
AK93184 Sequence
AK93184 Sequence
AK28473 Sequence
AR56546 Sequence
AR56546 Sequence
AR56546 Sequence
AR19012 Sequence
BD170377 Novel for
AR290927 Sequence
AR190122 Sequence
AR190122 Sequence
AR325099 Sequence
AR32509 Sequence
AR31509 Sequence
AR31509 Sequence
AR31509 Sequence
AR31100 Sequence
AR79100 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.
1 (Dases I to 24)
Seidman, C., Seidman, J., Watkins, H. and Rosenzweig, A.
Method for detecting hypertrophic cardiomyophathy associated
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Owens, R.J., Perry, M.J. and Lumb, S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutations
Patent: US 5429923-A 4 04-JUL-1995;
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5429923.
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Sequence 21 from Patent W09620281.
A52065 1 GI:2304690
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A94624
AX017662
CQ856685
                                                                                                                                                                   AR325098
AR325099
DOGP47701
AX462495
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CQ880137
CQ880249
BD170377
AR290927
AR190122
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AX791100
BD266478
           AX697195
AR355880
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AR284732
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                                                                                                                                                                                                                                                                                                                                                                                                             GI:910874
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112897
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AX663129 Sequence
CQB18593 Sequence
BD074127 Compositi
CQB87208 Sequence
AX793975 Sequence
AX79317 Sequence
AX79376 Sequence
BD274040 Identific
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A52065 Sequence 21
AR067674 Sequence
AR169819 Sequence
E22424 Method for
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AX061955 Sequence
AX514615 Sequence
                                                                        November 18, 2005, 11:12:34; Search time 665.886 Seconds (without alignments) 1746.433 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                             1839042
         GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                     4708233 segs, 24227607955 residues
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                  - núcleic search, using sw model
                                                                                                                  US-10-788-779-4
24
1 CTTCATGTTTCCAAAGTGCATGAT
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AR067674
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CQ818593
BD074127
CQ857208
AX793975
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AR120382
BD274040
BD274049
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AX061955
AX514615
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gb_htg:*
gb_in:*
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Match 1
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Result No.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 35)

Yamaji,N., Nishimura,K. and Sasamata,M.
Novel metallic protease

Deatent: UP 2001017183-A 19 23-JAN-2001;
YAMANOUCHI PHARMACEUT CO LTD
OS Homo sapiens (human)
PN JP 2001017183-A/19
PD 23-JAN-2001
PF 09-JUL-1999 JP 1999196584
PR NOBORU YAMAJI,KOICHI NISHIMURA,MIHO SASAMATA
PC CIZN15/09,CO7K16/40,CIZN1/15,CIZN1/19,CIZN1/21,CIZN5/10, PC CIZN15/00,CIZUS/50,CIZN15/00,CIZN15/00,CIZN15/00,CIZN15/00
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                                                                                                                      PAT 18-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               YOSHIKAZU ICHIHARA,AKIRA AWAYA
C12N15/09,C07K14/47,C12P21/02//(C12P21/02,C12R1:91),C12N15/00
Strandedness: Single;
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Lass 1 to 35)
Lass 1 to 35)
Lass 2 to 36)
Lass 3 to 36
Lass 3 to 36
Lass 3 to 36
Lass 4 to 9-FEB-1999;
EDUCATIONAL FOUNDATION FUJITA GAKUEN, RYUJI HUNAKOSHI
COMMENT OS UNidentified
PN JP 1999032779-A/4
PN JP 1999032779-A/4
PN JP 1999032779-A/4
PR 24-UUL-1997 JP 1997214074
PR CC12N15/09,C07XX4/4/7,C1"
CC Strandedness: Sir-
CC Strandedness: Sir-
CC Topology: Li-
FH Key
FT Sour
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    .35
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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                       3 TTTAAGCTTCCAAAGTGCATG 23
     2 TICATGITICCAAAGIGCAIG 22
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Novel metallic protease.
E58671
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JP 2001017183-A/19.
Homo sapiens (human)
Homo sapiens
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Owens, R.John., Perry, M.John., and Lumb, S.Mark.
Human phosphodiestrase type IVC, and its production and use
Patent: US 6291199-A 21 18-SEP-2001;
Location/Qualifiers
HUMAN PHOSPHODIESTERASE TYPE IVC, AND ITS PRODUCTION AND USE PALENT: WO 9620281-A 21 04-JUL-1996; CELLTECH THERAPEUTICS LTD (GB) Other publication AU 4270596 960719.

Location/Qualifiers
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Human phosphodiesterase type IVC, and its production and use
Patent: US 5851784-A 21 22-DEC-1998;
Location/Qualifiers
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                                                                                                                                                                                      67.5%; Score 16.2; DB 6; Length 34; llarity 85.7%; Pred. No. 6.7e+03; Conservative 0; Mismatches 3; Indels
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                                                                                     1. .34
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 21 from patent US 5851784.
AR067674
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 21 from patent US 6291199.
AR169819
AR169819.1 GI:17907735
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1 (bases 1 to 34)
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Best Local Similarity 85.7
Matches 18; Conservative
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Best Local Similarity 85.7
Matches 18; Conservative
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AR169819
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SCHULTZ,
SCOTT J PARKINSON
C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/68, G01N33/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A61K31/7088, A61K39/00, A61K39/395, A61K39/395, A61K48/00, A61P35/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Topology: Linear;
Composition binding specifically to colorectal cancer and
utilization
                                                                                                                                                                                                                                                                                                                                                                                                     unclassified.

1 (bases 1 to 27)

Whadman, S.A., Pearlman, J.M., Barber, M.T., Schultz, S. and Parkinson, S.A.

Composition binding specifically to colorectal cancer and utilization thereof the patent: JP 200151266-A 18 28-AUG-2001;

THOMAS JEFFERSON UNIVERSITY

S. Unidentified

P. JP 200151266-A/18
                                                                                                                                                                                                                                                        COmposition binding specifically to colorectal cancer and
                                                                                    Length 49;
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                                                                                  Score 14.8; DB 6;
Pred. No. 3.3e+04;
0; Mismatches 2;
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CQ857208/c
LOCUS CQ857208 30 bp DNA
DEFINITION Sequence 550 from Patent WO2004069997.
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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07-AUG-1998 JP 2000506228
07-AUG-1997 US 08/90864
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Strandedness: Double;
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                                                                                 Query Match 61.7%;
Best Local Similarity 88.9%;
Matches 16; Conservative (
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Enzymatic encoding
Patent: WO 2004039825-A 23 13-MAY-2004;
Nuevolution A/S (DK)
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Human leucine-rich repeat containing protein, expressed
predominantely in small intestine, HLRRSII
Patent: WO 02061086-A 36 08-AUG-2002;
Bristol-Myers Squibb Company (US)
Location/Qualifiers
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                             ce 1. .35
/organism='Homo sapiens (human)'.
Location/Qualifiers
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db xref="taxon:32630"
/note="Synthesized oligonucleotide.
                 Location/Qualifiers
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CQ818593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other sequences; artificial sequences.
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                                                                               1. .35
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                             Helicobacter pylori
Helicobacter pylori
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Helicobacteraceae, Helicobacter.
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Helicobacteraceae; Helicobacter.
                                                                                                                        Thiberge, J.M., Labigne, A., Coppee, J.Y. and Lacroix, C. Method for the production of a composition of dna sequences or the expression products thereof permitting the identification of the strains of helicobacter polori and use thereof in a prognostic or diagnostic method and produced by the Patent: Wo 2004069997-A 550 19-AUG-2004; INSTITUT PASTER (FR)
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                                                                                                                                                                                                                                                                                                                                                      Query Match 60.0%; Score 14.4; DB 6; Length 30; Best Local Similarity 75.0%; Pred. No. 5.5e+04; Matches 18; Conservative 0; Mismatches 6; Indels
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    .30
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/mol type="unassigned DNA"
/db_xref="taxon:210"
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CQB74317.1 GI:52747832
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other sequences; artificial sequences.
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                GI:51851583
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CQ857208
CQ857208.1
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AX793975/c
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BD274040.1 GI:33083808
JP 2025256030-A/7.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases I to 36)
Excer, D.J., Sampath, R., Griffey, R. and Mcneil, J.
Identification of molecular interaction sites in RNA for novel drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD274040 36 bp DNA linear PAT 17-JUL-2003 Identification of molecular interaction sites in RNA for novel drug
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                                                                                                                                                                                                                                                                                                                                                Gaps
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Bruggemann, M. Genetically modified non-human mammals and cells Genetically modified non-human mammals and cells Patent: WO 2004076618-A 13 10-SEP-2004; THE BABRAHAM INSTITUTE (GB)

    .28
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/note="Gamma 2a b reverse primer"

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ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/7
PD 20-AUG-2002
PP 12-MAY-1999 JP 2000548510
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PAT 27-AUG-2002

linear

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PAT 24-JAN-2001

linear

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E Unitabilities.

Kunsch, C.A., Choi, G.H., Johnson, S.L. and Hromockyj, A.

Kunsch, C.A., Choi, G.H., Johnson, S.L. and Hromockyj, A.

Streptococcus preumoniate antigens and vaccines

Patent: JP 2001505415-A 145 24-APR-2001;

HUMAN GENOME SCIENCES INC

PN JP 2001505415-A/145

PD 24-APR-2001

PF 30-OCT-1996 US 60/029960

PR 31-OCT-1996 US 60/029960

PR 31-OCT-1997 US 60/029960

PR 31-OCT-1997 US 60/029960

PR 31-OCT-1996 US 60/029960

PR 31-OCT-1997 US 60/029960

PR 4-OCT-1997 US 60/029960

PR 50/029960

PR 50/
                                                                                            (bases 1 to 36)
Choi.G.H., Kunsch, C.A., Barash, S.C., Dillon, P.J., Dougherty, B., Fannon, M.R. and Rosen, C.A.
Streptococcus pneumoniae antigens and vaccines
Patent: US 6573082-A 258 03-JUN-2003;
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llarity 77.3%; Pred. No. 8.6e+04;
Conservative 0; Mismatches 5; Indels
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Streptococcus pneumoniae antigens and vaccines.
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Sequence 3 from Patent WO0100837.
AX061955.1 GI:12539939
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AX061955/c
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BD063391
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JP 2002526030-A/16.
synthetic construct
other sequences; artificial sequences.
I (bases I to 36)
Ecker, D.J., Sampath, R., Griffey, R. and Moneil, J.
Identification of molecular interaction sites in RNA for novel drug
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PR 12-MAY-1998 US 60/055092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC
C12Q1/68, AGIK31/7105, AGIK48/00, C12N15/09, C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
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us-10-788-779-4.rge

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Location/Qualifiers
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                                                                                                             Query Match 58.3%;
Best Local Similarity 70.8%;
Matches 17; Conservative
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Best Local Similarity 77.3%;
Matches 17; Conservative (
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synthetic construct
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                                                                             Basbill polypeptide and polynucleotide from moraxella catharrhalis Patent: Wo 0100837-A 3 04-JAN-2001; SMITHKLINE BEECHAM BIOLOGICALS (S.A.) Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Detection of genetic polymorphisms
Patent: WO 02052044-A 6755 04-JUL-2002;
Riken (JP)
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Patent: WO 02052044-A 813 04-JUL-2002;
                                                                                                                                             1. .38
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Primer"
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                                other sequences; artificial sequences.
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AX520557
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AX514615
AX514615.1 GI:23561172
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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synthetic construct
                                                                 Thonnard, J.S.
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AX520557/c
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Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
                                                  Gaps
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Score 14; DB 6; Length 41;
Pred. No. 8.5e+04;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14; DB 6; Length 46;
Pred. No. 8.5e+04;
0; Mismatches 5; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Location/Qualifiers
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PAT 22-DEC-2003
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db. zref="taxon:32630"
/db. zref="taxon:32630"
/note="bescription of Artificial Sequence: based on genomic DNA sequence from Human Papilloma Virus"
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/organism='Unknown'.
Location/Qualifiers
                              unidentified
unclassified.
1 (bases 1 to 31)
Sha,N., Walinton,J. and Patel,N.
Patent: JP 2000245487-A 498 12-SEP-2000;
APIMETRICS INC
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                      JP 2000245487-A/498
12-SEP-2000
27-JAN-2000 JP 2000019392
27-JAN-1999 US 09/238.402
NIRA SHA,JANET WALINTON,NIRA PATEL
C12N15/09,C12Q1/68,C12N15/00
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synthetic construct
other sequences; artificial sequences.
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Sequence 41 from Patent WO03087829.
AX931884
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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    JP 2000245487-A/498
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AX931884/c
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    KEYWORDS
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Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
Rosen, C.A.
                    Gaps
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Patent: US 6737248-A 1998 18-MAY-2004;
Location/Qualifiers
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                                                                                                                                                        linear
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                   6; Indels
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Echt, C.S. and Nelson, C.D.
Microsatellite DNA markers and uses thereof
Patent: US 6733965-A 173 11-MAY-2004;
Location/Qualifiers
   73.9%; Pred. No. 8.5e+04; iive 0; Mismatches 6
                                                                                                                                                   AR537436 50 bp DNA Sequence 1998 from patent US 6737248. AR537436
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Sequence 173 from patent US 6733965.
AR533926.1 GI:53923959
                                                                                                                                                                                                                                                                                                                                                                                  /organism="unknown"
/mol_type="genomic DNA"
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BD002832
BD002832.1 GI:18630793
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Best Local Similarity 73.9°
Matches 17; Conservative
                 17; Conservative
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Unclassified.
Best Local Similarity
Matches 17; Conserv
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CQ880249.1 GI:54034016
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Best Local Similarity 80.0%;
Matches 16; Conservative 0
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synthetic construct
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Indectious etiologic agent detection probe and probe set, carrier, and genetic screening method
Patent: EP 146471-0-A 1 06-0CT-2004;
CANON KABUSHIKI KAISHA (JP)
Location/Qualifiers
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Gage, F.H., Palmer, T., Safar, F.G., Takahashi, J. and Takahashi, M.
Gage, F.H., Palmer, T., Safar, F.G., Takahashi, J. and Takahashi, M.
Method of isolating adult mammalian CNS-derived progenitor stem
cells using density gradient centrifugation
Patent: US G77738 + 10 27-JUL-2004;
Location/Qualifiers
                                                                                     1 (bases 1 to 47)
Blumenfeld,M., Chumakov,I., Bougueleret,L. and Cohen,A.
Biallelic markers related to genes involved in drug metabolism
Patent: US 6528260-A 784 04-MAR-2003;
Location/Qualifiers
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Sequence 10 from patent US 6767738.
AR565646
AR565646.1 GI:53981680
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Sequence 1 from Patent EP1464710.
CQ880137.1 GI:54033904
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                                                                                                                                                                             /organism="unknown"
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TGTCTCCAAAGTTGAYGAT 27
              GI:29721636
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/db_xref="Complementary DNA Sequence of Synthesized DNA probe PA-1"
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conter sequences; artificial sequences.

I bases 1 to 27)
Takaoka, Y. and Namba, H.
Novel formate dehydrogenase and process for producing the same
L patent: WO 0246427-A 7 13-UUN-2002;
KANEKA CORP, YASUKO TAKAOKA, HIROKAZU NAMBA
OS Artificial Sequence
PD 13-UUN-2002
PP 04-DEC-2001 WO 2001JP010569
PR 04-DEC-2000 JP 00P 368838
PI YASUKO TAKAOKA, HIROKAZU NAMBA
PC C12N15/53, C12N9/04, C12N1/21
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Suzuki,T., Ishii,M. and Fukui,T.
Infectious etiologic agent detection probe and probe set, carrier,
and genetic screening method
Patent: EP 1464710-A 113 06-OCT-2004;
CANON KABUSHIKI KAISHA (JP)
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                                                                                                    /note="Synthesized DNA probe named PA-1"
                                                                                                                                                                       Score 13.6; DB 6;
Pred. No. 1.4e+05;
0; Mismatches 4;
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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CQ880249
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PAT 20-APR-2002
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                                                                                                                                                                                                                                                                            1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 5611 12-FEB-2002;
Location/Qualifiers
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavco, P., McSwiggent for the treatment of diseases or conditions
related and reagent for the treatment endothelial growth factor receptor
Patent: US 6566127-A 2500 20-MAY-2003;
Location/Qualifiers
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Pred. No. 1.8e+05;
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US 6566127.
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AR325099.1 GI:33710907
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AR190123
        Mismatches
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/mol_type="unassigned RNA"
                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="unassigned DNA"
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/organism="unknown"
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Best Local Similarity 93.39
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AR325098/c
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AR325099/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown.
Unknown.
Unclassified.
I (bases 1 to 17)
I (bases 1 to 17)
Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
Pavco,P., McSwiggen,J. the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 5610 12-PEB-2002;
Location/Qualifiers
                                                                                                                                                                                                                Gaps
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Biallelic markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6537751-A 2662 25-MAR-2003;
Location/Qualifiers
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                             ce 1. .27 /organism='Artificial Sequence'
Location/Qualifiers
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                                                                                                                                                                             Query Match 56.7%; Score 13.6; DB 6; Length 27; Best Local Similarity 80.0%; Pred. No. 1.4e+05; Matches 16; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                             linear
Description of Artificial Sequence: primer-5
Key
                                                                               1. .27
/organism="synthetic construct"
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/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                     Sequence 2662 from patent US 6537751.
AR290927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR190122 17 bp DNA
Sequence 5610 from patent US 6346398.
AR190122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
/wol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TCATGTTTCCAAAGTGCATGAT 24
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Best Local Similarity 72.73
Matches 16; Conservative
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RESULT 33 AR190122/c

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RESULT 32 AR290927/c

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PAT 15-JUL-2002

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Sugimoto, Y., Thara, N. and Mizoshita, K.
Direct Submission
Submitted (04-MAR-2004) Yoshikazu Sugimoto, Shirakawa Institute of Animal Genetics, Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan (E-mail:kazusugi@siag.or.jp, Tel:81-248-25-5641, Fax:81-248-25-5725)
                                                                                                                                                                                                                                   Aegilops tauschii
Wataryota, Viridiplantae; Streptophyta; Bmbryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Aegilops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A comprehensive genetic map of the cattle genome based on 3802 microsatellites
Genome Res. 14 (10), 1987-1998 (2004)

    .23
/note="forward primer for microsatellite NRDIKM020"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABLOCOUR 23 bp DNA linear SYN 07-Synchetic construct DNA, forward primer for microsatellite NRDIKM020.
                                                                                                                                                                                                                                                                                                                              Bernard, M., Sourdille, P. and Guyomarch, H.
Microsatellite markers from Trilicum tauschii
Patent: EP 12/17079-A 239 26-UUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%; Score 13.4; DB 6; Length 20; 93.3%; Pred. No. 1.8e+05;
                                                                                                                   linear
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/organism="synthetic construct"
/mol_type="other DNA"
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                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Aegilops tauschii"
/mol_type="unassigned DNA"
/db_xref="taxon:37682"
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                                                                                                                 20 bp | Sequence 239 from Patent EP1217079.
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AB166618.1 GI:51850034
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TTTCCAAAGGCCATG 1
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synthetic construct
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Matches 14; Conservative
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AB166618/c
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KEYWORDS
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Canis familiaris
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 18)
Ostrander, E. A., Mapa, F. A., Yee, M. and Rine, J.
One hundred and one new simple sequence repeat-based markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Original source text: Canis familiaris (library: E. Ostrander, in pBluescript+) adult spleen DNA. Submitted by:
                                                                        1 (bases 1 to 17)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 2501 20-MAY-2003;
Location/Qualifiers
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ses C for 0.45 minutes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOGP47701 18 bp DNA linear
Dog (Clone: CXX.477) primer for STS 477, 5' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fred Hutchingon Cancer Research Center
Transplantation Biology Dept
1124 Columbia; Mailstop M318
Seattle, Wa 99104, USA
e-mail: EAGOSTRANGER®1b.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.
Annealing: 55 or 59 degrees C for 0.45 minut
POlymerization: 74 degrees C for 0.45 minutes
PCR Cycles: 33
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ension: 74 degrees C for 5.00 minutes.
Location/Qualifiers
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/db_xref="taxon:9615"
/tissue_type="spleen"
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/tissue_lib="E. Ostrander, ir
1. 18
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PCR identification; PCR primer; STS.
1 of 2
                                                                                                                                                                                                                                 /mol_type="unassigned RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the canine genome
Mamm. Genome 6 (3), 192-195 (1995)
                                                                                                                                                                                                            /organism="unknown"
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Best Local Similarity 93.39
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Best Local Similarity
Matches 14; Conserv
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KEYWORDS
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Query Match 55.8%; Score 13.4; DB 12; Length 23; Best Local Similarity 93.3%; Pred. No. 1.8e+05; Matches 14; Conservative 0; Mismatches 1; Indels (
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                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                          Novel RNase-like protein and its use
Patent: EP 0943679-A 7 22-SEP-1999;
INNOGENETICS NV (BE)
Location/Qualifiers
1 . 29
/organism="unidentified"
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/db_xref="taxon:32644"
                                                                                                                                                        A94624 29 bp
Sequence 7 from Patent BP0943679.
A94624.1 GI:6778935
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16 TTCATGTTACCAAAG 2
                                                                                                                                                                                                                            unidentified
unidentified
unclassified.
1 (bases 1 to 29)
                                                                                                                         RESULT 40
A94624/C
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DEFINITION
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Search completed: November 18, 2005, 17:42:53 Job time : 667.986 secs

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November 18, 2005, 05:29:23; Search time 165.262 Seconds (without alignments) 859.686 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                      4390206 seqs, 2959870667 residues
                                                                                                                                                                                                                        1 CTTCATGTTTCCAAAGTGCATGAT 24
                                                                  - nucleic search, using sw model
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                                                                                                                                                                                    US-10-788-779-4
24
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Perfect score:
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geneseqn1980s:*
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geneseqn2000s:*
geneseqn2001as:*
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geneseqn2002s:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* geneseqn2003cs:* genesegn2002bs:* genesegn2003as:* genesegn2003bs:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaq91124 Beta-card	Aca63114 Human bet	Adr05300 Human bet	Aah46257 Aldehyde/	Aat34642 Primer fo		_		Aad30162 HA-tagged	Adp21883 Ornithine	Adp21988 Ornithine	Ado04093 Identifie	Aax27821 CRCA-1 co	Ado41360 Oligo 3-2	Aal57225 Oligonucl	Aal57224 Oligonucl	Abx70212 Novel Hel	Adr23060 DNA/RNA D	Aal45772 Human aci	Abt 42676 Hillian G-n
SUMMARIES	ID	AAQ91124	ACA63114	ADR05300	AAH46257	AAT34642	AAX18400	AAH20236	ABS63500	AAD30162	ADP21883	ADP21988	AD004093	AAX27821	ADO41360	AAL57225	AAL57224	ABX70212	ADR23060	AAL45772	ABT42676
	DB	7	σ	13	4	7	~	4	9	9	12	12	12	0	12	10	10	9	13	9	8
	Query Match Length DB	24	24	24	41	34	35	35	25	38	20	20	49	27	34	41	41	30	30	33	37
ok	Query Match	100.0	100.0	100.0	68.3	67.5	66.7	66.7	63.3	62.5	61.7	61.7	61.7	8.09	8.09	60.8	60.8	60.0	0.09	0.09	0.09
	Score	24	24	24	16.4	16.2	16	16	15.2	15	14.8	14.8	14.8	14.6	14.6	14.6	14.6	14.4	14.4	14.4	14.4
	Result No.	н	7	М	Ω 4.	2	9	7	ω υ	ი ს	10	c 11	c 12	c 13	14	c 15	c 16	c 17	c 18	c 19	20

AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

Aaf87048 PCR prime Ad159164 Human ESM Ad158982 Human ESM Abv74729 Human cla		Adh27316 Ferritin Adh27295 Ferritin Adh27208 Ferritin Adh27208 Ferritin Adh27309 Ferritin Adh37305 Ferritin	Abkli366 NADH dehy Aav27468 Streptoco Aaa70860 Molecular Aaa70869 Molecular Abq84936 Streptoco Adc45339 S. pneumo	Aaf30041 Moraxella Abs55299 Human leu Aaa37264 Human PRO Aaf54390 Primer #7
4779	01101 10101 1014	28 12 ADH27316 28 12 ADH27295 28 12 ADH27208 29 12 ADH27308 29 12 ADH27309 32 13 ADR33465	33 6 ABK11366 36 2 AAV27468 36 3 AAAV70860 36 3 AAA70869 36 6 ABQ84936 36 10 ADC45339	38 4 AAF30041 41 6 ABS55299 46 3 AAA37264 46 4 AAFS4390
	14.2 59.2 14.2 59.2 14 58.3 14 58.3	14 588.3 14 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	14 58.3 14 588.3 14 588.3 14 588.3	14 58.3 14 58.3 14 58.3
22 23 24 24 24	25 26 28 28 28	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ы ш ш ш 4 4 6 г. в е о н	ე 4 4 4 4 8 4 4 8

ALIGNMENTS

Non-invasive method for diagnosis of hypertrophic cardio-myopathy useful for testing asymptomatic individual(s). Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy; diagnosis; primer; mutation; detection; ss. Watkins H, Rosenzweig A; Beta-cardiac myosin heavy chain PCR primer B' (HARD) HARVARD COLLEGE.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
(GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA. Example 1; Col 10; 22pp; English. AAQ91124 standard; cDNA; 24 BP. 92US-00989160. 92US-00989160 19-FEB-1996 (first entry) Seidman J, Seidman C, WPI; 1995-245715/32. 11-DEC-1992; 11-DEC-1992; 04-JUL-1995. US5429923-A. Synthetic. AAQ91124; RESULT 1 AAQ91124

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asymptomatic individuals suspected of having the disease. The method has a broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease and phenylketonuria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC; familial hypertrophic cardiomyopathy; SHC; Gaucher's disease; sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia; buchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease; phenylketonuria; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting a presence or absence of a mutation associated with hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or hemophilia, by detecting a mutation in an amplified product of a beta cardiac myosin heavy-chain DNA.
                                                                                                                                                                                   Gaps
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                                                                                                                                              100.0%; Score 24; DB 2; Length 24;
                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta cardiac myosin heavy chain PCR primer B'.
                                                                                                          Sequence 24 BP; 6 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                             Pred. No. 0.16;
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                   1 CTTCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                       CTTCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watkins H,
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                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                              ACA63114 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                               24; Conservative
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SEIDMAN J.
WATKINS H.
                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  ACA63114;
                                                                                                                                              Query Match
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                                                                                                                                                                Local
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                                                                                                                                                                               Matches
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ACA63114
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oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain DNA. The method is useful for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. This method is especially useful for diagnosing SHC and FHC, as well as for determining the estimated the life expectancy of a person with familial hypertrophic cardiomyopathy. In particular, the method is useful for determining an individual's genetic information, and diagnosing e.g. Gaucher's disease, haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease, phenylketonuria or cystic fibrosis. The present sequence is a nested PCR primer used to amplify a region of the beta cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting mutations associated with hypertrophic cardiomyopathy to diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac myosin heavy-chain DNA and detecting the mutation in the amplified product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (familial or sporadic, FHC, SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy, comprising amplifying beta-cardiac myosin heavy-chain DNA forming an amplified product, and detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy in the amplified product, thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also included are a set of DNA oligonuclectide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two oligonuclectides
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta cardiac myosin heavy chain mutation detection primer B'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHC;
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                                                                                                                                                                              myosin heavy chain cDNA containing an FHC-associated mutation
                                                                                                                                                                                                                                                  Score 24; DB 9; Length 24;
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                   Sequence 24 BP; 6 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 familial hypertrophic cardiomyopathy, sporadic hypertrophic cardiomyopathy.
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                                                                                                                                                                                                                                                                                                                                           CTTCATGTTTCCAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                                                            1 CTTCATGTTTCCAAAGTGCATGAT 24
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                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
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95US-00469172.
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                                                                                                                                                                                                                                                                                         24; Conservative
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SEIDMAN J.
WATKINS H.
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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(ROSE/)
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which amperity becar-catalate without for facilitating the diagnosis of hypertrophic cardiomyopathy by being capable of detecting a hypertrophic cardiomyopathy-associated mutation) and a kit for facilitating the diagnosis of hypertrophic cardiomyopathy (comprising a first container cardiomyopathy-associated mutation, a second container conding an RNA probe completely hybridisable to the beta-cardiac myosin heavy-chain DNA, where the RNA probe is capable of detecting a myosin cardiomyopathy-associated mutation, a second container conforms for amplifying beta-cardiac myosin heavy-chain DNA and instructions for using the components of the kit to detect the presence or absence of a hypertrophic cardiomyopathy cardiomyopathy-chain DNA). The method is used for detecting the presence or absence of a mutation associated with cardiomyopathy. Presently, the diagnosis of individuals hypertrophic cardiomyopathy relies on the presence of typical cardiomyopathy. Presently, the diagnosis of individuals cardiomyopathy. Presently, the diagnosis of individuals cardiomyopathy relies on the presence of typical cordiomyopathy relies or disorder was creveals that there are no extensive studies involving a large number of families which established that this particular disease or disorder was caused by point mutations in the beta cardiac myosin heavy-chain gene. The present sequence is a PCR primer used to am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain having a disease-related point mutation.
which amplify beta-cardiac myosin heavy-chain DNA (the set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiac myosin heavy
88888888888888888888888888888888888888
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/ Match 100.0%; Score 24; DB 13; Length 24; Local Similarity 100.0%; Pred. No. 0.16; nes 24; Conservative 0; Mismatches 0; Indels Seguence 24 BP; 6 A; 5 C; 4 G; 9 T; 0 U; 0 Other; Query Match

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Gaps

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0; Mismatches

Best Loc Matches

1 CTTCATGTTTCCAAAGTGCATGAT 24 CTTCATGTTTCCAAAGTGCATGAT 24 ð 셤

AAH46257 standard; DNA; 41 BP AAH46257; AAH46257/c RESULT 4

Aldehyde/ketone reductase 9 probe, SEQ ID NO:8. (first entry) 25-SEP-2001

Aldehyde/ketone reductase 9; human; recombinant production; malignant tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; immune disorder; inflammatory condition; cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.

Homo sapiens.

WO200146433-A1

28-JUN-2001

18-DEC-2000; 2000WO-CN000607.

99CN-00125681. 22-DEC-1999;

(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

Mao Y, Xie Y;

WPI; 2001-441679/47.

Aldehyde/ketone reductase 9 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammation.

Example 7; Page 16; 39pp; Chinese

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             The invention relates to aldehyde/ketone reductase 9 (AAB98900), nucleic acids encoding it (AAH46222), and a method for the recombinant production of the protein. The present invention additionally discloses an agonist of aldehyde/ketone reductase 9 for therapeutic use, and an antibody which specifically binds to aldehyde/ketone reductase 9. Aldehyde/ketone reductase of human immunodeficiency virus) infection, immune disorders and inflammatory conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification for polymucleotide can be used as a primer for nucleic acid amplification reactions or as a probe for hybridiation reactions, or in producing gene chips or microarrays. Sequences AAH46259. AAH46258 represent aldehyde/ketone reductase 9 probes used in an exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant phosphodiesterase (PDB) type IVC may be used to screen for inhibitors of PDB IVC. The inhibitors may be used in pharmaceutical for the treatment and prophylaxis of inflammatory diseases, especially inflamed lung associated with asthma. Multiple isoforms of PDB exist opening the possibility for individual inhibitors of each isoform. The distribution of PDB IV isoform mRNAs in different human rissues was analysed by northern blotting. Human multiple tissue northern blots were hybridised with isoform specific probes generated by PCR from the 3' non-translated region of each gene. Bither Hi-60 genomic DNA (probes A and C) or a CDNA library prepared from eosinophil enriched mRNA (probes B and D) were used as templates for the PCR reaction with two primers (AAT34642,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphodiesterase, screening, identification, inhibitor, inhibition, PDE, treatment, prophylaxis, inflammatory disease, inflamed lung, asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human phosphodiesterase type IVC and selective inhibitors - used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  68.3%; Score 16.4; DB 4; Length 41; 94.4%; Pred. No. 7.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                          Sequence 41 BP; 10 A; 11 C; 10 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer for human phosphodiesterase type IV D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TCATGTTTCCAAAGTGCA 20
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95GB-00012996.
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                                                                                                                                                                                                                                                                                                                                                                                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-321854/32.
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26-JUN-1995;
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SXS

RESULT 6

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AAX18400

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The invention relates to the novel human ADAM (A Disintegrin And Metalloprotease) -type metalloproteases MDTS4 (AAB73549) and MDTS5 (AAB73550). The metalloproteases can be used for the treatment of cancers and arthritis. The invention also relates to the genes encoding MDTS4 and MDTS5, vectors and host cells containing the MDTS4 or MDTS5 genes, the recombinant production of MDTS4 and MDTS5, and antibody specific for MDTS4 or MDTS5, and methods of screening for compounds which modulate the activity of MDTS4 and/or MDTS5. Sequences AAH20233- AAH20236 represent PCR primers used to isolate human MDTS5 cDNA (AAH20225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; human leucine-rich repeat small intestine I; HLRRSII; asthma; proliferative disorder; gastrointestinal disorder; renal disorder; neural disorder; reproductive disorder; calcium regulation; apoptosis; immune system, anaemia, human immune deficiency virus; HIV; cancer; blood coagulation disorder; autoimmune disorder; allergic reaction; inflammatory condition; cardiovascular disorder; ischaemia; neurological disorder; infectious disease; cytokine production; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease and its preparation for use as an anti-cancer and
                                                                                                                                             Human, MDTS5, ADAM-type metalloprotease, drug screening,
A Disintegrin And Metalloprotease, cancer, arthritis, PCR primer;
                                                                                                      Human ADAM-type metalloprotease MDTS5 PCR primer, SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%; Score 16; DB 4; Length 35; 79.2%; Pred. No. 1.1e+03; tive 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTCATCTTTCTAAGGTGGATGAT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTTCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 22; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                (YAMA ) YAMANOUCHI PHARM CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-arthritic therapeutic.
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                                                              (first entry)
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Best Local Similarity
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                                                              07-AUG-2001
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 new metal
                                                                                                                                                                                                                                                                                          23-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer; ss.
                     AAH20236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABS63500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
    a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a primer used in the method of the invention for gene or CDNA cloning membrane-combined proteins and secreted proteins. A CDNA library is prepared using a vector where a multiple cloning site (MCS) is introduced 3' of a known secreted protein cDNA or 3' of a cDNA with the C-terminal deleted from all membrane penetrating parts of a membrane-combined protein. It is transfected into a eukarycyte and expressed as a fusion protein using a promoter suitable for each bio species, and the cell expressing the fused membrane protein on the cell membrane is concentrated and isolated using a specific antibody against the N-terminal protein. The plasmid is recovered and transfected to E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene cloning of a protein - using a vector with a multiple cloning site introduced 3' of a known secreted protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer; gene cloning; membrane-combined protein; secreted protein;
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
AAT34643) used to amplify a cDNA of PDE gene D. See AAT34636-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                          ö
                                                                             Score 16.2; DB 2; Length 34;
Pred. No. 8.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 16; DB 2; Length 35; 79.2%; Pred. No. 1.1e+03; rive 0: Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35 BP; 7 A; 9 C; 10 G; 9 T; 0 U; 0 Other;
                                    Sequence 34 BP; 9 A; 9 C; 5 G; 11 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTTCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCATGTTTCCAAGGAGGAGGCT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated easily and comprehensively
                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer MIL2RAdBX2 for gene cloning
                                                                                                                                                                2 TICATGITICCAAAGIGCAIG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 4; 9pp; Japanese
                                                                                                                                                                                                       3 rrraagcrrccaaagrecare 23
                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH20236
ID AAH20236 standard; DNA; 35 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-00214074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97JP-00214074.
                                                                             67.5%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                           AAX18400 standard; DNA; 35
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 79.2
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUJITA GAKUEN.
FUNAKOSHI KK.
                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-183835/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP11032779-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                    AAX18400;
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RESULT 7

8

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Gaps

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The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin and increased levels of transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure. Antibodies to MCIP can be used in characterising the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy or as predictor of heart disease. The present sequence is a PCR primer used to isolate HA-tagged human MCIPI splice variant 4
                                                                                                                                                                                                                                                                                           Screening for modulators of muscle calcineurin interacting protein (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/mod_base= OTHER
/note= "OTHER= Phosphorothioate backbone. All cytidines
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "OTHER= 2'-0-Methoxyethyl (2'-MOE) nucleotides"
15..20
/ttag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; gene therapy; ornithine decarboxylase 1; ornithine decarboxylase 1 associated disorder; hyperproliferative disorder; cancer; human; antisense oligonucleotide; antisense technology; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ornithine decarboxylase 1 antisense oligonucleotide segid 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%; Score 15; DB 6; Length 38; 78.3%; Pred. No. 3.38+03; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38 BP; 14 A; 6 C; 5 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 78; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 rradagrircradandcarder 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TICATGITICCAAAGIGCAIGAI
                             07-JUL-2000; 2000US-0216601P.
13-FEB-2001; 2001US-00782953.
                                                                                                                                                                                                  B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP21883 standard; DNA; 20
                                                                                                 (TEXA ) UNIV TEXAS SYSTEM.
(WILL/) WILLIAMS S R.
(ROTH/) ROTHERMEL B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..5
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 78.3
les 18; Conservative
                                                                                                                                                                                               Williams SR, Rothermel
                                                                                                                                                                                                                                              WPI; 2002-179698/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP21883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated nucleic acid molecules (I) encoding human leucine-rich repeat small intestine I (HLRRSII) polypeptides. The nucleic acid molecules and polypeptides are useful for preventing.

CC treating and ameliorating medical conditions, such as proliferative, created to abstrant calcium regulation or apoptosis modulation, either directly or indirectly. They are also useful for treating, preventing and/or diagnosing diseases, disorders and/or conditions of: immune system carectly or indirectly. They are also useful for treating, preventing and/or diagnosing diseases, disorders and/or conditions of: immune system conditions of inminibiting the proliferation, differentiation, or mobilisation of immune cells, haematopoietic cells e.g. thrombocytopenia, anemnia, immune deficiency syndromes, e.g. human immune deficiency virus (HIV) infection, HTW-BLV infection; blood coaqulation disorders, e.g. Addison's disease, wasthenia gravis; asthma or allergic reactions; inflammatory conditions, cardiovascular disorders, e.g. arrhythmia, myocardial ischaemias, aneurological disorders, e.g. arrhythmia, myocardial ischaemias, aneurological disorders, e.g. measles, mumps, pneumonia, or viral, bacterial, and fungal infections. The HRRSII polypeptides are useful for and fungal infections. The HRRSII polypeptides are useful such an an and an anomal such and such are allerged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                 New isolated nucleic acid molecules encoding HLRRSI1 polypeptides, or their fragments and homologues, useful for preventing, treating and ameliorating medical conditions, e.g. proliferative, gastrointestinal, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muscle calcineurin interacting protein; MCID; cardiac hypertrophy; heart failure; cardiomyopathy; heart disease; human; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HA-tagged human MCIP1 splice variant 4 isolating PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.3%; Score 15.2; DB 6; Length 25; 85.0%; Pred. No. 2.5e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequences and PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 5 A; 7 C; 7 G; 4 T; 2 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                             Example 57, Page 287; 336pp; English.
                                                                                                                                                                                          Ramanathan C, Mintier G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTTCATGTTTCCAAAGTGCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCGTGGCTCCAAAGTGCA 4
                                                                                                                                           (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD30162 standard; DNA; 38 BP
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                                                 20-DEC-2001; 2001WO-US049739.
                                                                                              22-DEC-2000; 2000US-0257774P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                       WPI; 2002-619252/66
                                                                                                                                                                                                                                                                                                                                                              renal disorders
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08-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2002
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                                                                                                                                                                                        Feder J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
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AAD30162/c RESULT 9

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Gaps

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comprising 8-80
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 /note= "OTHER= 2'-0-Methoxyethyl (2'-MOE) nucleotides"
                                                                         /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                  New oligonucleotide compound that inhibits expression of ornithine decarboxylase 1, useful for preparing a composition for treating hyperproliferative disorder, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating hyperproliferative disorder, e.g. cancer. This sequence represents an ornithine decarboxylase 1 antisense oligonucleotide
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.7%; Score 14.8; DB 12; 88.9%; Pred. No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 16; SEQ ID NO 136; 69pp; English
                                       /*tag= c
/mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CATGTTTCCAAAGTGCAT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      m
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                                                                                                                                                                                                                               10-DEC-2002; 2002US-00316244.
                                                                                                                                                                                           10-DEC-2002; 2002US-00316244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-2002; 2002DK-00001652.
30-OCT-2002; 2002US-0422167P.
19-DEC-2002; 2002DK-00001955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-OCT-2003; 2003WO-DK000739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGTTTCAAAGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO04093 standard; DNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifier oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bifunctional complex; ss
                   15. .20
                                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                          Bennett CF, Dobie KW;
                                                                                                                                                                                                                                                                                                                                              WPI; 2004-440337/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004039825-A2
                                                                                                                 US2004110148-A1
                   modified base
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                                                                                                                                                     10-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD004093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO04093/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a new compound, having a sequence comprising 8-80 bp targeted to a nucleic acid encoding ornithine decarboxylase 1, specificially hybridises with the nucleic acid encoding ornithine decarboxylase 1 comprising 203-bp sequence and inhibits expression of ornithine decarboxylase 1. Also described are: inhibiting the expression of ornithine decarboxylase 1 in cells or tissues; screening for a modulator of ornithine decarboxylase 1; identifying a disease state; a kit or assay device comprising the compound, and treating an animal having a disease or condition associated with ornithine decarboxylase 1. The oligonucleotide compound is useful for preparing a composition for treating hyperproliferative disorder, e.g. cancer. This sequence represents an ornithine decarboxylase 1 antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "OTHER= Phosphorothioate backbone. All cytidines are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; gene therapy, ornithine decarboxylase 1;
ornithine decarboxylase 1 associated disorder;
hyperproliferative disorder; cancer; human; antisense oligonucleotide;
                 /note= "OTHER= 2'-0-Methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                        New oligonucleotide compound that inhibits expression of ornithine decarboxylase 1, useful for preparing a composition for treating hyperproliferative disorder, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ornithine decarboxylase 1 antisense oligonucleotide segid 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.7%; Score 14.8; DB 12; Length 20; 88.9%; Pred. No. 3.7e+03; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                    Example 15; SEQ ID NO 31; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CATGTTTCCAAAGTGCAT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CATGTTTCAAAGAGCAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP21988 standard; DNA; 20 BP.
                                                                                                                                 10-DEC-2002; 2002US-00316244
                                                                                                                                                                     10-DEC-2002; 2002US-00316244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...20
*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 88.9
Les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antisense technology; ss.
                                                                                                                                                                                                           (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                Dobie KW;
                                                                                                                                                                                                                                                                                      WPI; 2004-440337/41.
                                                       US2004110148-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                              Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-2004
                                                                                             10-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP21988
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diagnosis and method for using the same which provides with a quick diagnosis for 20 species of bacterial pathogens. The invention is useful for diagnosis of bacterial meningitis pathogens or can be conjugated to substrate (e.g., blochips) and serve as probes. The present sequence is an oligonucleotide used to diagnose Staphylococcus saprophyticus pathogen. This sequence is used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a nuleic acid kit for bacterial pathogen
              This sequence is a fragment of the CRCA-1 (colorectal cancer associated) transcript of the invention. The CRCA-1 transcript is a specific marker for colorectal cancer cells and detecting it is used to identify/confirm cells as colorectal cancer cells and to examine the extent of which they have migrated, especially for diagnosis, staging and post-operative monitoring, also for screening subjects at risk. The CRCA-1 DNA is used to express the corresponding expression products and its fragments are useful as oligonucleotide probes, primers and antisense agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid kit for diagnosis of bacterial pathogens that cause meningitis comprises nucleic acid sequences designed for 20 bacterial pathogens e.g., Staphylococcus aureus, S.epidermidis, Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligo 3-2 used to diagnose Staphylococcus saprophyticus pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.8%; Score 14.6; DB 12; Length 34; 81.0%; Pred. No. 5e+03; ive 0; Mismatches 4; Indels (
                                                                                                                                                                                        Score 14.6; DB 2; Length Pred. No. 4.9e+03; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial pathogen; diagnosis; meningitis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34 BP; 10 A; 6 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                            Sequence 27 BP; 6 A; 6 C; 6 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 10; 9pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chao
                                                                                                                                                                                                                                                      4 CATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                  cararerccaadcagcagar
                                                                                                                                                                                                                                                                                                                                                                    ADO41360 standard; DNA; 34 BP.
                                                                                                                                                                                         60.8%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus saprophyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-OCT-2002; 2002US-00281845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-2001; 2001TW-00127119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 saprophyticus, S.agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2004 (first entry)
                                                                                                                                                                                                        Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chiang Y, Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-224188/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSU P.
CHIANG Y.
HUANG H L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAO S Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004010129-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                  ADO41360;
                                                                                                                                                                                                                                                                                       56
                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIA/)
(HUAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HSUP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHAO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hsu P,
                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                     ADO41360
   *888888888888
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                                                                                                                                                                                                                                                                                    요
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                                                                                                                                                                                                                                                                                                 The present invention relates to a method (M1) for obtaining a bifunctional complex. (M1) comprises a display molecule part and a coding part, where a nascent bifunctional complex comprising a chemical reaction site and a priming site for enzymatic addition of a tag is reacted at the chemical reaction is the with reactent(s), and provided with respective tag(s) identifying the reactant(s) at the priming site using one or more enzymes. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                          at
                                                                                                                                                                                    Obtaining bifunctional complex with display molecule and coding part, where bifunctional complex with priming site for adding tag is reacted a reaction site with reactants and provided with tag identifying reactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRCA-1 transcript, a specific marker for colorectal cancer cells - used for in vitro diagnosis, staging and monitoring colorectal cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                          Lundorf MD, Felding J;
Sams C, Glad SS, Jensen KB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRCA-1; colorectal cancer associated transcript; marker; detection; colorectal cancer cell; diagnosis; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkinson SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.8; DB 12; Length 49;
Pred. No. 4.3e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 16 A; 12 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schulz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pearlman JM, Barber MT,
                                                                                            Gouliaev AH,
                                                                                                          Jakobsen SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 115; 133pp; English.
                                                                                                                                                                                                                                                                     Example 5; Page 125; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRCA-1 coding sequence fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TTCATGTTTCCAAAGTGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                2003UK-00001064.
2003US-0486199P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.7%;
88.9%;
19-DEC-2002; 2002US-0434425P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US016440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX27821 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 88.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assessing its metastasis.
                                                                                        Franch T,
                                                                                          P, Franch T. Holtmann A,
                                                           (NUEV-) NUEVOLUTION AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-180474/15.
                                                                                                                                                        WPI; 2004-376154/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAY00966.
                                                                                                                                                                                                                                      at priming site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9907726-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-1999
                                                                                                                      Pedersen H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waldman SA,
                                                                                          Freskgard
                                                                                                            sen EK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX27821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
8
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This invention relates to the novel human protein 46.53, containing a bromo structure, and the CDNA sequence encoding it. The invention may be useful in the treatment of diseases such as cancer and HIV infection. The present sequence is that of oligonucleocide probe I related to the human 46.53 protein of the invention and used in example 7 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing
                                                                                                                                                                                Polypeptide-human protein-46.53 containing bromo structure domain and polynucleotide for coding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein-protein interaction; ulcer; selected interacting domain; SID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                          60.8%; Score 14.6; DB 10; Length 41;
81.0%; Pred. No. 5.2e+03;
Live 0; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Labigne A;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 41 BP; 16 A; 8 C; 7 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Helicobacter pylori gene PCR primer #3183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Reuse H,
                                                                      (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Page 587; 642pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TTCATGTTTCCAAAGTGCATG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rrcaregreccadaarccare 17
                                                                                                                                                                                                                                        Example 7; Page 23; Opp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colland F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-2001; 2001WO-EP015428.
 18-APR-2001; 2001CN-00112636.
                                      18-APR-2001; 2001CN-00112636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JAN-2001; 2001US-0259302P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX70212 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rain J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYBR-) HYBRIGENICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-674910/72
                                                                                                                                               WPI; 2003-258240/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ulcers in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200266501-A2
                                                                                                             Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Legrain P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX70212;
                                                                                                           Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX70212/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   # X # X 4 X F X 8 X F F X 8 X C C C C C C X 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to the novel human protein 46.53, containing a bromo structure, and the cDNA sequence encoding it. The invention may be useful in the treatment of diseases such as cancer and HIV infection. The present sequence is that of oligonucleotide probe 2 related to the human 46.53 protein of the invention and used in example 7 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide-human protein-46.53 containing bromo structure domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                        Oligonucleotide probe 2 related to human protein 46-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide probe 1 related to human protein 46-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 41 BP; 17 A; 8 C; 6 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                            Human protein 46.53; cancer; HIV infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein 46.53; cancer; HIV infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 TTCATGGTGCCAAAATTCATG 17
 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TTCATGTTTCCAAAGTGCATG 22
                                  13 cargerreraadgreaagar 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 23; Opp; Chinese
CATGTTTCCAAAGTGCATGAT
                                                                                                                              ВР
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ID AALS7224/C
XX
XX
AC AALS7224;
XX
DT 04-DEC-2003 (first entry)
XX
DE Oligonuclectide probe 1 relat
XX
KW Human protein 46.53; cancer;
XX
CS Homo sapiens.
XX
PN CN1381487-A.
XX
PD 27-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2001; 2001CN-00112636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2001; 2001CN-00112636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide for coding it
                                                                                                             225/c
AAL57225 standard; DNA; 41
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-258240/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xie Y;
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     CN1381487-A.
                                                                                                                                                                                                     04-DEC-2003
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Mao Y,

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Gaps

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ORF DNA for strain typing.
                                                                                                                                                                                                                                              AAL45772;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABT42676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                      RESULT 19
AAL45772/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 20
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ID ABT4
XX
AC ABT4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transments or their expression products that allows typing of Helicobacter fragments or their expression products that allows typing of Helicobacter pylori strains. The method comprises preparing genomic DNA components of from clinical isolates and strains of H. Pylori that can be distinguished, particularly from their geographical origin or their particular associated pathology. Subsequently a set of non-ubiquitous particular associated pathology. Subsequently a set of non-ubiquitous particular associated pathology. Subsequently a set of non-ubiquitous present in the first stage and a composition may be prepared ontaining the in the first stage and a composition may be prepared containing the identified ORFs, or fragments, their expression products or antibodies against these expression products. The method of the invention may be used to provide unequivocal differentiation between clinical isolates of H. Pylori according to their geographical origin and isolates of H. Pylori infection is particularly associated with gastric and duodenal ulcers or inflammation, as well as cancer of the stomach or gastric system. The current sequence is that of a DNA/RNA hybrid PCR primer of the invention which was used to amplify H. pylori
                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preparing set of DNA fragments or expression products, useful for typing strains of Helicobacter pylori, by selecting non-ubiquitous open reading frames from genomic DNA.
              sequence represents a primer used to isolate polynucleotides encoding
Helicobacter pylori proteins for studies on protein-protein interactions
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                              DNA/RNA primer 550 used to amplify H. pylori strain typing ORF DNA.
                                                                                                                                                                                                                                                                                                                                                         strain typing; geographical origin; gastric ulcer; duodenal ulcer; inflammation; stomach cancer; gastric cancer; DNA/RNA hybrid; PCR;
used for treating or preventing ulcers in a human or animal. This
                                                                                                                ö
                                                                                ch 60.0%; Score 14.4; DB 6; Length 30; 1 Similarity 75.0%; Pred. No. 6.1e+03; 18; Conservative 0; Mismatches 6; Indels
                                                        Sequence 30 BP; 13 A; 6 C; 5 G; 3 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lacroix C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 550; 126pp; French.
                                                                                                                                         1 CTTCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coppee JY,
                                                                                                                                                             CTTCATTCATTCTTAGTGCATGAT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "RNA bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2003; 2003FR-00001235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2003; 2003FR-00001235
                                                                                                                                                                                                                                           ADR23060 standard; DNA; 30
                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .9
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori.
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                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                            strain typing;
                                                                                                                                                                                                                                                                                                    21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR2850667-A1
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                                                                                                                                                                                                                                                                                                                                                                                        primer; ss.
                                                                                                                                                                                                                                                                       ADR23060;
                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo acid phosphatase family protein 11 and encoding polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of human acid phosphatase family protein 11. The sequences can be used in the treatment of cancer, haemopathy, HIV infection, immune diseases and phlogosis. The present sequence is a PCR primer for the coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; acid phosphatase family protein 11; cancer; haemopathy;
cytostatic; haemostatic; virucide; immunomodulatory; antiinflammatory;
immune disease; HIV infection; phlogosis; gene therapy; PCR; primer; ss.
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                         Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human acid phosphatase family protein 11 cDNA PCR primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%; Score 14.4; DB 6; Length 33; 75.0%; Pred. No. 6.2e+03; ive 0; Mismatches 6; Indels
                                                                                                                     Indels
Sequence 30 BP; 13 A; 6 C; 5 G; 3 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33 BP; 9 A; 8 C; 5 G; 11 T; 0 U; 0 Other;
                                                      60.0%; Score 14.4; DB 13; 75.0%; Pred. No. 6.1e+03; ative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTAATGATGAGAAAGTGCATCAT 10
                                                                                                                                                                            1 CTTCATGTTTCCAAAGTGCATGAT 24
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                                                                                                                                                                                                                         28 CTTCATTCATTCTTAGTGCATGAT 5
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                                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                AAL45772 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABT42676 standard; DNA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUN-2002 (first entry)
                                                      Query Match 60.03
Best Local Similarity 75.03
Matches 18; Conservative
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nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-329869/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation.
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AAF87048 standard; DNA; 20

RESULT 21 AAF87048 (first entry)

18-SEP-2001

AAF87048;

PCR primer for Mash1 gene.

PCR primer; neuroectoderm cell; cell production; Parkinson's disease; early primitive ectoderm-like cell; EPL cell; cell therapy; transgenic animal; gene therapy; neuronal disease; Huntington's disease; lysosomal storage disease; multiple sclerosis; memory disorder; behavioural disorder; Alzheimer's disease; organ transplant; spinal cord disorder; Mashl; ss.

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This invention relates to an isolated nucleic acid molecule comprising a polynucleotide encoding a human G-protein receptor, including HGRBMY28, CC HGRBMY29, HGRBMY29, DOTYPEPTIGES. THE HGRBMY28 or HGRBMY29 polypeptides and nucleic acids are useful for treating.

CHGRBMY29 polypeptides and nucleic acids are useful for treating, preventing or ameliorating a medical condition, e.g. an immune disorder, an inflammatory disorder in which G-protein coupled receptors are either directly or indirectly associated with the disorder, a gastrointestinal disorder, a neural disorder at pulmonary cidisorder, a proliferative disorder, a cancre, a disorder related to aberrant p27 regulation, a disorder related to aberrant FBNI regulation, a disorder related to aberrant bMA repair regulation, a disorder related to aberrant call cycle regulation, a disorder related to aberrant condess, a male or female reproductive disorder related to aberrant condess, a male or female reproductive disorder related to aberrant condess, a male or female reproductive disorder a proliferative disorder, a cardiovascular disorder, a placental disorder, a fillicting the colon, cervix, lung, squamous cells or tissues, a renal disorder, a cardiovascular disorder, a placental disorder, and a disorder of the testes, heart or lymph nodes. The isolated polymuclectides of the invention may be used to treat disorders by gene therapy. This
                                                                                                                                                                                                                                         nephrotropic; cardiant; human G-protein receptor; HGRBMY28; HGRBMY29; HGPRBMY291; HGPRBMY292; HGRBMY29; HGRBMY29; HGRBMY29; HGRBMY29; immune disorder; pulmonary; inflammatory; haematopoietic; gastrointestinal; small intestine; cancer; proliferative; aberrant p27 regulation; FRNI; cell cycle; DNA repair; apoptosis; spleen; lymph node; reproductive; oesophageal; metabolic; endocrine; colon; cervix; lung; squamous cell; renal; cardiovascular; placental; testis; heart; gene therapy; ds.
                                                                                                                                                                                                     Neuroprotective, antiinflammatory, immunosuppressive, cytostatic, neural,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New G-protein coupled receptors, HGRBMY28 and HGRBMY29, and their variants, useful for treating, preventing or ameliorating e.g. hematopoietic, neural, pulmonary, gastrointestinal, inflammatory c
                                                                                                  Human G-protein coupled receptor HGPRBMY28 DNA SEQ ID 138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hawken DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feder J, Mintier G, Ramanathan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 24; Page 386; 501pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGPRBMY28 DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-APR-2001; 2001US-0283145P.
11-APR-2001; 2001US-02831G1P.
03-MAY-2001; 2001US-0286468P.
25-JUN-2001; 2001US-0306619P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2002; 2002WO-US011525
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-075538/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2002
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Alzheimer's and for transplantation comprises culturing early primitive

ectoderm-like cells in conditioned medium.

Producing neuroectoderm cells for treatment of Parkinson's and

20-APR-2000; 2000AU-00007045. 27-APR-2000; 2000AU-00007143.

Rathjen PD, Rathjen J; (BRES-) BRESAGEN LTD.

WPI; 2001-432908/46.

12-JAN-2001; 2001WO-AU000030. 14-JAN-2000; 2000AU-00005098.

WO200151611-A1. Unidentified

19-JUL-2001

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This sequence represents a PCR primer for the Mashl gene, used within the scope of the invention. The invention relates to a method for producing cope of the invention. The invention relates to a method for producing conceed early primitive ectoderm—like (BFD) cells and a neural-inducing conditioned primitive ectoderm—like (BFD) cells and a neural-inducing conditioned confident (CM) or extract of it, and (b) contacting the BFD cells with the CM or extract for a time sufficient to generate controlled cifferentiated for a time sufficient to generate controlled by the cuseful in human, or animal cells or partially differentiated progeny are confidentiated progeny and evaluation of biological molecules that induce differentiated progeny and evaluation of biological molecules that direct differentiated cells. It is also useful for producing differentiated cells. It is also useful for producing differentiated cells from neural ecoderm cells. The method can consequence confident maintaining neuroectoderm cells in vitro in homogeneous cell populations. It can also be used for producing the result of neuroectoderm cells in vitro in the result of neuroectoderm cells. The cells can be used in the result of neuroectoderm cells. The cells can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of neuronal diseases, including Parkinson's disease,
Huntington's disease, lysosomal storage diseases, multiple sclerosis,
memory and behavioural disorders, and Alzheimer's disease. The method can
also be used for preparation of tissue or organs for transplant. Neural
crest cells produced by the method are useful for the treatment of spinal
cord disorders and Schwann cells produced by the method are used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 4 A; 7 C; 2 G; 7 T; 0 U; 0 Other;
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Gaps

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Query Match 60.0%; Score 14.4; DB 8; Length 37; Best Local Similarity 75.0%; Pred. No. 6.4e+03; Matches 18; Conservative 0; Mismatches 6; Indels

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Gaps ; 0 59.2%; Score 14.2; DB 4; Length 20; 84.2%; Pred. No. 7.2e+03; Live 0; Mismatches 3; Indels Conservative Local Similarity nes 16, Conserva Query Match Matches

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The compound is useful for preparing a composition for treating diabetes, cancer, ischaemia or reperfusion injury, or angiogenic, immunological, cardiovascular or neurological disorder. This sequence represents an antisense oligonucleotide that can be used to modulate expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising 8-30 bp targeted to a nucleic acid encoding endothelial specific molecule-1 (ESM-1), that specifically hybridises with the nucleic acid ESM-1 and inhibits its expression. Also described are: a composition; inhibiting the expression of ESM-1 in cells or tissues; and treating an animal having a disease or condition associated with ESM-1.
                                                                                                                                                         cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; gene therapy; endothelial specific molecule-1; ESM-1; ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury; angiogenic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compound, having a sequence targeted to a nucleic acid encoding endothelial specific molecule-1 (ESM-1), useful for preparing a composition for treating e.g., diabetes, cancer or cardiovascular
                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "OTHER= phosphorothioate backbone. All cytidine
residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a new antisense compound, having a sequence
                                                                                                                            Human ESM-1 antisense oligonucleotide segid 1413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endothelial specific molecule-1 (ESM-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 1413; 555pp; English.
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "OTHER= 2'
                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-2003; 2003WO-US025833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-2002; 2002US-0404495P
                             ADL59164 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                  l. .5
/*tag≕ a
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weinstein EJ, Griggs DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .20
                                                                                                                                                                                                                                                                                                                            *tag=
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                                                                                                                                                                                                                                                                                                                                                                                               modified base
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                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                              03-JUN-2004
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                                                             ADL59164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder
                 ADL59164
RESULT
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DB 12; Length 20;

59.2%; Score 14.2;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                            cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; gene therapy; endothelial specific molecule-1; ESM-1; ESM-1; BSM-1 alated disorder; diabetes; cancer; ischaemia; reperfusion injury; angiogenic disorder; immunological disorder; cardiovascular disorder; neurological disorder; antisense technology; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising 8-30 bp targeted to a nucleic acid encoding endothelial specific molecule-1 (ESM-1), that specifically hybridises with the nucleic acid ESM-1 and inhibits its expression. Also described are: a composition, inhibiting the expression of ESM-1 in cells or tissues; and treating an animal having a disease or condition associated with ESM-1. The compound is useful for preparing a composition for treating diabetes cancer, ischaemia or reperfusion injury, or anglogenic, immunological, cardiovascular or neurological disorder. This sequence represents an antisense oligonucleotide that can be used to modulate expression of endothelial specific molecule-1 (ESM-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "OTHER= phosphorothioate backbone. All cytidine residues are 5-methylcytidines"
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mod_base= OTHER
/note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a new antisense compound, having a sequence
                                ..
                                Indels
. 7.2e+03;
3;
                                                                                                                                                                                                                                                                Human ESM-1 antisense oligonucleotide segid 1231.
                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 1231; 555pp; English.
                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER
                                                             19
                                                                                          crircardriricccaecrec 20
                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-2002; 2002US-0404495P.
                                                             CTTCATGTTTCCAAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-2003; 2003WO-US025833
                84.2%;
                                                                                                                                                                       ADL58982 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                base=
                                                                                                                                                                                                                                 03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= c
        Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Griggs DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PHAA ) PHARMACIA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-248358/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weinstein EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                           Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified base
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-2004
                                                                                                                                                                                                    ADL58982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder
                                                                                                                                        RESULT 23
                                                                                                                                                        ADL58982
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Human leukocyte gene expression profiling probe SEQ ID NO 4565
                                                                                                                                                                                                                          WPI; 2002-636525/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 16; Conserv
                                                                                      WO200257414-A2
                                                                                                                                                                                             Wohlgemuth J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2004
                                                                                                         25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG33666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                        Ly N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG33666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human clathrin light chain 13.64 (see ABB96794). The protein and its coding sequence can be used for treating various diseases, such as malignant tumours, haemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is a PCR primer, which was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                            New human clathrin light chain 13.64 polypeptide for treating malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and various inflammations.
                                                                                                                                                                                                               Human, clathrin light chain 13.64, tumour; haemopathy, HIV infection, immunological disease; inflammation; cytostatic; anti-HIV; PCR; primer;
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                           59.2%; Score 14.2; DB 12; Length 20; 84.2%; Pred. No. 7.2e+03; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.2%; Score 14.2; DB 6; Length 33; 84.2%; Pred. No. 7.8e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33 BP; 6 A; 12 C; 5 G; 10 T; 0 U; 0 Other;
          A; 8 C; 3 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 18 (Disclosure); 34pp; Chinese.
                                                                                                                                                                                             Human clathrin light chain 13.64 PCR primer #4.
                                                                                                                                                                                                                                                                                                                                                     (BODE-) BODE GENE DEV CO LTD SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGATGTTTCCAAATTGC 32
                                                                  1 CTTCATGTTTCCAAAGTGC 19
                                                                                    cricardrircccaggride 19
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                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ04574 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                               06-NOV-2000; 2000CN-00127271.
                                                                                                                                                                                                                                                                                                                                  06-NOV-2000; 2000CN-00127271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 84.2%,
"--hes 16; Conservative
                                                                                                                                    ABV74729 standard; DNA; 33
                                                                                                                                                                          (first entry)
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                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-644460/70.
                                   Local Similarity
hes 16; Conserv
          Sequence 20 BP; 2
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                                                                                                                                                                                                                                                       sapiens.
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                            Query Match
                                                                                                                                                       ABV74729
                                                                                                                                                                                                                                                                                                                                                                        Mao Y,
                                                                                                                                                                                                                                                       Homo
                                       Best Loc
Matches
                                                                                                                RESULT 24
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ID ABZ0
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17, leukocyte, gene expression profiling, allograft rejection; atherosclerosis; congestive heart failure, systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human DNA probe used to monitor expression of diagnostic genes SeqID990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human, ss; autoimmune; chronic inflammatory disease; SLE; systemic lupus erythematosis; rheumatoid arthritis; cholecystitis; Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis; ulcerative colitis; primary sclerosing cholangitis; appendicitis; diverticulitis; primary biliary sclerosis; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phillips J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prentice J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 50 BP; 16 A; 12 C; 12 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Altman P, Pr, Johnson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nuth J, Fry K, Matcuk G, A
Woodward R, Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 473; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P.
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cutoimmune and dronic inflammatory diseases. Specifically, it refers to the identification of genes that have a clinical utility as diagnostic tools for the management of, in particular, patients with systemic lupus erythematosis (SLB) or rheumatoid arthritis (RA). Accordingly, the present invention describes a method for determining the levels of multiple differentially expressed genes of a patient, in a concerted manner, in order to achieve an improved diagnostic assay with sensitivity and specificity for the disease in question. As such, these genes are useful for the diagnosis of various other inflammatory disorders including cholecystitis, slogren's disease, CREST syndrome, sclerosing cholangitis, appendicitis, diverticulitis, and primary sclerosing cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis. This oligonucleotide is a human DNA probe used to monitor the expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                          Diagnosing or monitoring autoimmune and chronic inflammatory diseases, such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, psoriasis and asthma by detecting the expression level of one or
                                                                                                                                                                                                                                                                                                                                                                    This invention relates to novel methods for diagnosing and monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.2%; Score 14.2; DB 10; Length 50; 84.2%; Pred. No. 8.3e+03; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50-mer oligonucleotide marker probe of the invention #117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50 BP; 16 A; 12 C; 12 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                           Ly N;
                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 990; 877pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EXPR-) EXPRESSION DIAGNOSTICS INC.
                                                                                                                                        (EXPR-) EXPRESSION DIAGNOSTICS INC
                                                                                                                                                                           Woodward R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTTCATGTTTCCAAAGTGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 CTTCATCTTCCCCAAGTGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP10108 standard; DNA; 50 BP.
                                                                     24-APR-2003; 2003WO-US013015,
                                                                                                     24-APR-2002; 2002US-00131827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-2002; 2002US-00131831.
20-DEC-2002; 2002US-00325899.
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Matches 16, Conservative
                                                                                                                                                                           Wohlgemuth J, Fry K,
                                                                                                                                                                                                           WPI; 2003-877243/81.
WO2003090694-A2
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                                  06-NOV-2003
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                                                                                                                                                                                                                                                                                                   more genes
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The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, wenchanglant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a 50 mer oligonuclectide marker for diagnosis and monitoring of allograft
                                                                                                     Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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genetic variation; biallelic marker; polymorphism; human;
                  Ξ
                  Prentice J, Morris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 59.2%; Score 14.2; DB 12; Length 50; Local Similarity 84.2%; Pred. No. 8.3e+03; hes 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human microarray DNA oligonucleotide SEQ ID NO 115249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50 BP; 16 A; 12 C; 12 G; 10 T; 0 U; 0 Other;
                  Ľ,
                                                                                                                                                                                                Claim 2; SEQ ID NO 117; 1762pp; English.
                  Fry K, Woodward R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rejection and other disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACK15268 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                   WPI; 2004-400724/37.
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                  Wohlgemuth J,
                                     Rosenberg S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mittmann MP;
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                                                                                                                                                                the genes.
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cotton (Gossypium hirsutum) plant referred to as PV-GHBK04 or cotton event 757. The invention provides polynucleotide sequences contained within cotton event 757 and methods for detecting DNA from the cotton
                                                                                                                                                                                        present invention relates to a Lepidoptera resistant transgenic
                                                               Claim 3; Page 16; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 30
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                                                                                               The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises bybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA melecules by primer extensions or in screening segments of DNA that have been containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence date for this patent can also be obtained in electronic format directly from USPTO at sequence. Thull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Claim 1; SEQ ID NO 115249; 9pp; English.
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Best Local Similarity 100.
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Synthetic.
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plant event 757 in a sample. The methods are useful for determining whether the progeny of a sexual cross contain a transgene of interest. The present sequence represents a PCR primer that may be used to detect DNA derived from the cotton event 757 in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting a conserved structures in an RNA sequence by generating an offspring group from the parent group and selecting at least one group from the parent and offspring groups with the highest fitness.
                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                       Length 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferritin related oligonucleotide Bin#5 structure 3.
                                                                                                                                                            Sequence 27 BP; 11 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                   58.3%; Score 14; DB 10; Lv
77.3%; Pred. No. 9.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14; DB 12;
Pred. No. 9.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fogel GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved structure in an RNA sequence. The p
the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                2 TTCATGTTTCCAAAGTGCATGA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADH27316 standard; DNA; 28
                                                                                                                                                                                                   Query Match
Best Local Similarity 77.3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-062371/06.
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Best Local Similarity
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The present invention describes a method for detecting a conserved structure in an RNA sequence. The method comprises: (a) placing 2 structures in an RNA sequences from 2 RNA sequences from 2 organisms into a parent group; (b) generating an offspring group from the parent comparing the fitness of the parent and offspring groups; (d) selecting at least one group from the parent and offspring groups; and (e) selecting at least one group from the parent and offspring groups; into the highest fitness, where the conserved structure in the RNA is present the highest faction group. The method is useful for detecting a conserved structure in an RNA sequence. The present sequence is used in the exemplification of the present invention.
                        detection; conserved structure; RNA structural element; fitness; ss.
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                                                                                                                                                                                                                                                                                                                                                                              Detecting a conserved structures in an RNA sequence by generation offspring group from the parent group and selecting at least on from the parent and offspring groups with the highest fitness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.3%; Score 14; DB 12; Length 28; larity 77.3%; Pred. No. 9.4e+03; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferritin related oligonucleotide Bin#1 structure 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffey RH, Fogel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TICATGITICCAAAGIGCAIGA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 13; 52pp; English
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es 17; Conserv
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                                                               Synthetic
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least one group
      Gaps
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    Indels
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                                                                                                                                                                                                                                                                                              Ferritin related oligonucleotide Bin#2 structure 3.
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  Mismatches
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                                      2 TTCATGTTTCCAAAGTGCATGA
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Best Local Similarity 77.3
Matches 17; Conservative
17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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Matches
                                                                                                                                     RESULT 31
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Gaps

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Porto VW;

GB,

generating an least one group

Porto VW;

Fogel GB,

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                                                                                                                                                                                         The present invention describes a method for detecting a conserved structure in an RNA sequence. The method comprises: (a) placing 2 structures from structures generated for 2 RNA sequences from 2 organisms into a parent group; (b) generating an offspring group from the parent group; (c) determining fitness of the parent and offspring groups; (d) comparing the fitness of the parent and offspring groups; (d) selecting at least one group from the parent and offspring groups; ind (d) selecting at least one group from the parent and offspring groups with the highest fitness, where the conserved structure in the RNA is present within the at least one group. The method is useful for detecting a conserved structure in an RNA sequence. The present sequence is used in the exemplification of the present invention.
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                                                                                      one group
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                                                          Detecting a conserved structures in an RNA sequence by generating an offspring group from the parent group and selecting at least one groufrom the parent and offspring groups with the highest fitness.
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                                                                                                                                                   Example 1; Fig 13; 52pp; English.
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                WPI; 2004-062371/06.
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The invention relates to a method of treating a nucleic acid sample with components under nicking conditions, where the components comprise a nicking agent, and the conditions cause the nicking agent to nick the nucleic acid sample to thus produce a family of initiating of a nigonucleotide fragments to a characterization of analy of initiating oligonucleotide fragments to a characterization process to thus provide results. The method is useful for creating an assay panel of diagnostic oligonucleotides that can identify any organism or individual. The method is useful for characterization patterns. The method, kit or composition is useful for identifying the source organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant, con-human animal or human. The method is particularly useful for rapidly fingerprinting DNA to identifying prokaryotic and eukaryotic species in subspecies, and especially strains or individuals of the subspecies. It is especially useful for identifying different bacterial strains involved in e.g., nosocomial infections. Furthermore, the method is useful for diagnosing bacterial disease in plants and humans, monitoring for bacterial content and/or contemination in the environment, monitoring processes for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying nucleic acid sample source, useful for identifying bacterial strains involved in nosocomial infections, comprises treating the nucleic acid sample with components comprising a nicking agent under nicking
the highest fitness, where the conserved structure in the RNA is present
             within the at least one group. The method is useful for detecting a conserved structure in an RNA sequence. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; nicking agent; assay panel; diagnosis; expression pattern; DNA fingerprinting; nosocomial infection; microbiological assay; bacterial contamination; genome mapping; bioremediation.
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                                                                                                                                                Length 29;
                                                                                                                                                                                          Indels
                                                                                                                                           Query Match 58.3%; Score 14; DB 12; L
Best Local Similarity 77.3%; Pred. No. 9.5e+03;
Matches 17; Conservative 0; Mismatches 5;
                                                                                                       G; 9 T; 0 U; 0 Other;
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                                                                                                       Sequence 29 BP; 7 A; 7 C; 6
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ADR33465/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polypeptide of NADH-dehydrogenase 51 Kd subunit 10, the cDNA encoding it, and its fragment, analogue or derivative. Also included are vectors expressing the protein, a host cell comprising the vector, the isolation of modulators of the protein and an anti-NADH-dehydrogenase 51 antibody. The protein and nucleic acid are used in diagnosis and treatment of a malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases, various inflammations, metabolic disturbance of carbohydrate, lipid and protein. The present sequence is a PCR primer used to clone the cDNA encoding the NADH- dehydrogenase 51Kd subunit 10
  monitoring quality assurance/quality control of
                  laboratory tests involving microbiological assays, tracing bacterial contamination and/or outbreaks of bacterial infections, genome mapping, monitoring bioremediation sites, and for monitoring agricultural sites for test crops, bacteria and recombinant molecules. This sequence corresponds to nucleic acid used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; PCR; NADH dehydrogenase 51Kd subunit 10; malignant tumour; haemopathy; human immunodeficiancy virus infection; HTV; primer; immunological disease; inflammation; cytostatic; haemostatic; virucide; immunomodulatory; antiinflammatory; metabolic disturbance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADH-dehydrogenase 51 and encoded polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                          ö
                                                                                                                                                                              ch 58.3%; Score 14; DB 13; Length 32; 1 Similarity 77.3%; Pred. No. 9.6e+03; 17; Conservative 0; Mismatches 5; Indele
                                                                                                                                      Sequence 32 BP; 10 A; 8 C; 6 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33 BP; 8 A; 8 C; 3 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADH dehydrogenase 51Kd subunit 10 PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI
                                                                                                                                                                                                                                                              3 TCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                                29 TCATTTTCCATAAAGCATGGT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 13; 35pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-2001; 2001WO-CN000991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-2000; 2000CN-00116593
                                                                                                                                                                                                                                                                                                                                                                                                         ABK11366 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
bacterial contamination,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-090538/12.
                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK11366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mao Y,
                                                                                                                                                                                                                                                                                                                                                                   RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                          ABK11366
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The present sequence represents a cloning primer used in an example from the present invention which describes proteins from Streptococcus preumoniae. Nucleic acid sequence encoding Streptococcus pneumoniae. Or proteins can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acids are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The proteins can be used similarly to detect specific antibodies in standard immunosasays, especially for diagnosing or monitoring infections. Antibodies which bind the proteins are used to detect corresponding antigens, to purify the proteins and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose. The cloning primers used in the present invention are given in AAV27437 to AAV27562 and AAV39870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                        Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis; detection; pneumonia; otitis media; meningitis; cloning primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                      Streptococcus pneumoniae ORF cloning primer SEQ ID NO:258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.3%; Score 14; DB 2; Length 36;
llarity 77.3%; Pred. No. 9.8e+03;
Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36 BP; 11 A; 10 C; 6 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hromockyj A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 106; 118pp; English
8 TGATGTTTCCCATATACATGAT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TCATGTTTCCAAAGTGCATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rcaagcriccaaacregrigar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0029960P
                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US019422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                           AAV27468 standard; DNA; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA70860 standard; DNA; 36
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-272224/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                      WO9818930-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             30-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-1996;
                                                                                                                                                                                   02-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunsch CA,
                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                               AAV27468;
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Best Local S
Matches 17
                                                                         RESULT 37
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ID AAA7
XX
                                                                                            AAV27468
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Best Local Similarity 77.3 Matches 17; Conservative

Query Match

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Gaps

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58.3%; Score 14; DB 6; Length 33; 77.3%; Pred. No. 9.7e+03; ive 0; Mismatches 5; Indels

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Modulator; identification; molecular interaction; virtual library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying compounds which modulate activity of target biomolecules, used to provide compounds which can be used as pharmacological,
                                                                                                                                                                                                                                                                                                                                                                                                                                      used to provide compounds which can be
agricultural and industrial compounds.
                                                  Molecular interaction site RNA #55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 66; 405pp; English
                 27-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                     Ecker DJ, Griffey R, C:
Hofstadler S, Mcneil J;
                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-086439/07.
                                                                                                                                                                                                                                                   12-MAY-1998;
12-MAY-1998;
                                                                                                                                                  WO9958947-A2
                                                                                                                                                                                                                    12-MAY-1999;
                                                                                                                                                                                    18-NOV-1999
                                                                                                                      Xenopus sp.
This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating in silico a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a internal loop region; (b) 4 nucleotides forming a first side of a nucleotides forming a second side of the second ds region; (e) 4 nucleotides forming and loop region; (f) 4 nucleotides forming and loop region; (g) 4 nucleotides forming a second side of the internal loop region; (g) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (d) a purified and isolated RNA fragment comprising the human sequence of an internal loop region; (z) a purified and isolated RNA fragment comprising the human sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNGAPACAUANUCURAGAAAANUC (II). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural
                                                                                               Modulator; identification; molecular interaction; virtual library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying compounds which modulate activity of target biomolecules, used to provide compounds which can be used as pharmacological, agricultural and industrial compounds.
                                                                                                                                                                                                                                                                                                                                                    Mohan V;
                                                                                                                                                                                                                                                                                                                                                    Swayze E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.3%; Score 14; DB 3; Length 36; llarity 77.3%; Pred. No. 9.8e+03; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36 BP; 7 A; 11 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                    Crooke ST, Sampath R,
                                                                Molecular interaction site DNA #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 63; 405pp; English
                                                                                                                                                                                                                                   99WO-US010361.
                                                                                                                                                                                                                                                                 98US-00076404
98US-0085092P
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                   Ecker DJ, Griffey R, Cı
Hofstadler S, Mcneil J;
                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-086439/07.
                                                                                                                                                                 WO9958947-A2
                                                                                                                                                                                                                                  12-MAY-1999;
                                                                                                                                                                                                                                                                   12-MAY-1998;
                                                                                                                                                                                                                                                                                    12-MAY-1998;
                               27-APR-2001
                                                                                                                                                                                                  18-NOV-1999
                                                                                                                                  Xenopus sp.
AAA70860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Mohan V;

Swayze E,

Sampath R,

Crooke ST,

99WO-US010361. 98US-00076404 98US-0085092P

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This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and alibrary of compounds and comprises (a) identifying at least one molecular interaction site of predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with thair respective ability to of the compounds ranked in accordance with thair respective ability to method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary curucture defined by: (a) 3 nucleotides forming a first side of an internal loop region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of an incleotides forming a second side of the internal loop region; (e) 4 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the internal loop region; and isolated RNA fragment comprising the human sequence of units of the first side of and isolated RNA fragment comprising the human sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 58.3%; Score 14; DB 3; Length 36; 1 Similarity 45.5%; Pred. No. 9.8e+03; 10; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36 BP; 7 A; 11 C; 9 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TTCATGTTTCCAAAGTGCATGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
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Best Local Similarity
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Matches
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ABQ84936
ID ABQ849
XX
AC ABQ849
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Gaps

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2 TTCATGTTTCCAAAGTGCATGA 23

Best Local Similarity Matches 17; Conserv

AAA70869 standard; RNA; 36 BP.

RESULT 39 AAA70869

AAA70869

04-SEP-2002 (first entry)

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ABQ84792 to ABQ84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABP54557 to ABP54669. The S. pneumoniae antigens have antibacterial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polynucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ88130 represent primers used in the cloning of S. pneumoniae ORFS (open reading frames) which are used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus pneumoniae antigens, useful for detecting Streptococcus and for preventing or attenuating disease caused by Streptococcus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fannon MR;
                                                                                                                                                Streptococcus pneumoniae; epitope; vaccine; antigenic protein; antibacterial; Streptococcal infection; detection; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dougherty B,
                                                                        Streptococcus pneumoniae ORF cloning primer SEQ ID NO:258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.3%; Score 14; DB 6; Length 36; Best Local Similarity 77.3%; Pred. No. 9.8e+03; Matches 17; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36 BP; 11 A; 10 C; 6 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 62; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-2001; 2001US-00765272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-00961083
                                                                                                                                                                                                                                                                 Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHOI/) CHOI G H.
(KUNS/) KUNSCH C A.
(BARA/) BARASH S C.
(DILL/) DILLON P J.
(DOUG/) DOUGHERTY B.
(FANN/) FANNON M R.
(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-479261/51
                                                                                                                                                                                                                                                                                                                                                                                  US2002061545-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-2002.
                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi GH,
Rosen CA;
NAMES OF COLORS OF STREET STRE
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Gaps ;

Search completed: November 18, 2005, 11:52:25 Job time : 168.262 secs

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2M0047P10

AA995598 06225703.6 CC049873 0180518-0 BZ661378 SALK 0245 CG712334 1119026A1 BH850177 SALK 0709 BW593923 BW593923 H95706 YE95910.61 AL477015 T. brucei AL481755 T. brucei AL481755 T. brucei AL481755 T. brucei AL481755 T. brucei AL881754 AL81756 T. Brucei AL881757 T. Brucei

T. brucei qw07c06.x

SALK 1378 1M0148F03 SALK 1013 T. brucei 2M0109M08

1M0558A05 SALK_0645

SALK 0915 SALK 0248 1119026A1 SALK 0709 BW593923

0180518-0

nucleic

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Run on:

Sequence:

Searched:

Database

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0 0 0 0 0 0 0 0 0 0 0

Result

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ьнылогзэ 44 bp DNA linear GSS 02-MAY-2002 SALK 048259 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_048259, genomic survey sequence. ВН810239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="caron:3702"
/clone="SALK 048259".
/clone="SALK 048259".
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
Shequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is single pass sequence recovered from the left border of TDNA.
                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torray Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;

    44
/organism="Arabidopsis thaliana"

                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/ecotype="Col-0"
                                                                                  BW593923
H95706
TAZ02B01Q
A1280742
BZ766776
AZ388487
BH866468
TAZ32A04Q
AZ830439
                     AA995598
CC049873
                                         BZ290816
BZ661378
CG712334
BH850177
                                                                                                                                                                                BZ584043
AZ826147
AZ762777
BH911010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: TDNA tagged
  Email:
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Query Match
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  ORIGIN
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AL974349 Danio rer
AA423162 ve36b01.r
AA330873 vz71e07.s
A172854 uc10c07.r
A2651473 1M0522N07
AZ651473 1M0522N07
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BX891114 Arabidops
CC888123 SALK 1513
BZ762504 SALK 1050
BE54888 601073346
BX572262 Arabidops
BK77262 Arabidops
BH79038 SALK 6580
BH79038 SALK 6580
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T73611 yc36h11.s1
AZ307496 IM0009F14
AU014420 AU014420
CL213211 A045A04 G
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AV845171 AV845171
                                                                    November 18, 2005, 11:22:09; Search time 1147.98 Seconds (without alignments) 795.779 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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          5.1.6
Compugen Ltd.
                                                                                                                                                                                         34239544 seqs, 19032134700 residues
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                US-10-788-779-4
24
1 CTTCATGTTTCCAAAGTGCATGAT 24
          GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                                  Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                nucleic search, using sw model
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AZ307496
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BH790838
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AA930873
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AA386692
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gb_htc:*
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gb_est5:*
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Match Length
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                                                                                                                                                                                 AV845171 AV845171 Nori Satch unpublished cDNA library, cleavage stage embryo Ciona intestinalis cDNA clone rcicl09p13 3', mRNA sequence.
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This sequence was generated from the SP6 end of BAC 46K23. 46K23 is part of the Danlokey BAC Library created by R. Plasterk and N.V.
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Bukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona, Phlebobranchia, Cionidae, Ciona.

1 (bases 1 to 42)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="rcicl09p13"
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/dev_stage="cleavage stage embryo"
/clone_lib="Nori Satoh unpublished cDNA library, cleavage
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                         Gaps
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Danio rerio genomic clone DKEY-46K23, genomic survey sequence.
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                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
       Pred. No. 2.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Ciona intestinalis"
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Direct Submission
81.8%; Preu. ....
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/db_xref="taxon:7719"
                                                                           2 TTCATGTTTCCAAAGTGCATGA 23
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AL974349.1 GI:25185781
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Department of Zoology
                                                                                                                                                                                                                                                                                          Ciona intestinalis
                        18; Conservative
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       Similarity
     Best Local
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AV845171/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 43) Marra, M.; Hillier, L., Allen, M.; Bowles, M.; Dietrich, N.; Dubuque, T.; Geisel, S.; Kucaba, T.; Lacy, M.; Le, M.; Martin, J.; Morris, M.; Schellenberg, K.; Steptoe, M.; Tan, F.; Underwood, K.; Moore, B.; Theising, B.; Wylie, T.; Lennon, G.; Soares, B.; Wilson, R.
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                        Gaps
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project Contact: Marza M/Mouse EST Project Contact: Marza M/Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Porset Park Parkway, Box 8501, St. Louis, MO 63108 Pax: 314 286 1800
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                                                                                                                                                                                                                                                                                   Length 47;
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Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                              59.2%; Score 14.2; DB 9;
84.2%; Pred. No. 1e+05;
iive 0; Mismatches 3;
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/db xref="taxon:7955"
/clone="DRAY-46K23"
/tissue_type="Testis"
/note="Tector pIndigoBAC-536"
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                                                                          /organism="Danio rerio"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Matches 16; Conservative
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A1172854

wolloc07.rl Soares mammary_gland_NDAWG Mus musculus cDNA clone
IMAGE:1397580 5' Similar to gb:M90696 CATHEPEIN S PRECURSOR
(HTMAN); , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 48)
Marray, M.; Hillier, J., Allen, M.; Bowles, M.; Dietrich, N.; Dubuque, T.; Geisel, S.; Kucaba, T.; Lacy, M.; Le, M.; Martin, J.; Morris, M.; Schellenberg, K.; Steptoe, M.; Tan, F.; Underwood, K.; Moore, B.; Theising, B.; Wylie, T.; Lennon, G.; Soares, B.; Wilson, R.; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:909296
                                                                                                  Gaps
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Contact: Marra M/Mouse RST Project
Contact: Marsh Whouse RST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fars: 314 286 1800
                                                            Length 48;
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Best Local Similarity 77.3%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 5; Indels
                                                         Score 14; DB 1; 1
Pred. No. 1.3e+05;
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Seg primer: -28mil rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                      58.3%; Scor. 77.3%; Pred. No. ...
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/dev_stage="4 weeks"
lab_host="DH108"
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The WashU-HHMI Mouse EST Project
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/db_xref="taxon:10090"
/clone="IMAGE:1397580"
                                                                                                                                         3 TCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                34 TCATGTCTCCCAAGTGGTTCAT 13
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                                                                                                                                                                                                                                                                                                                                                           48 bp mRNA linear EST 23-APR-1998 vz71e07.81 Soares mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1331940 3' Similar to gb:M90696 CATHEPSIN S PRECURSOR (HUMAN);, mRNA sequence.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:691484
                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra Manuse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                      Query Match 58.3%; Score 14; DB 1; Length 43; Best Local Similarity 77.3%; Pred. No. 1.2e+05; Matches 17; Conservative 0; Mismatches 5; Indels
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Seg primer: -28mil rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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clone="IMAGE:1331940"
                                                                                                                                                                                                                                         1 CTTCATGTTTCCAAAGTGCATG 22
                                                                                                                                                                                                                                                             37 CTCCATGTCTCCATTGTGGATG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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Bonaldo.
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AA930873/c
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ACCESSION VERSION KEYWORDS

RESULT 7

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TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/John | Jib host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone | Jib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated from a frapated polymurcleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                     AZ651473 40 bp DNA linear GSS 14-DEC-2000 1M0522N07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0522N07 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 40)
Dunn, D., Aoyagi, A., Barber, M., Bacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.7%; Score 13.6; DB 8; Best Local Similarity 80.0%; Pred. No. 1.9e+05; Matches 16; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 10000 Std Error:
Plate: 0522 row: N column: 07
Seg primer: CGTTGTAAAACGACGGCCAGT
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Location/Qualifiers
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34 TCATGTCTCCCAAGTGGTTCAT 13
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Mus musculus
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 48)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/mol type="mRNA"
/strain="CS7EL/6"
/db xref="taxon:1009"
/clone="IMAGE:76090"
                                                            34 TCATGTCTCCCAAGTGGTTCAT 13
                              3 TCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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FEATURES

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Gaps

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5 ATGTTTCCAAAGTGCATGAT 24

8

3 TCATGTTTCCAAAGTGCATGAT 24

ORIGIN

Length 40; 4; Indels GSS 13-DEC-2000

GSS

KEYWORDS

ACCESSION VERSION

LOCUS DEFINITION AZ637079/c

RESULT 9

셤

SOURCE

REFERENCE AUTHORS JOURNAL COMMENT

TITLE

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Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Barrell, Oxford University Press, 1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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(bases 1 to 42)

Hillier,L. Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
                                                                                                                                                                              TA46H06P 1inear GSS 13-DI
T. brucei sheared genomic DNA clone 46h06, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                               Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/organism="Trypanosoma brucei"
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/strain="TREU927"
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      T73611.1 GI:690286
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource Library Managements (Inter J. Naw.) ax. org/resources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oilgonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                        AZ637079 26 bp DNA linear GSS 13-DEC-2000 1M0496F09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0496F09 F, genomic survey sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0496 row: F column: 09
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0496F09"
                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                 23 Argrircccaccrcaaggar 4
                                                                                                                                                                                                                                                                    AZ637079
AZ637079.1 GI:11759185
/sex="Male"
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Best Local Similarity
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source

FEATURES

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9 TICCAAAGIGCAIGA 23

Matches

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harocoury, whose DNA resources (thtp://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil #4732114 [gb] AR125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone llb="Mouse lokb plasmid UUGCNH library"
/note="Vector: PWD4Zny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 31;
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                                                                                                                   Std Error:
                                                                                                          Insert Length: 10000 Std Error: Plate: 0009 row: F column: 14 Seg primer: CGTTGTAAAACGACGGCCAGT class: plasmid ends
                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                     High quality sequence stop: 31. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="UUGC1M0009F14"
                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male
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Best Local Simi
Matches 15;
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                                                                                                                                                                                                                                                                                                                                                                                      High qality sequence starts: 1 High qality sequence stops: 1 Source: IMAGE Consortium, LLML This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information: Trace considered overall poor quality Insert Length: 1676 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="49 years old"
/lab host="SOLR cells (kanamycin resistant)"
/clone_lib="Strattagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Digo dr. Hepatectomy from normal male caucasian. Average
insert size: 11 kb; Uni-ZAP XR Vector: ~5' adaptor sequence: 5'
sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
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1M0009F14F Mouse 10kb plasmid UUGCIM library Mus musculus genomic CODE UUGCIM0009F14 F, genomic survey sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 31)
                                                                             Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                             Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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/organism="Homo_sapiens"
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/db_xref="GDB:499878"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anger primer: -21ml3
Seq primer: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
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clone="IMAGE:82821"
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Insert Size: 1676
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AUTHORS
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pTlbetageo gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
http://genetrap.gsf.de/project/web_new/database/result clone.html?
clone_id=A045A04' ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.html'
l' Inhouse Sequence Identifier: 08991
                                                                                                                              /clone lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 35)
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/cell_type="Embryonic stem cell"
/cell_line="ES cells 12952 (formerly 129/Sv)
/celn=[lib="GGTC Gene Trap Library GV03C04"
/note="Vector: pTlbetageo"
                                                                                                                                                                                                                                                                                                          55.0%; Score 13.2; DB 1; Length 33; 83.3%; Pred. No. 2.8e+05; ive 0; Mismatches 3; Indels
                'organism="Schizosaccharomyces pombe"
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/mol_type="mRNA"
/strain="129 Sv"
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/clone="A045A04"
                                                                         /db_xref="taxon:4896"
/clone="spc09814"
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                                /mol_type="mRNA"
/strain="972"
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55.0%; Score 13.2; DB 9; Length 35; 83.3%; Pred. No. 2.8e+05;

Query Match Best Local Similarity

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Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.

Direct Submission

Unsect Submission

Submitted (11-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Submitted (11-MAR-2004) Weisshaar B., Max-Planck-Institut fuer

Suechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

Details on the protocols used for generation of the sequence are

described in References 1-3. Re-examination of the sequence

is of low reliability. Therefore, no information on a potential

insertion site is deduced. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated

'GABI.' Information on line availability can be found at:

Location/Qualifiers
                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana T-DNA flanking sequence GK-049G05-013871, genomic survey sequence.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/clone="GK-049G05-013871"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Weisshaar, B.
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/mol type="genomic DNA"
/strain="Columbia 0"
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22755829
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/ecotype="Col-0"
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Unpublished (2001)
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Direct Submission.

Direct Submission.

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Submitted (31-Mak-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (11-Mak-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (31-Mak-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungeforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone K21P3. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
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plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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GABI-Kat SimpleSearch: a flanking sequence tag (FST) database
the identification of T-DNA insertion mutants in Arabidopsis
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                                                               Length 41;
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I-DNA derived sequences were removed."
                                                           55.0%; Score 13.2; DB 9; 83.3%; Pred. No. 2.8e+05; ive 0; Mismatches 3;
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/strain="Columbia 0"
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lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 45)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
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/clone="SALK 15365.21.90.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                           55.0%; Score 13.2; DB 9; 83.3%; Pred. No. 2.8e+05;

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    /organism="Arabidopsis thaliana"
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601073346F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3459586 5',
mRNA sequence.
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Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                 SALK 105087.19.80.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK 105087.19.80.n, genomic
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/clone="SALK 105087.19.80.n"
/clone lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
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Pred. No. 3.3e+05;
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/organism="Arabidopsis
/mol_type="genomic DNA"
/ecotype="Col-0"
     29 bp
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Fax: 858 558 6379
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                                                          survey sequence.
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Arabidopsis thaliana T-DNA flanking sequence GK-544G08-020964,
                                                                                                                                                                                                                                                                                                                                                                                       /mol type="minute suprems"
/mol type="minute suprems"
/db xref="taxon:9606"
/clone="IMAGE:345586"
/tissue_type="cervical carcinoma cell line"
/lab host="DHING"
/lone=lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
Technologies."
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Rosso,M.G., Li,Y., Strizhov,N. and Weisshaar,B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM8452 row: k column: 11
High quality sequence stop: 37.
Location/Qualifiers
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BJ076538 BJ076538 NIBB Mochii normalized Xenopus tailbud library Xenopus
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/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
(bases 1 to 43)
       Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., dadadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                      BH790838 1.05.x Arabidopsis thaliana TDNA inear GSS 02-APR-2 SALK 058022.27.05.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_058022.27.05.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g41627.
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Pax: 858 558 6379
                                                                                                          Length 43;
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                                                                                                                                                            Indels
                                                                                                       54.2%; Score 13; DB 2; Le llarity 76.2%; Pred. No. 3.5e+05; Conservative 0; Mismatches 5;
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     Average insert size 1.8 kb.
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Arabidopsis thaliana
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/ecotype="Col-0"
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                                  Technologies.
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Unpublished (2001)
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This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At1932090. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MDI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mgo.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAc16 I (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA
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/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_68"
/note="Grgan: ling; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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1 (Dases 1 to 43)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                            /clone="GK-544G08-020964"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
n column: 20
High quality sequence stop: 43.
Location/Qualifiers
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                                                                                                                                                                                                                                                            organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13; DB 9; I
Pred. No. 3.5e+05;
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                    DNA"
                                                                                                                                                                                                                                                                                                                                       'db xref="taxon:3702"
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                                                                                                                                                                                                                                                                                    /mol_type="genomic_D
/strain="Columbia 0"
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                                                                                                                                                                                                                                                                                                                                                                                                              ecotype="Col-0"
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76.2%;
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BE788148
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GSS 16-FEB-2001
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Railam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Duvae whole genome scaffolding with paired end reads from 10kb Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ794096 16-FEB-200 36 bp DNA linear GSS 16-FEB-200 2M0047P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0047P10 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                             Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: mob.REGA+ET
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                    /dev stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error
no47 row: P column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:10090"
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Location/Qualifiers
                                                                                                                                                                                                                                                                  /clone="IMAGE:330001"
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                                           MGI: 211401
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DEFINITION
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 28)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Marlin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                    Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 44)

Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                    Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
Bmail: tshini@genes.nig.ac.jp
The information of this clone is available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
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mADADIST SOARES MOUSE D3NMF19.5 Mus musculus cDNA clone
IMAGE:330001 5' similar to SW:CATK_RABIT P43236 CATHEPSIN K
PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.2%; Score 13; DB 4; Length 44;
81.2%; Pred. No. 3.5e+05;
tive 0; Mismatches 3; Indels
laevis cDNA clone XL051f21 3', mRNA sequence.
                                                                                    Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL051f21"
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The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://xenopus.nibb.ac.jp.
Location/Qualifiers
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                    BJ076538
BJ076538.1 GI:17521454
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W11835.1 GI:1286140
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Matches 13; Conserv
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ecotype="Col-0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (91)4732114 [9b]ARD20072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the innert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC796901 36 bp DNA linear GSS 01-JUL-2003 SALK 144210.22.90.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_144210.22.90.x, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 36)
Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Sadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J. R.

A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                          /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                    lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is single pass sequence recovered from the left border of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.3%; Score 12.8; DB 8; Length 36; 70.8%; Pred. No. 4.2e+05; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis Genome Unpublished (2001) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies (10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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Arabidopsis thaliana
organism≃"Mus musculus"
                     mol type="genomic DNA"
strain="C57BL/6J"
                                                                       'db_xref="taxon:10090"
'clone="UUGC2M0047P10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTTCATGTTTCCAAAGTGCATGAT 24
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
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CC796901
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CC796901/c
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA995598 43 bp mRNA linear EST 27-AUG-1998 os22h03.s1 NCI CGAP Kid5 Homo sapiens cDNA clone IMAGE:1606133 3' similar to TR:014949 014949 LOW MOLECULAR MASS UBIQUINONE-BINDING
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/db_xref="txxon:3702"
/clone="SALK 144210.22.90.x"
/clone="SALK 144210.22.90.x"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 43) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                 Length 36;
                                                                                                                                                                                                                                                                                                                                                                        7; Indels
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                                                                                                                                                                                                                                                                                                              53.3%; Score 12.8; DB 9; ilarity 70.8%; Pred. No. 4.2e+05; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trace considered overall poor quality Insert Length: 475 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1606133"
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Unpublished (1997)
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Matches

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LOCUS CC049873/c

RESULT 28

ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

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/organizem-controlled by Amol type="genomic DNA"
/mol type="genomic DNA"
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/clone="PCR was performed on Arabidopsis thaliana lines
- which contains one or more TDNA insertion
- which contains one or more TDNA insertion
- elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At1929620 and 300 bases of the 5' end of At1929630. Class: TDNA tagged.
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                                                                                                                                                                                                                                                                                                                                              Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA PER: 858 558 6379 East: 858 558 6379 East: 858 558 6379 East: 858 558 6379
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Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

    .26
    /organism="Arabidopsis thaliana"

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Arabidopsis thaliana (thale cress)
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/clone="015-518-3-7to12-B06"
/clone="1b="UniformWu MuTAIL Library"
/note="Wector: TOO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo assymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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                        53.3%; Score 12.8; DB 1; Length 43; 87.5%; Pred. No. 4.3e+05; 1ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
00 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
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/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
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/organism="Zea mays"
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Unpublished (2003)
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RESULT 29 BZ290816/c DEFINITION

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/db xref="taxon:3702"
/clone="SALK 02484.36.30.x"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Iiliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 32)

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Stanford University
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Fax: 650 125 8221
Fax: 650 125 8221
Formal: walbot@stenford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 119026 row: A column: 11
Class: transposon-tagged.
Location/Qualifiers
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/tissue_type="leaf"
/dev_grage="adult"
/lab_host="lulto" - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
                                                           This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
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/multivar="mixed background W23/A188/B73/K55"
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                                                                                                                                              1. .31
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
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Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Sadarinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA, was grown at UC San Diego in 2002. Was extracted from leaf strips, double digested using BamHi and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                            Length 32;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                            Score 12.6; DB 9;
Pred. No. 5.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               1 CTTCATGTTTCCAAAGTGC 19
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                                                                                                                                                                                                                                                                                         52.5%;
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                                                                                                                                                                                                                                                                                                                                                     15; Conservative
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/mol_type="mRNA"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                    and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TTCATGTTTCCAAAGTGCA 20
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Best Local Similarity 78.9°
Matches 15; Conservative
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TA202B01Q/c
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Ciona savignyi"
/mol_type="mRNA"
/mol_type="mRNA"
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/clone_lib="Yutaka Satou unpublished cDNA library (csef2)"
                   BW593923 Yutaka Satou unpublished cDNA library (csef2) Ciona savignyi cDNA clone csef028024 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 25-NOV-1996
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                                                                                                                                                            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

1 (Dases 1 to 38)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona savignyi (Satou, Shin-i, Kohara, Satoh)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primatee, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 40)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yt95g10.s1 Soares pineal gland N3HPG Homo sapiens CDNA clone INAGE:232098 3' similar to gb|M73048|HUMU3AAAA Human U3 small H95706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 52.5%; Score 12.6; DB 5; Length 38; 1 Similarity 75.0%; Pred. No. 5.3e+05; 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                      Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Eax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence starts: 1 High quality sequence stops: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                   Contact: Yutaka Satou
Department of Zoology
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H95706.1 GI:1108848
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Homo sapiens
                                                                                                                                  Ciona savignyi
                                                                                                                                                      Ciona savignyi
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Matches 15; Conserv
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                     LOCUS
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BW593923
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/dlone="IMAGE:23098"
/lab host="BH10B (ampicillin resistant)"
/clone=lib="Soares_pineal_gland_N3HPG"
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/note="Organ: pineal_gland_N3HPG"
/set farmaccon for the pineal_gland_Nath not 1 = 011go(dr) primer
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/set farmaccon for not 1 
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AL477015.1 GI:11843470
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Rockville, MD. Genomic DNA isolated from a cloned population of
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
innert libraries for whole genome shotgun sequencing small
innert libraries for whole genome shotgun sequencing projects. In
Barrell, Oxford University Press, 1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: polyT not found Insert Length: 597 Std Brror: 0.00 Seq primer: Promega -21ml3.

Location/Qualifiers
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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GSS 13-MAR-2003

LOCUS DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

RESULT 36

g

AI280742

Matches

ORIGIN

ORGANISM

AUTHORS

TITLE

JOURNAL

COMMENT

REFERENCE

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AZ388487 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 43)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 37)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used car be found at http://signal.salk.edu/tdna_protocols.html"
43 bp DNA linear GSS 13-MAR-2 SALK 137836.19.55.x Arabidopsis thaliana TDNA insertion lines survey sequence.
BZ766776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db xref="taxon:3702"
/clone="SALK 137836.19.55.x"
/clone lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.5%; Score 12.6; DB 8; Length 43; 78.9%; Pred. No. 5.4e+05; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
TH: 858 453 4100 x1752
Pax: 858 558 6379
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                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/ecotype="Col-0"
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Mus musculus
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GSS.
                                                                                                                                                           GI:28939329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: TDNA tagged
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NT-CGAP clone distribution information can be
found through the I.M.A.G.E., Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                  AI280742 43 bp mRNA linear EST 23-NOV-1998 qw07c06.xl NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:1990378 3' similar to TR:Q39949 Q39949 HYDROXYPROLINE-RICH PROTEIN. ;, mRNA
                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors"
/lab_host="mulous"
/clone_lib="NCI_CGAP_Ut3"
/note="Organ: uterus, Vector: pCWV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 43)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                             Gaps
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Pred. No. 5.4e+05;
0; Mismatches 4; Indels
                                                                                                                                                      Score 12.6; DB 9; Length 41; Pred. No. 5.3e+05; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  www-bio.llnī.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality
Seg primer: -40UP from Gibco
High quality sequence scop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1990378"
                                                   /db_xref="taxon:5691"
/clone="202b01"
                                                                                                                                       52.5%; bc. 78.9%; Pred 0; h
                               strain="TREU927"
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0
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78.9%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                Similarity
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                                                                                                                                                         Query Match
Best Local
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Gaps ; 0

source

FEATURES

RESULT 37 BZ766776/c

g

Matches

ORIGIN

JOURNAL

COMMENT

ROUTCE

FEATURES

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/clone="SALK_101369"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="FCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
Trypanosoma a tight saize distribution (
c give a tight saize distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
Unpublished (2001)

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

Email: eckerosalk.edu
This is single pass sequence recovered from the left border of This is sequence lies within 300 bases of the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TA232A04Q 42 bp DNA linear GSS 13-DE
T. brucei sheared genomic DNA clone 232a04, reverse sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 6.6e+05;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Trypanosoma brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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AL481755.1 GI:11847265
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Best Local Similarity 72.7%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                              At3g60570.
Class: TDNA tagged
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TA232A04Q/c
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JOURNAL
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SOURCE
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                                      COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114]pD|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was light adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH866468 1inear GSS 05-AUG-2002 SALK_101369 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_101369, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosid8; euroside II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 41)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Adonso,J.M., Leisse,T.J., Rarnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="R. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                         84112, usa
Far: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                        Plate: 0148 row: F column: 03
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Mus musculus"
                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 37. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="UUGC1M0148F03"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TCATGTTTCCAAAGTGCATGAT 24
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BH866468.1 GI:22102366
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Best Local Similarity 72.79
Watches 16; Conservative
Unpublished (2000)
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

LOCUS DEFINITION

ACCESSION

RESULT 39

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ORIGIN

BH866468

GSS 13-DEC-2000

Gaps

; 0

Search completed: November 18, 2005, 21:12:43 Job time : 1150.98 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

November 18, 2005, 00:26:13 ; Search time 46.6312 Seconds (without alignments) 842.154 Million cell updates/sec Run on:

US-10-788-779-4 24 1 CTTCATGTTTCCAAAGTGCATGAT 24 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1202784 segs, 818138359 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:* Issued Patents NA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
1	24	100.0	24	-	US-07-989-160-4	Sequence 4, Appli
7	16.2	67.5	34	7	US-08-577-492-21	21,
٣	16.2	67.5	34	m	US-09-079-630-21	21,
C 4	15.6	65.0	25	4	US-09-396-196G-53744	
S	14.8	61.7	25	4	US-09-396-196G-21176	2117
9 0	14.8	61.7	25	4	US-09-396-196G-21177	
C 7	14.8	61.7	25	4	US-09-396-196G-21178	Sequence 21178, A
0 0	14.6	60.8	25	4	US-09-396-196G-23224	
o 0	14.6	60.8	27	٣	US-08-908-643C-34	
c 10	14	58.3	25	4	US-09-396-196G-59686	
11	14	58.3	25	4	US-09-396-196G-122551	
12	14	58.3	36	m	US-08-961-083-258	
13	14	58.3	36	4	US-09-536-784-258	258,
14	14	58.3	20	4	US-08-956-171E-1998	1998,
15	14	58.3	20	4	US-08-781-986A-1998	
16	13.8	57.5	20	4	US-09-232-785-173	173, 7
-	13.8	57.5	25	4	US-09-396-196G-21175	
c 18	13.8	57.5	25	4	US-09-396-196G-109424	
-	13.8	57.5	25	4	US-09-396-196G-109425	
20	13.8	57.5	47	4	US-09-671-317-784	
21	13.6	56.7	20	4	US-09-913-192A-10	10, 7
22	_	56.7	25	m	US-08-544-381B-80	80,
c 23	13.6	56.7	25	4	US-09-396-196G-41037	
24	13.6	56.7	25	4	US-09-396-196G-59155	
25	13.6	56.7	25	4	US-09-396-196G-122534	
0		56.7	47	4	US-09-422-978-2662	2662,
c 27	13.4	55.8	17	m	US-08-584-040-5610	

	sednence sell, Ap	Sequence 2500, Ap	Sequence 2501, Ap	Sequence 2500, Ap	Sequence 2501, Ap	Sequence 10, Appl	305	Sequence 33631, A	Sequence 33632, A	Sequence 45409, A	Sequence 45410, A	Sequence 70209, A	Sequence 3015, Ap	Sequence 3250, Ap	Sequence 835, App	٥, ٨	26	Sequence 12297, A	
	US-08-584-040-5611	US-09-371-772B-2500	US-09-371-772B-2501	US-09-685-664B-2500	US-09-685-664B-2501	US-07-768-437-10	US-09-396-196G-30572	US-09-396-196G-33631	US-09-396-196G-33632	US-09-396-196G-45409	US-09-396-196G-45410	US-09-396-196G-70209	US-09-422-978-3015	US-09-422-978-3250	US-09-443-199C-835	US-07-763-512-9	US-09-396-196G-5610	US-09-396-196G-12297	
•	7)	4	4	4	4	٦	4	4	4	4	4	4	4	4	4	H	4	4	
	7	17	17	17	17	18	25	25	25	25	25	25	47	47	20	21	25	25	
	22.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.8	55.0	55.0	55.0	
	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.2	13.2	13.2	
6	Z)	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
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ALIGNMENTS

APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: SATKINS, HUGH
APPLICANT: ROSENZWIS, HUGH
APPLICANT: ROSENZWIS, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDED ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510 STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSELE
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DAEE: 11-DEC-1993
CLASSIFICATION: 435
ATTCANEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/POCKET NUMBER: 33,505
REFERENCE/POCKET NUMBER: 33,505
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEBURSS: single Sequence 4, Application US/07989160; Patent No. 5429923; GENERAL INFORMATION: MOLECULE TYPE: CDNA US-07-989-160-4 US-07-989-160-4

Gaps ö Query Match 100.0%; Score 24; DB 1; Length 24; Best Local Similarity 100.0%; Pred. No. 0.07; Matches 24; Conservative 0; Mismatches 0; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.2; DB 3; Length 34; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.;
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NOS: 127806
SEQ ID NOS: 3744
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/577,492
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: GB 9426227.6
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9512996.1
FILING DATE: 26-UNM-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-396-196G-53744/c
; Sequence 53744, Application US/09396196G
; Patent No. 6821724
                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/079,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TTCATGTTTCCAAAGTGCATGA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 rrraagcrrccaaagrecare 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Cherry, David A.
REGISTRATION UNDREE: 35,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.5%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 34 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: mus musculus US-09-396-196G-53744
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                             USA
                                                                                                                                                                                                                                                     FILING DATE:
                                                                  19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-079-630-21
                                             COUNTRY:
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                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Owens, Raymond John
APPLICANT: Lunb, Simon Mark
TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
TITLE OF INVENTION: ITS PRODUCTION AND USE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSES: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784ris
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6291199ris
One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.5%; Score 16.2; DB 2; Length 34; 85.7%; Pred. No. 3e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND TITLE OF INVENTION: ITS PRODUCTION AND USE COMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIT: 19103

ZIT: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: WordPerfect 6.1

CURRENT APPLICATION NUMBER: US/08/577,492
FILING DATE: 22-DEC-1995
CLASSIFFCATION: 435
PRIOR APPLICATION NUMBER: GB 942627.6
FILING DATE: 23-DEC-1994
PRIOR APPLICATION NUMBER: GB 942627.6
FILING DATE: 23-DEC-1994
PRIOR APPLICATION NUMBER: GB 951296.1
FILING DATE: 26-UTN-1995
ATTORNEY AGENT INFORMATION:
1 CTTCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/09079630
Patent No. 6291199
GENERAL INFORMATION:
APPLICANT: Perry, Martin John
APPLICANT: Lumb, Simon Mark
                                                                                                      Sequence 21, Application US/08577492
Patent No. 5851784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TTCATGTTTCCAAAGTGCATG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cherry, David A.
REGISTRATION NUMBER: 35,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.7
Matches 18; Conservative
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TOPOLOGY: lin
                                                                RESULT 2
US-08-577-492-21
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US-09-079-630-21
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Length 25;

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SPECIFICALLY BIND TO CELLS AND METHODS OF
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Pred. No. 1.5e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23224/C
; Sequence 23224, Application US/09396196G
; Patent No. 682124
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Methods of Genetic Analysis
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REPERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23224
                 APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
ITLE OF INVENTION: Methods of Genetic Analysis
FILE REPERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21178
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                          Score 14.8; DB 4;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Barber, Michael T.
Schultz, Stephanie
Parkinson, Scott J.
TITLE OF INVENTION: TART
COLORECTAL CANCER
USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/08908643C; Patent No. 6120995
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TICATGITICCAAAGIGCAIG 22
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81.0%;
                                                                                                                                                                                                                                                                                                                                                        61.7%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         6 TGTTTCCAAAGTGCATGA
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.8°
Best Local Similarity 81.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Mus musculus
US-09-396-196G-21178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mus musculus
US-09-396-196G-23224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-908-643C-34/c
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Pred. No. 1.3e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.7%; Score 14.8; DB 4; Length 25; 88.9%; Pred. No. 1.3e+03; ive 0; Mismatches 2; Indels
                                                 US-09-396-196G-21176/c

i Sequence 21176, Application US/09396196G

i Patent No. 6821724

i GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Mack

APPLICANT: Affymetrix, Inc.

ITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT FILIAGO DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21176

LENGTH: 25

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21177
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %3-09-396-196G-21178/c
%Sequence 21178, Application US/09396196G
%Patent No. 6821724
%GENERAL INFORMATION:
% APPLICANT: Michael Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21177, Application US/09396196G Patent No. 6821724
25 TTCAACTTCCCAAAGTGCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 TGTTTCCAAAGTGCATGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 TGTTTCCAAAGTGCATGA 23
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.7
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-21176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-396-196G-21177/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-396-196G-2117
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Gaps

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FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: BrOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 309-8504
INPORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: mus musculus
                                                                            JS-09-396-196G-122551
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6120995ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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81.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-396-196G-59686/C
; Sequence 59686, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
APPLICANT: Michael Mittmann
; APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Nack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
; PRIOR PILING DATE: 1998-09-15
; NUMBER OF SEQ ID NOS: 127806
; SEQ ID NO 59686
; LENGTH: 25
; TAPPE. NATE OF SEQ ID NOS: 127806
; SEQ ID NO 59686
; LENGTH: 25
                                                                                                                                                        COMPUTER: 3.5 inch disk, 1.44 Mb COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDER: 0.5 (0.1)

CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBR: US/08/908,643C FILING DATE: 0.7-Aug-1997

CLASSIFICATION NUMBER: cuknom>
PILING DATE: cuknom>
PILING DATE: cuknom>
PILING DATE: cuknom>
PILING DATE: cuknom>
APTORNNY/AGENT INFORMATION:
NAME: Mark Deluca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-2209
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 34: US-08-908-643C-34
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STRANDEDNESS: double
                                                                                             COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
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Best Local Similarity 81.0
Matches 17; Conservative
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Matches 17; Conservative
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; ORGANISM: mus musculus
US-09-396-196G-59686
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US-08-961-083-258

Sequence 258, Application US/08961083

Patent No. 6159469

GENERAL INFORMATION:
APPLICANT: Choi et. al.
TILLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
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ZIE: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
Sequence 12251, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT APPLICATION NUMBER: 60/100,678
PRIOR PILLING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastERQ for Windows Version 4.0
SEQ ID NO 122551
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.3%; Score 14; DB 4; 18est Local Similarity 77.3%; Pred. No. 2.9e+03; Matches 17; Conservative 0; Mismatches 5
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
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Michael R. Pannon
NUMBER OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus Polynucleotides and Sequences 5255
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION NUMBER: 06/009,861

PRICATION NUMBER: 08/781,986

APPLICATION NUMBER: 08/781,986

APPLICATION NUMBER: 08/781,986

APPLICATION NUMBER: 46,789

RETERBENEZ JOHNANTION:

NAME: MARK J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE JOCKET NUMBER: PE248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.3%; Score 14; DB 4; 1
Best Local Similarity 73.9%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1998:
US-08-956-171E-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1998, Application US/08781986A
Fatent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aur
CORRESPONDENCE: 5255
NUMBER OF SEQUENCES: 5255
STREET: 9410 Key West Avenue
STREET: 9410 Key West Avenue
CITY: ROCKYILLE
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TICATGITICCAAAGIGCAIGAI 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20850
COMPUTER READABLE FORM:
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US-08-781-986A-1998
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                                                                                                                                                                                                                                                                                                                                   Sequence 258, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
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WEDIUM TYPE: Diskett, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII TEXT.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/536,784

FILING DATE: 30-00C-1997

CLASSIFCATION: CUNKNOWN>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,083

APPLICATION DATA:

APPLICATION NUMBER: 108/97

ATTORNEY/AGENT INFORMATION:

NAME: MSCHENTINE OCT-30-1997

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 41,971

REFERENCE/DOCKET NUMBER: 41,971

REFERENCE/DOCKET NUMBER: 41,971

REFERENCE/DOCKET NUMBER: 6301,309-8504

TELLEPAX: (301) 309-8512
                                                                    58.3%; Score 14; DB 3; Length 36; 77.3%; Pred. No. 3.1e+03; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 58.3%; Score 14; DB 4; Length 36; Best Local Similarity 77.3%; Pred. No. 3.1e+03; Matches 17; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-09-536-784-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1998, Application US/08956171E
PATENT NO. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
G11 H. Choi
PATENCK S. Dillon
Craig A. Rosen
                                                                                                                                                                 3 TCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                               3 rcaagcriccaaacregrigar 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 258:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                               Query Match
Best Local Similarity 77.3
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
linear
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; TOPOLOGY:
US-08-961-083-258
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                                                                                                                                                                                                                                                  57.5%; Score 13.8; DB 4; Length 25; 88.2%; Pred. No. 3.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 18
US-09-36-1966-109424/C
; Sequence 109424, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Mack
; APPLICANT: Affwertix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT APPLICATION NUMBER: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR PILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 109425, Application US/09396196G
Fatent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
FRICR APPLICATION NUMBER: 00/100,678
FRICR APPLICATION NUMBER: 60/100,678
FRICR APPLICATION NUMBER: 60/100,678
FRICR APPLICATION NUMBER: 60/100,678
FRICR FASTESCO FOR WINDOWS VERSION 4.0
SEQ ID NOS: 127806
SSCTWARE: FASTESCO FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                 0; Mismatches
    ; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21175
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-21175
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                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.2.
Thes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 19
US-09-396~196G-109425/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: International Paper Co.
APPLICANT: International Paper Co.
APPLICANT: Echt, Craig. S
APPLICANT: Belt, Craig. S
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 4481/IE188051
CURRENT APPLICATION NUMBER: US/09/232,785
CURRENT FILING DATE: 1999-01-19
PRIOR PELICATION NUMBER: 09/232,884
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 397
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 173
LENGTH: 20 '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
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US-09-396-196G-21175/C
; Sequence 21175, Application US/09396196G
; Patent No. 681724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; TITLE OF INVENTION Wethods of Genetic Analysis
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.3%; Score 14; DB 4; J
73.9%; Pred. No. 3.3e+03;
tive 0; Mismatches 6
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
FELECOMMUNICATION NUMBER: 91,446
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8504
INFORMATION FOR SEQ ID NO: 1998:
SEQUENCE CHARACTERISTICS:
THE TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1998:
SEQUENCE CHARACTERISTICS:
THE TELEPHONE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TTCATGTTTCCAAAGTGCATGAT 24
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US-09-232-785-173
, Sequence 173, Application US/09232785
, Patent No. 6733965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TTCATGTTTCCAAAGTG 18
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Best Local Similarity 73.9
Matches 17; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDRESS: double
; TOPOLOGY: linear
US-08-781-986A-1998
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ORGANISM: Pinus taeda L.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Croin, Maureen T.
APPLICANT: Croin, Maureen T.
APPLICANT: Miyada, Charles Garrett
APPLICANT: Hubbell, Earl A.
APPLICANT: Chee, Mark
APPLICANT: Chee, Mark
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Sheldon, Redward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes for TITLE OF INVENTION: Arrays of Nucleic Acid Probes for TITLE OF INVENTION: Detecting Cystic Fibrosis NUMBER OF SEQUENCES: 250
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,381B
FILING DATE: 10-OCT-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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APPLICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
PRIOR APPLICATION NUMBER: PCT/US94/12305
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12305
FILING DATE: 02-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,064
FILING DATE: 02-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CATGITICCAAAGIGCAIGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CATGTATTCAAAGACCATGA 20
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REFERENCE/DOCKET NUMBER: 015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-544-381B-80
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                                                                                                                                                             Blumenfeld, Marta

Blumenfeld, Marta

APPLICANT: Chumakov, Ilyaie

APPLICANT: Chumakov, Ilyaie

APPLICANT: Cohon, Annick

TITLE OF INVENTION: BIALELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

TITLE REPRENKOE: 62. US3. CIP

CURRENT APPLICATION UNMBER: US/09/671,317

CURRENT APPLICATION NUMBER: US/09/671,317

FRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 09/536,178

PRIOR APPLICATION NUMBER: US 00/126,269

PRIOR PILING DATE: 1999-04-30

PRIOR PILING DATE: 1999-04-30

SOFTWARE PARENT OF US 00/131,961

NUMBER: PARENT PILING DATE: 1999-04-30

SOFTWARE PARENT 
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APPLICANT: SAFAK, FRED H.
APPLICANT: SAFAK, FRANCIS G.
APPLICANT: TAKAHASHI, JUN
APPLICANT: TAKAHASHI, MASAYO
ITTLE OF INVENTION ISOLATION OF STEM CELLS AND METHODS OF USE THEREOF
FILE REFERENCE: SALZ250-1
CURRENT APPLICATION NUMBER: US/09/913,192A
CURRENT FILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-11
PRIOR FILING DATE: 1999-02-11
PRIOR FILING DATE: 1999-02-11
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 18
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                       Query Match 57.5%; Score 13.8; DB 4; Length 25; Best Local Similarity 88.2%; Pred. No. 3.6e+03; Matches 15; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 24
; OTHER INFORMATION: 10-266-203 : polymorphic base C or T
US-09-671-317-784
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Patent No. 6767738
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TGTCTCCAAAGTTGAYGAT 27
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Best Local Similarity 78.9
Matches 15; Conservative
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Gaps

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APPLICANT: Cohen. Daniel
APPLICANT: Cohen. Daniel
APPLICANT: Cohen. Marta
APPLICANT: Chunakov, Ilya
APPLICANT: Chunakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1999-10-21
EARLIER FILING DATE: 1999-11-23
EARLIER FILING DATE: 1996-11-23
EARLIER FILING DATE: 1996-11-3
EARLIER FILING DATE: 1996-11-3
EARLIER FILING DATE: 1996-11-3

EARLIER FILING DATE: 1996-11-3

LENGTH: 47
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Pred. No. 5e+03;
1; Mismatches 5; Indels
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Pred. No. 4.5e+03;
0; Mismatches 4; Indels
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; OTHER INFORMATION: 99-13113-234 : polymorphic base G or A
US-09-422-978-266.
  Indels
  4.
                                                                                                                                                                                                                                                                  APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
FURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PAPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
  0; Mismatches
                                                                                                                                                       RESULT 25
US-09-396-125534
Sequence 122534, Application US/09396196G
Perent No. 6821724
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-422-978-2662/c; Sequence 2662, Application US/09422978; Patent No. 6537751; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TCATGTTTCCAAAGTGCATGAT 24
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Best Local Similarity 72.7%;
Matches 16; Conservative
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Best Local Similarity 80.09
Matches 16; Conservative
  16; Conservative
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FEATURE:
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  Matches
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                                                                                                                                                          Score 13.6; DB 3; Length 25;
Pred. No. 4.5e+03;
0; Mismatches 4; Indels
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; Sequence 59155. Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Mack
; PRICATION TION: MICHOGO of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT FILING DATE: 1999-09-15
; PRIOR PILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 127806
; SEQ ID NO 59155

LENTH: 25
                                                                                                                                                                                                                                                                                                                                                                           Sequence 41037/c
Sequence 41037 Application US/09396196G
Fatent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TILLE OF INVENTION: Methods of Genetic Analysis
FILE REPRENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
FRICR APPLICATION NUMBER: 60/100,678
FRICR FILING DATE: 1998-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41037
LENGTH: 25
                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-544-381B-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTTCATGTTTCCAAAGTGCA 20
                                                                                                                                                                                                                                                    4 CATGTTTCCAAAGTGCATGA 23
                                                                                                                                                                                                                                                                                            4 CATTTTTGCAAAGTTCATTA 23
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80.0%;
                                                                                                                                                       Query Match
Best Local Similarity 80.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
25 base pairs
                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OKGANISM: mus musculus
US-09-396-196G-59155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-396-196G-41037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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Gaps

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Gaps

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APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinckhoomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MBHB00, 976-07 (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1999-08-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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TITLE OF INVENTION: METHOD AND REACENT FOR THE TITLE OF INVENTION: METHOD AND REACENT FOR THE TITLE OF INVENTION: CRODITIONS RELATED TO LEVELS TITLE OF INVENTION: GROWTH FACTOR NUMBER OF SEQUENCES: 8502 CORRESPONDENCE ADDRESS: ADDRESSE: LYON & IVON
                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" DISKETTE, 1.00 FORRATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: January 11, 1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: October 26, 1995
ATTORNEY AGENT INFORMATION:
MANNEY MACHINE MACHINE INFORMATION:
MANNEY MACHINE MACHINE INFORMATION:
MANNEY MACHINE M
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%Sequence 2500, Application US/09371772B

%Patent No. 650MAION:

GENERAL INFORMATION:

% APPLICANT: Ribozyme_Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218/064
                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 67-3510
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5611:
SEQUENCE CHARACTERISTICS:
FRUGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J.
REGISTARION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (213) 489-1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.8
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-584-040-5611
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                                                                                                                                                                                                                       Sequence 5610, Application US/08584040

Patent No. 6346338

GENERAL INFORMATION:
APPLICANT: Pavoc, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
ITLE OF INVENTION: TREATMENT OF DISEASES
ITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
ITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
ITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
ITLE OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRESCEE: LYON & LYON
STREET: 633 West Fifth Street
STREET: Salite 4700
CITY: Los Angeles
STRATE: California
COUNTY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY, AGENT INFORMATION:
NAME: WALDUEG, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECHONE: (213) 4899-1600
TELECHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5611, Application US/08584040
Patent No. 6346398
GENERAL INPORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
                                  33 TCATGAATTYAAAATTCATGAT 12
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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TYPE: nucleic acid
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Best Local Similarity
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US-08-584-040-5611/c
                                                                                                                                                                                                  US-08-584-040-5610/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: ]
US-08-584-040-5610
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AREALCANII: BACDOLGUO, VARINGE
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recptor
FILE REFERENCE: MEHBOO-876-K (400/021)
CURRENT APPLICATION NUMBER: US/09/685,664B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-081.00
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Sequence 10, Application US/07768437

Patent No. 5371009

GENERAL INFORMATION:

APPLICANT: MEUBERGER, MICHAEL S.

APPLICANT: MEYER, KERSTIN B.

TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO ENHANCERS NUMBERS OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHWAN DARRY & CUSHWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.8%; Score 13.4; DB 4; Length 17; Best Local Similarity 93.3%; Pred. No. 5.2e+03; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                               55.8%; Score 13.4; DB 4; Length 17; 93.3%; Pred. No. 5.2e+03; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 32
US-09-685-664B-2501/C
1S-09-685-664B-2501, Application US/09685664B
Patent No. 6818447
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: StinchComb, Dan
APPLICANT: StinchComb, Dan
APPLICANT: Escobedo, Jaime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
NUMBER OF SEQ ID NOS: 8231
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin version 3.0 SEQ ID NO 2501
LENGTH: 17
TYPE: RNA
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                                                                                                                                                                                                  Query Match
Best Local Similarity 93.34
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus
US-09-685-664B-2501
                                                                                                  TYPE: RNA
ORGANISM: Mus musculus
                                                                                                                                                   US-09-685-664B-2500
                                                                             LENGIH: 17
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US-09-371-772B-2501/C

Sequence 2501, Application US/09371772B

Sequence 2501, Application US/09371772B

Pacent No. 6566127

GENERAL INFORMATION:

APPLICANT: Pavco, Pam

APPLICANT: Stinchoub, Dan

APPLICANT: Stinchoub, Dan

APPLICANT: Stinchoub, Jame

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION NUMBER: US/09/371,772B

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR PELING DATE: 1995-10-26

PRIOR PELING DATE: 1995-01-08

NUMBER OF SEQ ID NOS: 14225

SSOTUM NOS: 14225

SSOTUM NOS: 14225

SSOTUM NOS: PatentIn Version 3.0

SEQ ID NO 2501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WENDUL (Sequence 2500, Application US/0968564B)

Sequence 2500, Application US/0968564B

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Raviggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Pactor Recptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Pactor Recptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Pactor Recptor

TITLE OF INVENTION: WINBER: US 60/002, 974

PRIOR APPLICATION NUMBER: US 60/005, 974

PRIOR PLING DATE: 1995-10-26

PRIOR FILING DATE: 1995-10-108

PRIOR FILING DATE: 1995-08-10

PRIOR PLING DATE: 1999-08-10
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0
                                                                                                                                                                           Score 13.4; DB 4; Length 17;
Pred. No. 5.2e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.8%; Score 13.4; DB 4; Length 17; 93.3%; Pred. No. 5.2e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                           55.8%;
SOFTWARE: PatentIn version 3.0 SEQ ID NO 2500
                                                                                                                                                                                                                                                                           7 GTTTCCAAAGTGCAT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 GTTTCCAAAGTGCAT 21
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                                                                                                                                                                                                                                                                                                                         16 GTTTCCAAAGAGCAT 2
                                                                                                                                                                      Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                      ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-371-772B-2501
                                                 LENGTH:
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Gaps

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55.8%; Score 13.4; DB 4; Length 25; 93.3%; Pred. No. 5.6e+03; live 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 36
US-09-196G-33612/C
i Sequence 33632, Application US/09396196G
i Patent No. 6821724
i GENERAL INFORMATION:
APPLICANT: Mitchael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: AFFUNCANT: Nethods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION WUNBER: 60/100,678
FILE REFERENCE: 1999-09-15
FRIOR PILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE FASESEQ for Windows Version 4.0
SEQ ID NO 33632
TAVED: NAX
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; Patent No. 6821724
; GENERAL INPORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 310.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT APPLICATION NUMBER: 60/100,678
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFFWARE: FRASÉEQ for Windows Version 4.0
; SEQ ID NO 45409
  TITLE OF INVENTION: Methods of Genetic Analysis
                       FILE REPERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33631
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 TCCAAAGTGCATGAT 24
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US-09-396-196G-33631
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
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US-09-396-196G-45409
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                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.8%; Score 13.4; DB 4; Length 25; 73.9%; Pred. No. 5.6e+03; ive 0; Mismatches 6; Indels
           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/768,437

FILING DATE: 19910925

CLASSIFICATION: 435

ATTONREY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16773

REGISTRATION NUMBER: 16773

REGISTRATION NUMBER: 16773

TELEFRONE (202) 861-3000

TELEFRA: (202) 862-0944

TELEFRA: (202) 862-0544

TELEFRA: (202) 862-0544

TELEFRA: (202) 862-0545

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TELEFRA: (202) 862-0544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-396-196G-30572/c
; Sequence 30572, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: APPLICANT: AFFWETTIX, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/396,196G CURRENT FILING DATE: 1999-09-15 PRIOR APPLICATION NUMBER: 60/100,678 PRIOR FILING DATE: 1998-09-17 NUMBER OF SEQ ID NOS: 127806 SOFTWARE: FRSEESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-396-196G-33631/c
; Sequence 33631, Application US/09396196G
; Patent No. 6821724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TTCATGTTTCCAAAGTGCATGAT 24
PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TTCATGTTTCCAAAG 16
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APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 73.9°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-30572
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LENGTH: 25
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                                                                                                                                                                        55.8%; Score 13.4; DB 4; Length 25; 93.3%; Pred. No. 5.6e+03; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.8%; Score 13.4; DB 4; Length 25; 93.3%; Pred. No. 5.6e+03; ive 0; Mismatches 1; Indels
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US-09-396-196G-70209/C
i Sequence 70209, Application US/09396196G
i Batent No. 6821724
i GENERAL INFORMATION:
APPLICANT: Michael Mittmann
i APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
CURRENT APPLICANT: 3101.1
CURRENT APPLICANT: 1990-09-15
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FBateSEQ for Windows Version 4.0
SEQ ID NO 70209
LENGTH: 25
LE
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US-09-396-196G-45410
Sequence 45410, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
FRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
ERNOTH: 25
                                                                                                                                                                                                                                                                                                                          1 CTTCATGTTTCCAAA 15
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                                                                                                                                                                            Query Match
Best Local Similarity 93.3
Matches 14; Conservative
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                                 TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-45409
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Best Local Similarity
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; ORGANISM: mus mus
US-09-396-196G-45410
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LENGTH: 25
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RESULT 40

US-09-422-978-3015/c
; Sequence 3015. Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; TITLE OF INVENTION Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER PILING DATE: 1998-04-21
; RARLIER PILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3015
; LEMCTH. 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
CCATION: 24
COTHER INFORMATION: 99-21687-313 : polymorphic base G or A
US-09-422-978-3018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November 18, 2005, 11:21:59 Job time : 47.6312 secs
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1 CTTCATGTTTCCAAAGTGCATGA 23
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                                     24 CTTGATGGTTATAAAGAACATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapiens
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27538, A 27539, A 27549, A 170463, 180820, 394513, 53744, A 219368,

Sequence Sequence Sequence

Sequence

Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

606061, 180, App 37, Appl 19916, 413418, 132433, 50302, A 51276, A 185437,

Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Perfect score:

Sequence:

nucleic

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Run on:

Scoring table:

Searched:

. Database :

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Sequence 4, Application US/08469172;
Publication No. US20030054343A1
GENERAL INFORMATION:
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: MATKINS, HUGH
APPLICANT: MATKINS, HUGH
APPLICANT: MATKINS, HUGH
APPLICANT: MATKINS, HUGH
APPLICANT: NOSENZWEIG, ANTHONY
ITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
          US-11-036-317-478233

US-11-060-756-27539

US-11-060-756-27539

US-11-060-756-180820

US-11-060-756-180820

US-11-060-756-180820

US-11-060-756-180820

US-10-109-900-193188

US-10-109-900-193188

US-10-109-900-193188

US-10-900-19317

US-10-91-19317

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,172
FILLING DATE:
CLASSIFFCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 STATE STREET, Suite
Massachusetts: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
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US-08-469-172-4
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114.8
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114.8
Sequence 4, Appli
Sequence 125280,
Sequence 25437,
Sequence 403636,
                                                                                                                            (without alignments)
615.265 Million cell updates/sec
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                                                                                                         November 18, 2005, 06:36:48 ; Search time 322.586 Seconds
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             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-956-157-125280
US-11-036-317-256437
US-10-719-956-403636
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        9794790 seqs, 4134909567 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-469-172-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         - nucleic search, using sw model
                                                                                                                                                                                                      1 CTTCATGTTTCCAAAGTGCATGAT
                                                                                                                                                                                                                                      IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Match Length
                          Copyright
                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0 Maximum DB seq length: 50
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100.0
75.8
70.0
65.8
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Score

Result

18.2 16.8 15.8

48069, A 262242, 827966, 838178,

Sequence Sequence S

Sequence

Sequence

472576, 551468, 771700, 247281, 115420,

Sequence

Sequence Sequence

Sequence Sequence Sequence Sequence

989895,

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100.0%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10788779

Publication No. US20040152121A1

GENERAL INFORMATION:

SEIDMAN, CHRISTINE

SEIDMAN, JOHN
WATKINS, HUGH

ROSENZWEIG, ANTHONY

TITLE OF INVENTION: A METHOD FOR DETECTING

DISEASE-ASSOCIATED MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: MASAGIMENCES

COUNTRY: W.S.A.

ZIP: 02109

COMPUTER: ENDADALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

APPLICATION NUMBER: US/10/788,779

FILING DATE: 27-Feb-2004

CLASSIFICATION NUMBER: US/07/989,160

FILING DATE: CAMPRONDATA

APPLICATION NUMBER: US/07/989,160

FILING DATE: 11-DEC-1933

ATTORNAY, AGENT INFORMATION:

NAME: HANLEY, ELIZABETH A.

REGISTRATION NUMBER: 33,505

REGISTRATION NUMBER: 33,505

REGISTRATION NUMBER: 33,505

REGISTRATION NUMBER: GML-111

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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TELECOMMUNICATION INFORMATION:
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTARION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GML-111
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-7401
TELEFAX: (617) 227-7591
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTTCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 crrcargrirccaaagrgcargar 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-10-788-779-4
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US-08-469-172-4
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APPLICANT: Wyeth
APPLICANT: Worth
APPLICANT: Woults, William
APPLICANT: MOULE, ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARES: Patentin version 3.2
SEQ ID NO 125280
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ### Sequence 256437

| Sequence 256437, Application US/11036317 |
| Sequence 256437, Application US/11036317 |
| Publication No. US20050214823A1 |
| GENERAL INFORMATION: |
| APPLICANT: Williams, Alan |
| APPLICANT: Blume, John |
| TITLE OF INVERTION: Method of Analysis of Alternative Splicing in Mouse |
| FILE REFERENCE: 3654.1 |
| CURRENT APPLICATION NUMBER: US/11/036,317 |
| CURRENT PILING DATE: 2005-01-13 |
| PRIOR PILING DATE: 2004-01-13 |
| NUMBER OF SEQ ID NOS: 991174 |
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 |
| LENGTH: 25
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                                                                                                                                           Score 24; DB 20; Length 24;
Pred. No. 0.32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.8%; Score 18.2; DB 22; ilarity 87.0%; Pred. No. 1.7e+02; Conservative 0; Mismatches 3;
                                                                                                                                           Query Match 100.0%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.3 Matches 24; Conservative 0; Mismatches
TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-788-779-4
                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 125280, Application US/10956157; Publication No. US20050118625A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                             1 CTTCATGTTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                      1 CTTCATGTTCCAAAGTGCATGAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TTCATGTTTCCAATGTACCTGAT 25
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US-10-956-157-125280
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Best Local Similarity
Matches 20; Conserv
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us-10-788-779-4.rnpb

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TYPE: DNA
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Sequence 365552, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01.13
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Publication No. US20050214823A1

GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVERTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174
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US-10-719-956-403636

Sequence 403636, Application US/10719956

Publication No. US20040146910A1

GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.
CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT PLING DATE: 2003-11-20

PRIOR PILING DATE: 2002 11 20

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-403636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 89.5
Matches 17; Conservative
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US-11-036-317-363552
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US-11-036-317-363552
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US-11.060-756-27538
US-11.060-756-27538
Sequence 27538, Application US/11060756
Sequence 27538, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
MOUNTED FULLOANT: Wheth
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION UNDERS. US/11/060,756
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT PILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SSOTWARE: PatentIn version 3.2
LENGTH: 25
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Publication No. US20050221354A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFUL NOS: 27539
LENGTH: 25
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                  Indels
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89.5%; Pred. No. 2.3e+03;
iive 0; Mismatches 2;
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Pred. No. 2.3e+03;
0; Mismatches 2;
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                                                                                                                                                                                                                                                     3 TGTGTCCAAGTGCATGTT 21
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                                                                                                                                          65.8%;
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Matches 17; Conservative
                                                                                                                                                                                17; Conservative
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Matches 17; Conservative
                                                          TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-478233
                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: probe US-11-060-756-27538
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US-11-060-756-27539
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                  SEQ ID NO 478233
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 394513, Application US/10719900
; Sequence 394513, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; AFPLICANT: Yue Mei Zhou
; TILE OF INVENTION: Methods of Genetic Analysis of Mouse;
; TILE OF INVENTION: Methods of Genetic Analysis of Mouse;
; TILE OF INVENTION: Methods of Genetic Analysis of Mouse;
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT APPLICATION NUMBER: 60427,808
; PRIOR APPLICATION NUMBER: 60427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 394513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.0%; Score 15.6; DB 22; Length 25; Best Local Similarity 81.8%; Pred. No. 2.8e+03; Matches 18; Conservative 0; Mismatches 4; Indels (
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; Sequence 53744, Application US/10809189
; Publication No. US20050048531A1
; GENERAL IMPORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 127806
; SOFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53744
; LENGTH: 25
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                                                                                                                                                        Query Match 65.8%; Score 15.8; DB 26; Best Local Similarity 89.5%; Pred. No. 2.3e+03; Matches 17; Conservative 0; Mismatches 2;
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CORGANISM: Mus musculus
US-10-719-900-394513
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US-10-809-189-53744
                      ; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-180820
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-10-719-900-394513
SEQ ID NO 180820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
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APPLICANT: Wyeth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT PAPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
LENGTHARE: 25
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Publication No. US200502213541
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Target Genea
FILE REFRENCE: AMO1083 (031896-042000)
CURRENT APPLICATION UNMER: US/11/060,756
CURRENT PELICATION NUMBER: US/11/060,756
CURRENT PELICATION NUMBER: US/11/060,756
CURRENT PELICATION NUMBER: US/11/060,756
SOFTWARE: PALENTIN OF SEQ ID NOS: 303284
SOFTWARE: PALENTIN Version 3.2
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APPLICANT: Woth
APPLICANT: Worth
APPLICANT: Wounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT PAPILIAND NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 27549
LENGTH: 25
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Pred. No. 2.3e+03;
0; Mismatches 2; Indels (
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                                                                        ; Sequence 27549, Application US/11060756; Publication No. US20050221354A1; GENERAL INFORMATION:
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89.5%;
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Best Local Similarity 89.5'
Matches 17; Conservative
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; ORGANISM: probe
US-11-060-756-170463
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US-11-060-756-180820
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                                               US-11-060-756-27549
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; Bublication No. US20050214823A1
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REPRENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 606061
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Publication No. US20050164246A1
GENERAL INFORMATION:
APPLICANT: Fan, Jian-Bing
APPLICANT: Bibikova, Marina
TITLE OF INVENTION: Methods and Compositions For Diagnosing
TITLE OF INVENTION: Lung Cancer with Specific DNA Methylation Patterns
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                                                                                                                                           Sequence 219368 Application US/10719956
; Sequence 219368 Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; TITLE REFERENCE: 3527.1
; CURRENT FILING DATE: 2003-11-20
; RIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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  TTCATGTTTCCAAAGTGCATGA 23
                                             Trcaactrcccaaagrccarca 4
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CRGANISM: Rattus norvegicus
US-10-719-956-219368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 16
US-11-036-317-606061/c
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US-10-719-956-219368/c
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Sequence 37, Application US/10882761
Publication No. US20040265890A1
GENERAL INFORMATION:
APPLICATION NO. US20040265890A1
GENERAL INFORMATION:
TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
TITLE OF INVENTION: PREDOMINATELY IN SMALL INTESTINE, HLRRSI1
TITLE OF INVENTION: BREDOMINATELY IN SMALL INTESTINE, HLRRSI1
CURRENT APPLICATION NUMBER: US/10/882,761
CURRENT APPLICATION NUMBER: US 10/029,347
PRIOR APPLICATION NUMBER: US 10/029,347
PRIOR APLICATION UNBER: 3001-12-20
NUMBER OF SEQ ID NOS: 45
SSOTUMARE: Patentin version 3.2
SSOTUM NOS: 15
LENGTH: 25
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GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION:

FILE REPERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthesized oligonucleotide.
US-10-882-761-37
                                                                                                                                                                                                                                                                                                                                                             64.2%; Score 15.4; DB 2 94.1%; Pred. No. 4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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FILE REFERENCE: 67234-100
CURRENT APPLICATION NUMBER: US/10/973,783
CURRENT FILING DATE: 2004-10-25
FRIOR FILING DATE: 2004-06-14
FRIOR FILING DATE: 2004-06-14
FRIOR FILING DATE: 2003-05-14
FRIOR FILING DATE: 2003-05-15
NUMBER: OF SEQ ID NOS: 1513
SEQ ID NO 180
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; Publication No. US20050026164A1
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Best Local Similarity 85.09
Matches 17; Conservative
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Matches 16; Conservative
                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-10-973-783-180
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US-10-719-900-199176/c
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US-10-882-761-37/c
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Publication No. US20050136395A1

Publication No. US20050136395A1

Publication No. US20050136395A1

APPLICANT: Michael Mittmann

TITE OF INVEMINION: Methods of Genetic Analysis of SARS Virus

TITE OF INVEMINION: Methods of Genetic Analysis of SARS Virus

CURRENT APPLICATION NUMBER: US/10/843,527

CURRENT APPLICATION NUMBER: 60/469,545

PRIOR PILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 238196

SOFTWARR: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 51277
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Sequence 51276, Application US/10843527

Publication No. US20050136395A1

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: Eric Schell

TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.1

CURRENT APPLICATION NUMBER: US/10/843,527

CURRENT FILING DATE: 2004-05-10

PRIOR APPLICATION NUMBER: 60/469,545

PRIOR PILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 238196

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                    GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: Eric Schell
TILE REFERENCE: 360.1
CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT PILING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR PILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 238196
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 50302
LENGTH: 25
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85.0%; Pred; No. 4.4e+03;
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85.0%; Pred. No. 4.4e+03;
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     Publication No. US20050136395A1
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Best Local Similarity 85.0%
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: SARS Virus
US-10-843-527-51276
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APPLICANT: Wounts, William
TITLE OF INVENTION: HUWAN OSTEOARTHRITIS AND HUWAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 132433
LIENGH: 25
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                                                                           Length 25;
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                                                                                                                         Indels
                                                                    Query Match
63.3%; Score 15.2; DB 22;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                               US-10-719-900-413418/c
; Sequence 413418, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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Sequence 132433, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:
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US-10-843-527-50302/c
; Sequence 50302, Application US/10843527
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Best Local Similarity 85.0
Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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ORGANISM: Probe Sequence
US-10-956-157-132433
; ORGANISM: Mus musculus
US-10-719-900-199176
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; ORGANISM: Mus musculus
US-10-719-900-413418
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JS-10-843-527-186411
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; Sequence 185436, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
   APPLICANT: Michael Mitmann
   APPLICANT: Bric Schell
   TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
   FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT APPLICATION NUMBER: 60/469,545
PRIOR APPLICANTON NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
; WUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 185436
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Sequence 185437, Application US/10843527

Publication No. US20050136395A1

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: Eric Schell

TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.11

CURRENT APPLICATION NUMBER: US/10/843,527

CURRENT FILING DATE: 2003-65-10

PRIOR PILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 238196

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 185437
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Pred. No. 4.4e+03;
0; Mismatches 3; Indels (
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4.4e+03;
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                                                                                                   Query Match 63.3%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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Matches 17; Conservative
                     ; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-51277
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US-10-843-527-185437
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US-10-843-527-185437
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LENGTH: 25
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; Publication No. US20050214823A1; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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| Sequence 147524, Application US/11036317
| Publication No. US20050214823A1
| Publication No. US20050214823A1
| GENERAL INFORMATION:
| APPLICANT: Williams, John
| APPLICANT: Blume, John
| TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
| FILE REFERENCE: 3654.1
| CURRENT PELING DATE: 2005-01.13
| CURRENT PILING DATE: 2005-01.13
| PRIOR APPLICATION NUMBER: US 60/536,639
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Pred. No. 4.4e+03;
0; Mismatches 3;
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85.0%;
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Best Local Similarity 85.0°
Matches 17; Conservative
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Best Local Similarity 85.0°
Matches 17; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-81554
                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: SARS Virus
US-10-843-527-186411
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us-10-788-779-4.rnpb

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3 TCATGTTTCCAAAGTGCATG 22
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; Sequence 472576, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Williams, John
; TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REPERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; RIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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i Sequence 551468, Application US/11036317

j Publication No. US20050214823A1

j GENERAL INFORMATION:
    APPLICANT:
    MIlliams, Alan

j TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
    FILE REFREENCE: 3554.1

j CURRENT PILING DATE: 2005-01-13
    PRIOR PILING DATE: 2004-01-13
    NUMBER OF SEQ ID NOS: 991174
    SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
    LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.3%; Score 15.2; DB 26; Length 25; 85.0%; Pred. No. 4.4e+03; 1ve 0; Mismatches 3; Indels
                                                                                                                                                                                           Length 25;
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 147524
LENGTH: 25
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85.0%; Pred. No. 4.4e+03;
tive 0; Mismatches 3;
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Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                     TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-147524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-472576
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ORGANISM: Mus musculus
US-11-036-317-551468
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hes 17; Conserv
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Matches
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Sequence 771700, Application US/11036317
; Sequence 771700, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICAMT: Williams, Alan
; APPLICAMT: Blume, John
; TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3664.1
; CURRENT PLICATION NUMBER: US/11/036,317
; CURRENT PLICATION NUMBER: US 60/536,639
; PRIOR PILING DATE: 2004-01-13
; NUMBER: OF SEQ ID NOS: 991174
; SOFTWARE: Wicroarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 771700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.3%; Score 15.2; DB 26;
85.0%; Pred. No. 4.4e+03;
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Best Local Similarity 78.3%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 5;
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US-10-681-773-115420/c
is Sequence 115420, Application US/10681773
is Publication No. US20040146890A1
is GENERAL INFORMATION:
is APPLICANT: Mei, Rui
is APPLICANT: Shen, Mei, Rui
is APPLICANT: Shen, Mei, Rui
is APPLICANT: Shen, Mei, Rui
is APPLICANT: Kennedy, Giulia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 247281, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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20 TCAGGTTTCCAAAGCGCTTG 1
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Best Local Similarity 85.09
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus
US-11-036-317-771700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRANISM: Mus musculus US-10-719-900-247281
                                                                                              RESULT 32
US-11-036-317-771700/c
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US-10-316-244-136/c
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                                                                      TYPE: DNA
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GENERAL INFORMATION.
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION WEthod of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIOR PILING DATE: 2004-01-13
PRIOR FILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-681-773-120711/c

Sequence 12071, Application US/10681773

Publication No. US20040146890A1

GENERAL INFORMATION:
APPLICANT: Mateuzaki, Hajime
APPLICANT: Mei, Rui
APPLICANT: Mei, Rui
APPLICANT: Remedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
FILE REPRENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
CURRENT FILING DATE: 2003-10-07
PRIOR FILING DATE: 2002-05-14
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 124031
SEQ ID NO 120711

LENGTH: 25
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TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
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                    FILE REFERENCE: 3522.2
CURRENT PELLING UNIMBER: US/10/681,773
CURRENT PELLING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: 60/470,475
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Pred, No. 5.5e+03;
Signdels 5; Indels
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                                                                                                                                                                                                                                                                                                                                                 Query Match 62.5
Best Local Similarity 78.3
Matches 18; Conservative
                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapien
US-10-681-773-115420
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; ORGANISM: Homo sapien
US-10-681-773-120711
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US-11-036-317-989895
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Sequence 31, Application US/10316244
Sequence 31, Application US/10316244
Sequence 31, Populication US/10316244
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MOULATION OF ORNITHINE DECARBOXYLASE 1 EXPRESSION
FILE REFERENCE: HTS-0096
CURRENT APPLICATION NUMBER: US/10/316,244
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 219
LENGTH: 20
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Publication No. US20040110148A1

GREERAL INFORMATION:
GREERAL REPRESSION
FILLE REPRESCE:
FILLS REPRESCE:
FILLS REPRESCE:
GURRENT FILING DATE:
CURRENT FILING DATE:
UNDHER OF SEQ ID NOS: 219
SEQ ID NO 136
LENGTH: 20
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                                                                                                                                                            Query Match 62.5%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 989895
LENGTH: 25
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88.9%; Pred. No. 6.5e+03;
tive 0; Mismatches 2;
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Pred. No. 6.5e+03;
0; Mismatches 2;
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88.9%;
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Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                          ) ORGANISM: Mus musculus
US-11-036-317-989895
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ORGANISM: H. sapiens
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; Sequence 26242, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; FRIOR APPLICATION NUMBER: 06/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER: OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; ERWITH: 25
; TENGENT: 25
Sequence 48069, Application US/10719900
; Bublication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION:
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: WEALD SERVICE: 3528.1
; CURRENT PAPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48069
; LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-48069
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; ORGANISM: Mus musculus
US-10-719-900-262242
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Search completed: November 18, 2005, 15:41:05 Job time : 323.586 secs

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Sequence:

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PAT 26-JUL-1995
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1 (bases 1 to 25)
Seidman, C., Seldman, J., Watkins, H. and Rosenzweig, A.
Method for detecting hypertrophic cardiomyophathy associated
                  AX573495
BD081415
BR107707
AR153673
CC0862312
BD197942
AX801708
AX8067397
AX0367397
AX757197
AX717766
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Location/Qualifiers
1. .25
/organism="unknown"
/mol_type="unassigned DNA"
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5429923.
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AX573495

AR107101

AR107101

CQ862312

BD197342

CX36597

AX801708

AX030985

AX157197

AX15797

AX15797
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AX080051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP 1999127899-A/7. unidentified
Query Match
Best Local Similarity
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unclassified.
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                                   source
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
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KEYWORDS
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LOCUS
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BD258702 Regulatio
AX406739 Sequence
BD180726 Array of
AX098688 Sequence
AX098690 Sequence
AX098692 Sequence
AX204762 Sequence
AX204764 Sequence
AX204764 Sequence
AX204764 Sequence
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E25007 Oligonucleo
A19073 Oligonucleo
AR059408 Sequence
AR178489 Sequence
CC0856719 Sequence
                                                          November 18, 2005, 11:12:34; Search time 693.631 Seconds (without alignments) 1746.433 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                               4708233 segs, 24227607955 residues
                                                                                                                  1 CTGGGCTTCACTTCAGAGAGAAAA 25
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Maximum Match 1008
Listing first 45 summaries
                                           núcleic search, using sw model
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BD258702
AX406739
BD180726
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AR204762
ARZ04764
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CQ826719
CQ826720
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seq length: 50
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Best Local Similarity 75...
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                Unknown.
Unclassified.
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Matches 18; Conserv
  Unknown.
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CQ826719
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Little,M., Breitling,F.B., Seehaus,T., Duebel,S. and Klewinghaus,I.
Preparation and use of a human antibody gene bank (human antibody
libraries)
Patent: EP 0440147-A 19 07-AUG-1991,
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         Oligonucleotide probe species-specific to bacterium of Bacteroides Patent: JP 1999127899-A 7 18-MAY-1999; YAKULT BIOSCIENCE KENKYU ZAIDAN
                                                                                                                                CI2Q1/68,CI2NIS/09//(CI2Q1/68,CI2R1:01),(CI2NIS/09,CI2R1:01),
CI2NIS/00,
(CI2NIS/00,CI2R1:01)
Strandedness: Single;
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/organism='Unidentified'
Location/Qualifiers
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Sequence 28 from patent US 5840479.
AR059408.1 GI:5985858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="unassigned RNA"
/db_xref="taxon:32644"

    .21
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Location/Qualifiers
                                                   Unidentified
JP 1999127899-A/7
18-MAY-1999
29-OCT-1997 JP 1997297085
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Yukiko, T. and Kikuji, I.
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oligonucleotide.
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A19073.1 GI:513993
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AR059408
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Little, M., Breitling, F. Berthold., Seehaus, T., Dubel, S. and Klewinghaus, I.
Klewinghaus, I.
Preparation and use of gene banks of synthetic human antibodies ('synthetic human-antibody libraries')
Patent: US 5840479-A 28 24-NOV-1998;
Location/Qualifiers
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Patent: EP 1431387-A 22 23-JUN-2004;
Roche Diagnostics GmbH (DE); F. HOFFWANN-LA ROCHE AG (CH)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.
1 (bases 1 to 30)
Little,M., Breitling,F.Berthold., Seehaus,T., Dubel,S. and
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Patent: US 6319690-A 19 20-NOV-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.6%; Score 14.4; DB 6; Length 30; ilarity 75.0%; Pred. No. 5.3e+04; Conservative 0; Mismatches 6; Indels
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75.0%; Pred. No. 5.3e+04;
iive 0; Mismatches 6;
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                                                                                                                                                                              /organism="unknown"
/mol_type="unassigned DNA"
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Sequence 22 from Patent EP1431387.
CQ826719
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/organism="unknown"
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PAT 17-JUL-2003
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PN JP 2002441795-A/6495
PN JP 2002541795-A/6495
PN 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PT 12-APR-1999 US 60/129390
PT 12-APR-1999 US C12N15/09, A61K38/00, A61P43/00, A61P43/00, C12N5/10, PC C12N15/02, PC C12N15/02, C12P21/02, A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC C12P21/02, A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC C12P21/02, A61K31/711, C12N5/10, C12R1:91), (C12P21/02, PC C12P21/02, PC PC C1
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AGIX37/02,
(C12N5/00,C12R1:91)
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candida albicans
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Bregulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 6495 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
                                                                                                                                                         ;
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Patent: WO 02270211A 3 04-APR-2002;
Cytonet GmbH & Co. KG (DE)
Location/Qualifiers
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Location/Qualifiers
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    .29
    /organism="unidentified"

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Sequence 3 from Patent W00227021.
AX406739
AX406739.1 GI:21439664
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/db_xref="taxon:32644"
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                                                 20 GACTTACCTTCAGAGGAGA 38
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JP 2002541795-A/6495.
     4 GGCTTCACTTCAGAGGAGA
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Matches 17; Conserv
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PC (C12P2
PC A61K37
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Jones, P.G. and Holt, D.C.
Jones, P.G. and Holt, D.C.
Jones, P.G. and Holt, D.C.
Jones and Holt, D.C.
Jones BINDING PROTEINS AND TRANSGENIC PLANTS CONTAINING THEM
PACHALL WO 9932650-A 32 01-JUL-1999;
JONES PAUL GLYN (GB); ZENECA LTD (GB)
Location/Qualifiers
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Patent: EP 1431387-A 23 23-JUN-2004;
Roche Diagnostics GmbH (DE); F. HOFFMANN-LA ROCHE AG (CH)
Location/Qualifiers
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                                                                                                                       Query Match 57.6%; Score 14.4; DB 6; Length 37; Best Local Similarity 75.0%; Pred. No. 5.3e+04; Matches 18; Conservative 0; Mismatches 6; Indels
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84.2%; Pred. No. 6.7e+04;
iive 0; Mismatches 3; Indels
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

    .37
    'organism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

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| Organism="unidentified"
|mol_type="unassigned DNA"
|db_xref="taxon:32644"
|clone="VH3'"
                                                                                                                                                                                                                                                                                                                                                                                              37 bp
Sequence 23 from Patent EP1431387.
CQ826720
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Sequence 32 from Patent W09932630.
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A94788.1 GI:6779042
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Best Local Similarity 84.2
Matches 16; Conservative
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Unclassified.
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                                                                                   Similarity
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Matches 17;
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AR098689
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JUNICHI MINENO, MASATOMO ROKUSHIMA, NARIKAZU SOTOZONO, KIYOZO PI
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PC C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N37/00,C12N15/00 CC
besigned Oligomucleotide probe for detecting in vitro CC
transcribed RNA of
CC Lamda DNA fragment 1
FH Key Location/Qualifiers
FT source 1.40
/organism='Artificial Sequence'.
                                                                                   Gaps
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synthetic construct
synthetic construct
ther sequences; artificial sequences.

(base 1 to 40)
Mineno,J., Rokushima,M., Sotozono,N., Asada,K. and Kato,I.
Parray of mucleic acid
Parent: JP 2002330767-A 18 19-NOV-2002;
TAKARA BIO INC
S Artificial Sequence
PN JP 2002330767-A/18
PD 19-NOV-2002
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Location/Qualifiers
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Kool, E.T.

Highly sensitive multimeric nucleic acid probes
Patent: US 6077668-A 46 20-UUN-2000;
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
/db_xref="taxon:5476"
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Sequence 46 from patent US 6077668.
AR098688
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Array of nucleic acid.
BD180726.1 GI:30791644
JP 2002330767-A/18.
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                                          Query Match
Best Local Similarity
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AR098688/c
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FEATURES
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Highly sensitive multimeric nucleic acid probes
Patent: US 6077668-A 48 20-JUN-2000;
Location/Qualifiers
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                                                                           Score 14; DB 6; I
Pred. No. 8.5e+04;
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Sequence 47 from patent US 6077668.
AR098689
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Sequence 48 from patent US 6077668.
AR098690
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/organism="unknown"
/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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PAT 20-JUN-2002
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                                                         Query Match 56.0%; Score 14; DB 6; Length 49; Best Local Similarity 77.3%; Pred. No. 8.5e+04; Matches 17; Conservative 0; Mismatches 5; Indels
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Circular DNA vectors for synthesis of RNA and DNA
Patent: US 6368802-A 48 09-APR-2002;
Location/Qualifiers
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Kool, B.T.
Circular DNA vectors for synthesis of RNA and DNA Patent: US 6368802-A 50 09-APR-2002;
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Sequence 48 from patent US 6368802.
AR204764
AR204764.1 GI:21502174
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/organism="unknown"
/mol_type="unassigned DNA"
  /organism="unknown"
/mol_type="unassigned DNA"
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AR204766
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CQ008790
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S 1 (bases 1 to 49)

S Kooll.E.T.

Circular DNA vectors for synthesis of RNA and DNA

AD Patent: US 6368802-A 47 09-APR-2002;

Location/Qualifiers
                                                                                      M Unknown.

Wolassified.

B 1 (bases 1 to 49)

KS Kool, E.T.

Highly sensitive multimeric nucleic acid probes

AL Patent: US 6077668-A 50 20-JUN-2000;

Location/Qualifiers
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Circular DNA vectors for synthesis of RNA and DNA
Patent: US 6368802-A 46 09-APR-2002;
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           AR098692 49 bp 1
Sequence 50 from patent US 6077668.
AR098692 AR098692.1 GI:12808458
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Seguence 46 from patent US 6368802.
AR204762
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Sequence 47 from patent US 6368802.
AR204763.1 GI:21502172
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JP 2001518304-A/58.
Homo sapiens (human)
Homo sapiens
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                    CTGGGCTTCACTTCAGA 17
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                                     20 CTTGGCTTCAGTTCAGA 4
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   PAT 16-JAN-2004
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CC biotiniylated phosphoaramidite residue
CC biotiniylated prosphoaramidite residue
FH Key Location/Qualifiers
FT misc feature (2).
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Secreted proteins and polynucleotides encoding them
Batent: JP 2002505074-A 10 19-FEB-2002;
SATISTIVITE INC
SATISTICIAL Sequence
BN JP 2002505074-A/10
PD 19-FEB-2002
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                                                                                                                                                           Shimkets, R.A. and Leach, M.

Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

Patent: WO 0147944A 7430 05-JUL-2001;

Curagen Corporation (US)

Location/Qualifiers
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/note="Nucleotide deleted between bases 25 and 26
Accession number cg43994815"
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Secreted proteins and polynucleotides encoding them. BD138865
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JP 2002505074-A/10.
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often sequences, artificial sequences.
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   linear
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llarity 77.3%; Pred. No. 8.5e+04;
Conservative 0; Mismatches 5; Indels
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21-NOV-1997 US 08/975936, 26-OCT-1998 US
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   DNA
CQ008790 50 bp DN Sequence 7430 from Patent WO0147944. CQ008790.1 GI:41015507
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/organism="Homo sapiens"
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Best Local Similarity
Matches 17; Conserva
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 48)

E 1 (bases 1 to 48)

E 2 (alanowski, M.A., Caparon, M.H., Casperson, G.F., Gregory, S.A., Klein, B.K. and Mckearn, J.P.

Klein, B.K. and Mckearn, J.P.

Fused protein containing angiostatin component and utilization thereof in antitumor therapy

D Patent: JP 2001518304-A 58 16-OCT-2001;

EN JP 2001518304-A/58

PN JP 2001518304-A/58

PR 30-SEP-1998 JP 2000513958

PR 30-SEP-1997 US 60/060609
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Fused protein containing angiostatin component and utilization
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C12N15/09, A61K38/00, A61K48/00, A61P9/10, A61P35/00, C07K14/52,
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0-OCT-1997 US 60/060609
MARK A BOLANOWSKI, MAIRE H CAPARON, GERALD F CASPERSON, SUSAN
GREGORY,
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                                                                                                                                                                                                                                                                        Chen, J., Taylor, D.D., Weiner, M.P. and Ye, F. Wultiplexed gene analysis on a mobile solid support Patent: EP 1249503-A 78 16-OCT-2002; SMITHKLINE BEECHAM CORPORATION (US)
   linear

    .38
    forganism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"

   DNA
                                                                                                                                                synthetic construct
synthetic construct
other sequences; artificial sequences.
AX573495 38 bp
Sequence 78 from Patent EP1249503.
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PAT 17-JUL-2003
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PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
                                                                                             PAT 10-SEP-2004
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JAMES A MCSWIGGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthesized Hammerhead Ribozyme
The letter 'n' stands for any base or bases forming a loop or
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Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
Method and reagnt for treating diseases or conditions concerning
patent: JP 2002509721-A 968 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHO PI JAMES A MCSWIGGEN PC CI2NIS/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06,
                                                                                                                                                                                                                                                            Burczynski, M., Twine, N., Dorner, A.J. and Trepicchio, W.L. METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /i Patent: WO 2004072265-A 945 26-AUG-2004; Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. Dorner, Andrew J. (US); Trepicchio, William L. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that may contain multiple nucleic acid analogues or deoxynucleotides.
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    .29
/organism='Artificial Sequence'

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                                                                                             CQ862312 25 bp DNA Sequence 945 from Patent WO2004072265.
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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27-MAR-1998 US 60/079678
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          5 GGACTAACTGCAGAGGAGAA 24
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JP 2002509721-A/968
02-APR-2002
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CQ862312.1 GI:51983301
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                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                              Homo sapiens
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BD197942
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KEYWORDS
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1 (bases 1 to 50)

Penger, C.K., Granstrom, D.E., Gajadhar, A.A. and Dubey, J.P.

Sarcocystis neuronadiagnostic primer and its use in methods of equine protozoal myeloencephalitis diagnosis

Patent: US 6110665-A 60 29-AUG-2000;
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Unclassified.
1 (bases 1 to 25)
Kraus, G., Wong-Staal, F., Talbott, R.L. and Poeschla, E.M.
Polypeptides encoded by novel HIV-2 proviruses
Patent: US 6235881-A 19 22-MAY-2001,
Location/Qualifiers
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/organism='Homo sapiens (human)'.
                                                                                                                                             Length 48;
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Pred. No. 1.1e+05;
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Pred. No. 1.1e+05;
0; Mismatches 4;
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Best Local Similarity 78.9%; Pred. No. 1.1e
Matches 15; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                            Sequence 60 from patent US 6110665.

    .25
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    /mol_type="unassigned DNA"

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="unknown"
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Best Local Similarity 78.9
Matches 15; Conservative
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Patent: WO 9804716-A 5 05-FEB-1998;
VANCOV TOWY (AU) ; SCHNEIDER RENE (AU) ; CRC WASTE MAN & POLL CONTR LTD (AU) ; JURY KAREN (BB)
LOCATION/Qualifiers
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Score 13.6; DB 6; Length 33; Pred. No. 1.4e+05; 0; Mismatches 4; Indels
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54.4%; Score 13.6; DB 6;
Best Local Similarity 80.0%; Pred. No. 1.46+05;
Matches 16; Conservative 0; Mismatches 4;
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    .36
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    /db_xref="taxon:32644"

                                                                                                                                                                                                                                                                                       Unclassified.
1 (bases 1 to 36)
Schneider,R., Vancov,T. and Jury,K.
                                                                                                                                                                                                                                                                                                                                                          Patent: US 6329160-A 5 11-DEC-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vancov, T., Schneider, R. and Jury, K.
                                                                                                                                                                           Sequence 5 from patent US 6329160.
AR366334
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Sequence 5 from Patent WO9804716.
AXO30985
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/mol_type="mRNA"
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                                                                    5 GCTTCACTTCAGAGGAGAAA 24
                                                                                                GCTTTCCTTAAGAGGATAAA 26
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   Query Match
Best Local Similarity 80.0%;
Matches 16; Conservative 0
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AR366334/c
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AX030985/c
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AX767197
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                                                                                                               Query Match 54.4%; Score 13.6; DB 6; Length 29; Best Local Similarity 76.2%; Pred. No. 1.4e+05; Matches 16; Conservative 0; Mismatches 5; Indels
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/db xref="texon:32630"
/note="Synthetic DNA"
                  1. .29
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/mol_type="genomic RNA"
/db_xref="taxon:32630"
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/db xref="texon:32630"
/note="Oligonucleotide"
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CQ867997
                                                                                                                                                                                                                                                                                            DNA
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Sequence 7 from Patent WO03057730.
AX801708
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                                                                                                                                                                                                           2 GGCTTCACTGATGAGNCGAAA 22
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Ulfendahl, P.J. and Wong, K.C.
                     Homo sapiens (human)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

Patent: WO 014051-A 1200 07-JUN-2001;

Curagen Corporation (US)

Location/Qualifiers
                                                                                                                                                                                                              /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotides for Vh - OL 413"
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1 Similarity 80.0%; Pred. No. 1.4e+05;
16; Conservative 0; Mismatches 4; Indels
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                                                                                                                       Hellendoorn, K., Baker, M. and Carr, F.J. Modified anti-thf alpha antibody Parent: WO 03042247-A 126 22-MAY-2003; Merck Patent GmbH (DE)
                                                                                             other sequences; artificial sequences
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Sequence 126 from Patent WO03042247.
AX767197
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 7 from Patent WO03004045.
AX671483
AX671483.1 GI:29329792
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                                  AX767197.1 GI:32260748
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synthetic construct
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Robataille, J.M. and Hayden, M.R.
Processes for identifying therapeutic agents useful in treating
diseases involving fidd gene
batent: WO 03005304-A 11 16-JANN-2003;
Xenon Genetics, Inc. (CA); The University of British Columbia (CA)
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                                                                                              Macdonald, M. L., Goldberg, Y. P. and Hayden, M. R.
Methods for identifying therapeutic agents for treating diseases involving wnt polypeptides and wnt receptors
Patent: WO 03004045-A 7 16-JAN-2003;
Xenon Genetics, Inc. (CA), The University of British Columbia (CA)
Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX026972
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Novel polypeptides and nucleic acids encoded thereby
Curagen Corporation (US)
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Primers for identifying typing or classifying nucleic acids Patent: WO 0065088-A 1075 02-NOV-2000; Amersham Pharmacia Biotech AB (SE)
Location/Qualifiers
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Genotyping reagents, kits and methods of use thereof
Patent: WO 0129262-A 130 26-APR-2001;
                                                                 | 1.25
| forganism="synthetic construct"
| forganism="synthetic construct"
| for type="unassigned DNA"
| db xref="taxon:32630"
| force="HLA-C Heterozygote Primer Sequence"
                                                                                                                                                                                              Length 25;
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 130 from Patent W00129262.
AX115007
AX115007.1 GI:14031949
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Patent: WO 0053229-A 31 14-SEP-2000;
BACHER ADELBERT (DE) ; FISCHER MARKUS (DE)
Location/Qualifiers
                                                                                                                                                                                                                         Gaps
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Orchid BioSciences, Inc. (US)
Location/Qualifiers
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/db_xref="taxon:32630"
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Patent: DE 19942174-A 14 21-JUN-2000;
BACHER ADELBERT (DE)
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Sequence 14 from Patent DE19942174.
                                                                               /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
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Sequence 31 from Patent WO0053229.
AX035992
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ilarity 73.9%;
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Query Match 53.6%; Score 13.4; DB 6; Length 36;
Best Local Similarity 73.9%; Pred. No. 1.78+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps
Qy 2 TGGGCTTCACAGGGGAAA 24
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Search completed: November 18, 2005, 17:42:55 Job time: 695.731 secs

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November 18, 2005, 05:29:23; Search time 172.148 Seconds (without alignments) 859.686 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aag91125 Beta-card	Aca63115 Human bet	Adr05301 Human bet	Aba02364 Human nuc	Adh43094 CRAM prot	Acc58874 Doubly la	Acc58875 Doubly la	Aci46238 Human mic	Abx12624 Human zin	Abx12626 Human zin	Abx12627 Human zin	Aax59982 Oligonucl	Adq28791 PCR prime	Acc42057 Human SCN	Abz84436 Toxicolog	Adp88540 Bovine pa	Adp88541 Bovine pa	Aba02365 Human nuc	Aci31972 Human mic	Adp14058 Renal cel
SUMMARIES	QI	AAQ91125	ACA63115	ADR05301	ABA02364	ADH43094	ACC58874	ACC58875	ACI46238	ABX12624	ABX12626	ABX12627	AAX59982	ADQ28791	ACC42057	ABZ84436	ADP88540	ADP88541	ABA02365	ACI31972	ADP14058
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ALIGNMENTS

AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing Non-invasive method for diagnosis of hypertrophic cardio-myopathy useful for testing asymptomatic individual(s). Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy; diagnosis; primer; mutation; detection; ss. Ä Watkins H, Rosenzweig Beta-cardiac myosin heavy chain PCR primer C. (BGHM) BRIGHAM & WOMENS HOSPITAL. (GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA. Example 1; Col 10; 22pp; English. BP. 92US-00989160. 92US-00989160. AAQ91125 standard; cDNA; 25 19-FEB-1996 (first entry) (HARD) HARVARD COLLEGE. Seidman C, WPI; 1995-245715/32. 11-DEC-1992; 11-DEC-1992; US5429923-A. 04-JUL-1995. Seidman J, Synthetic. AAQ91125; RESULT 1 AAQ91125

oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (sporadic or familial, SHC and FHC) comprises detecting a mutation associated with hypertrophic cardiomyopathy in an amplified product of a beta cardiac myosin heavy chain DNA. The mutations associated with SHC/FHC are detected in the myosin gene isolated from blood, by detecting mis-matched areas in RNA-DNA hybrid double strands (RNA from the normal gene, DNA from the suspect asample). FHC associated point mutation can be classified and used to determine life expectancy in affected individuals e.g. using a Kaplan-Meier curve for the classified type of FHC causing point mutation. Also included are an RNA probe comprising ribonucleotides arranged in a sequence which is complementary to at least a portion of beta-cardiac myosin heavy-chain DNA and a set of DNA oligonucleotide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two
asymptomatic individuals suspected of having the disease. The method has be broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     familial hypertrophic cardiomyopathy; SHC; Gaucher's disease; sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia; Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease; phenylketonuria; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting a presence or absence of a mutation associated with hypertrophic cardiomypathy, useful for diagnosing cystic fibrosis or hemophilia, by detecting a mutation in an amplified product of a beta cardiac myosin heavy-chain DNA.
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                                                                                                                                                                       Similarity 100.
25; Conservative
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(SEID/) SEIDMAN J.
(WATK/) WATKINS H.
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         DNA. The method is useful for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. This method is especially useful for diagnosing SHC and FHC, as well as for determining the estimated the life expectancy of a person with familial hypertrophic cardiomyopathy. In particular, the method is useful for determining an individual's genetic information, and diagnosing e.g. Gaucher's disease, haemophilia, undennes muscular dystrophy, sickle cell ansemia, Tay-Sachs disease, phenylketonuria or dystrophy, sickle cell ansemia, Tay-cath of primer used to amplify a region of the beta cardiac myosin heavy chain cDNA containing an FHC-associated mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting mutations associated with hypertrophic cardiomyopathy to diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac myosin heavy-chain DNA and detecting the mutation in the amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amplified product, and detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy in the amplified product, thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also included are a set of DNA oligomuclectide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two oligomucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to detecting the presence or absence of a mutatio associated with hypertrophic cardiomyopathy (familial or sporadic, FHC, SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy, comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, beta cardiac myosin, heavy chain, PCR; primer, ss, FHC, SHC, familial hypertrophic cardiomyopathy, sporadic hypertrophic cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human beta cardiac myosin heavy chain mutation detection primer C.
                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                             100.0%; Score 25; DB 9; Length 25; 100.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                              G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosenzweig A;
                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                      1 CTGGGCTTCACTTCAGAGGAGAAA 25
                                                                                                                                                                                                                                                                                                                                          CTGGGCTTCACTTCAGAGGAGAAAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; SEQ ID NO 5; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watkins H,
                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-00989160.
95US-00469172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2004; 2004US-00788779.
                                                                                                                                                                                                              Sequence 25 BP; 8 A; 5 C; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR05301 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                Local Similarity 100.
nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seidman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROSENZWEIG A.
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SEIDMAN J.
WATKINS H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004152121-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR05301;
                                                                                                                                                                                                                                                   Query Match
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(ROSE/)
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                                                                                                                                                                                                                                                                                    Matches
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cc which amplify beta-cardiac myosin heavy-chain DNA (the set of cligonuclectide primers being useful for facilitating the diagnosis of hypertrophic cardiomyopathy being capable of detecting a hypertrophic cardiomyopathy (comprising the diagnosis of hypertrophic cardiomyopathy (comprising a first container holding an RNA probe completely hybridisable to the beta-cardiac myosin heavy chain DNA, where the RNA probe is capable of detecting a chaptrophic cardiomyopathy associated mutation, a second container of pretricions for uspilitying beta-cardiac myosin heavy-chain DNA and instructions for uspilitying beta-cardiac myosin heavy-chain DNA). The method is used for amplified beta-cardiac myosin heavy-chain DNA). The method is used for cardiomyopathy for facilitating the diagnosis of individuals cardiomyopathy. Presently, the diagnosis of individuals cardiomyopathy. Presently, the diagnosis of individuals cardiomyopathy. Presently, the diagnosis of individuals cardiomyopathy relies on the presence of typical clinical symptoms and the demonstration of unexplained ventricular companions of part, on the discovery that hypertrophic cardiomyopathy relies on the presence of typical chypertrophy. The present invention is non-invasive and based, at least in the beta actaiac myosin heavy-chain gene. Prior art creveals that there are no extensive studies involving a large number of families which established that this particular disease or disorder was caused by point mutations in the beta cardiac myosin heavy-chain gene. The present sequence is a PCR primer used to amplify a region of the beta cardiac myosin heavy-chain gene. The present sequence is a PCR primer used to amplify a region of the beta cardiac myosin heavy-chain gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiac myosin heavy chain having a disease-related point mutation.
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0; Gaps
ch 100.0%; Score 25; DB 13; Length 25; 1 Similarity 100.0%; Pred. No. 0.11; 25; Conservative 0; Mismatches 0; Indels
                                                                                                 CTGGGCTTCACTTCAGAGAGAAAA 25
                                                                              1 CTGGGCTTCACTTCAGAGGAGAAA 25
     Query Match
Best Local Similarity
                         Best Loc
Matches
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ABA02364 standard; DNA; 41 (first entry) 22-FEB-2002 ABA02364; RESULT 4 ABA02364 THE STATE OF THE S

Human nucleotide reductase 9 probe, SEQ ID NO:8.

Human; nucleotide reductase 9; recombinant production; malignant tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; cancer; blood disease; HIV infection; human immunodeficiency virus; immune disorder; inflammatory condition; purine; pyrimidine; metabolism disorder; embryonic disorder; growth disorder; gene therapy; cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.

Homo sapiens

WO200181385-A1.

01-NOV-2001.

23-APR-2001; 2001WO-CN000591.

27-APR-2000; 2000CN-00115483.

(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI

Mao Y, Xie Y;

WPI; 2002-026142/03.

Human reductase nucleotide 9 and encoded polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation

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The invention relates to human nucleotide reductase 9 (AAMS2683), nucleic acids encoding it (ABA02159), and a method for the recombinant production of nucleotide reductase 9. The protein has a molecular weight of 9 kD. The present invention additionally discloses an antagonist of nucleotide reductase 9 for therapeutic use, and an antibody which specifically binds to nucleotide reductase 9. Nucleotide reductase 9, and nucleotides which encode it may be used for treating a variety of diseases, such as malignant tumours, blood diseases, HIV (human immunodeficiency virus) infection, immune disorders, inflammatory conditions, disorders of purine and pyrimidine metabolism, and embryonic and growth disorders. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polynucleotide can be used as a primer for nucleic acid amplification reactions or as a probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hybridisation reactions, or in producing gene chips or microarrays.
Sequences ABA02364-ABA02365 represent human nucleotide reductase 9 probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in an exemplification of the invention
                         Example 7; Page 15; 35pp; Chinese.
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Seguence 41 BP; 10 A; 5 C; 9 G; 17 T; 0 U; 0 Other;

Gaps ö Length 41; 5; Indels Score 16; DB 6; Pred. No. 1.7e+03; 0; Mismatches 64.0%; 79.2%; 19; Conservative Local Similarity Query Match Best Loca Matches

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ADH43094 standard; DNA; 30 BP. 25-MAR-2004 (first entry) ADH43094; ADH43094

9 CRAM protein related primer sequence #SEQ ID Neuroprotective, neutralisation, CRAM, collapsing-response mediator protein-associated molecule, gene therapy; mitochondria, drug development, neural disease, pathosis, PCR, primer;

Synthetic.

WO2004001038-A1.

31-DEC-2003

19-JUN-2003; 2003WO-JP007766.

19-JUN-2002; 2002JP-00179105.

ORG. (NEWI-) NEW IND RES

Yanagi S;

WPI; 2004-099123/10.

Genes and proteins participating in neutralization of cells or tissues, useful in gene therapy and regeneration medicine, applicable in diagnosis, drug development for neural diseases and study of mechanism of pathosis.

Example 1; SEQ ID NO 6; 101pp; Japanese.

The invention relates to a method for inducing neutralisation of cells or tissues by using a protein binding to CRAM (collapsing-response mediator protein-associated molecule) protein or its encoded gene. The proteins and their encoded genes are useful in gene therapy and regenerative

BP.

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Probe; nucleic acid detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-OCT-2001; 2001US-0336432P.
                                                                                                                                                                                                                                                                                                                                                                                                                                21-OCT-2002; 2002WO-US033699.
     ACC58875/c
ID ACC58875 standard; DNA; 31
                                                                                                                                                                           Doubly labelled DNA probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bruce I, Davies M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-505122/47
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                                                                                                                             08-SEP-2003
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                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection or quantification of nucleic acid analyte, by hybridizing a nucleic acid probe having non-identical covalently attached dyes, with nucleic acid analyte, and measuring change in fluorescence of the probes.
medicine, e.g. by inducing neutralisation of mitochondria. They are also applicable in diagnosis, drug development for neural diseases and studying the mechanism of pathosis. The current sequence represents CRAM protein related PCR primer sequence.
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85.0%; Pred. No. 3.8e+03;
ive 0; Mismatches 3; Indels (
                                                                                                                                                                           61.6%; Score 15.4; DB 12; Length 30; 94.1%; Pred. No. 3.1e+03; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30 BP; 7 A; 11 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                             Sequence 30 BP; 5 A; 8 C; 7 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe, nucleic acid detection;
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                                                                                                                                                                                                                                                                              2 TGGGCTTCACTTCAGAG 18
                                                                                                                                                                                                                                                                                                                                24
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ID ACC58874;

ACC58874;

ACC58874;

ACC58874;

XX ACC58874;

XX O8-SEP-2003 (first entry)

XX O6-SEP-2003 (first entry)

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C9 Index of based to attach the intro
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                                                                                                                                                                    Query Match
Best Local Similarity 94.1'
Matches 16; Conservative
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nes 17; Conservative
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Wolter A;

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The present sequence is an example of nucleic acid probes of the invention. The probe may be doubly labelled with non-identical covalently attached dyes, i.e. thiazole orange and MDCC. A bifunctional branched linker is used to attach the dyes to the oligonucleotide. The probe generates a fluorescent signal upon hybridisation to a complementary nucleic acid based on the interaction of an intercalator or DNA groove binder with the formed double-stranded DNA. Nucleic acid probes of the invention can be used in homogeneous assays, real-time PCR monitoring, transcription assays, expression analysis on nucleic acid microarrays and other microarray applications such as genotyping
Detection or quantification of nucleic acid analyte, by hybridizing a nucleic acid probe having non-identical covalently attached dyes, with nucleic acid analyte, and measuring change in fluorescence of the probes.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31 BP; 8 A; 11 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                      Example 9; Page 33; 110pp; English.
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nes 17; Conserv
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RESULT 7

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Human zinc finger protein 33.22, encoding polynucleotide, antagonist and recombinant preparation, useful for treating tumors and diabetes.
                                                                                                                                                                                                                                                                                                                          The invention describes a human zinc finger protein -33.22, encoding polynucleotide, antagonist, and recombinant preparation. This sequence represents a PCR primer used to amplify DNA encoding the human zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a human zinc finger protein -33.22, encoding polymuclectide, antagonist, and recombinant preparation. This sequence represents a probe used to detect DNA encoding the human zinc finger protein 33.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human zinc finger protein 33.22, encoding polynucleotide, antagor
recombinant preparation, useful for treating tumors and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.2%; Score 14.8; DB 8; Length 33; 88.9%; Pred. No. 5.9e+03; live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33 BP; 12 A; 6 C; 7 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                              Example 5; Page 18 (Disclosure); 32pp; Chinese.
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                                                      (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TTCACTTCAGAGGAGAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 TACACTTCAGAAGAGAAA 30
       22-MAR-2001; 2001CN-00105731.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        finger protein 33.22
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                                                                                                                                                    WPI; 2003-176047/18.
                                                                                                       Xie Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABX12626;
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                                                                                                     Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, an analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises comprises and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid components of a gene and a cross-species comparises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the cucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific cucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific cucleic acids further comprises a tag sequence. The array of nucleic acid for any gene, in mapping the 5' termin of mRNA molecules by companions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the form inspro are analso be obtained in electronic format directly from tisput a marcher analso be obtained.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.2%; Score 14.8; DB 9; Length 25; 88.9%; Pred. No. 5.7e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; zinc finger protein 33.22; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 8 A; 4 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human zinc finger protein 33.22, PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from USPTO at segdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 46229; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
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                                              15-MAR-2002; 2002US-00098263.
                                                                                                16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAR-2001; 2001CN-00105731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 CTTCACTTCAGAGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX12624 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                 (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                              WPI; 2003-567953/53.
                                                                                                                                                                                                  Mittmann MP;
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05-JUN-2003
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antagonist and

ABX12624;

X4X6X4X6X4X6X4X

RESULT 9 ABX12624

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Gaps

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JP2004194654-A.
29-OCT-1997;
               29-OCT-1997;
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                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                         RESULT 13
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                                                                                                                                                                                                                                                             Human zinc finger protein 33.22, encoding polynucleotide, antagonist and recombinant preparation, useful for treating tumors and diabetes.
                                                                                                                                                                                                                                                                                                    The invention describes a human zinc finger protein -33.22, encoding polymucleotide, antagonist, and recombinant preparation. This sequence represents a probe used to detect DNA encoding the human zinc finger protein 33.22
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species-specific, Bacteroides, microbe, identification, Rikenella, Porphyromonas, Prevotella, probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide probe specific for Porphyromonas gingivalis.
                                                                                                                                                                                                                                                                                                                                                          59.2%; Score 14.8; DB 8; Length 41; 88.9%; Pred. No. 6.1e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                           Sequence 41 BP; 20 A; 6 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                    Example 7; Page 20 (Disclosure); 32pp; Chinese.
                                                                                                                   Human; zinc finger protein 33.22; probe; ss
                                                                                                    Human zinc finger protein 33.22, probe #2.
                                                                                                                                                                                                                (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                     TACACTICAGAAGAGAAA 20
24
          TACACTICAGAAGAGAAA 20
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                                                      ABX12627 standard; DNA; 41 BP.
                                                                                                                                                                                                 22-MAR-2001; 2001CN-00105731
                                                                                                                                                                                22-MAR-2001; 2001CN-00105731
                                                                                                                                                                                                                                                                                                                                                                                          7 TTCACTTCAGAGGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX59982 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                     (first entry)
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nes 16; Conservative
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                                                                                                                                                                                                                                Xie Y;
                                                                                                                                   Homo sapiens
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                                                                                     13-MAY-2003
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                                                                      ABX12627
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Matches
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New oligonucleotide probe species-specific to a Bacteroides group microbe - useful for identification of the microbe.
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Specifically, it refers to a bacteriophage chosen from a levi virus of the Leviviridae family, which is a small globular form RNA phage or a micro virus of the Microviridae family, which is a small globular form ENA phage. The bacteriolytic gene in the construct is under the control of a phage lambda lactose promoter, and further contains a gene encoding a coat protein as well as an inducer of gene expression i.e. isopropyl beta-D-1 thio-galactopyranoside (IPTG). The present invention describes a composition useful for treating infectious disease through the bacteriolysis of bacteria such as Escherichia coli infections occurring in both humans and animals. Furthermore, it is a highly reliable, safe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pharmaceutical composition useful for treating infectious diseases, comprises gene construct containing bacteriolytic gene of bacteriophage, and carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAXS9976-93 represents oligonucleotide probes that are species-specific Bacteroides group microbes. The probes are useful for species-specific identification of a Bacteroides group microbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer SP-23 to amplify B-IV group phage bacteriolysis gene Seq 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacteriophage; infectious disease; pathogenic; bacteriolysis; ss; antimicrobial; bacteriolytic; PCR; primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 5 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.6; DB 2;
Pred. No. 6.8e+03;
                                                                                                                                                  (YAKU-) ZH YAKULT BIOSCIENCE KENKYU ZAIDAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; SEQ ID NO 11; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGGGCTTCACTTCAGAGGAG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 7; 9pp; Japanese.
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97JP-00297085
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ilarity 81.0%;
Conservative (
                                                                       97JP-00297085
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                                                                                                                                                                                                                          WPI; 1999-350346/30.
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Best Local Similarity
Matches 17; Conserv
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The present invention describes a method (M) for determining the ion channel disease genotype of an individual. Also described: (1) an isolated KXONG1 nucleic acid molecule (I) comprising a sequence (S1, see ACC41977 to ACC41980), or a nucleic acid sequence that is fully complementary to S1, where the isolated nucleic acid molecule is less than 5 kilobases in length; (2) an array of oligonucleotides comprising (I); and (3) an isolated nucleic acid molecule (II) comprising at least one base variation from that of an ion channel associated gene sequence comprising a polymorphic nucleotide identified in Tables 4 and 5 in the specification, with the polymorphic nucleotide, where the isolated nucleic acid molecule is less than about 5 kilobases in length. (M) is nucleic acid molecule is less than about 5 kilobases in length. (M) is useful for determining ion channel disease genotype of an individual, where the individual has or is suspected of having an ion channel disease selected from long QT syndrome, cardiac arrhythmias, epilepsy, hearing
                                                                                                                                                                                ö
specific antimicrobial method for targeting pathogenic bacteria and nuse it does not comprise a medical agent it also prevents the risk of erating drug-resistant microbes. This oligonucleotide sequence is a primer given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            decreased ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; KCNQ1; KCNE1; HERG; SCN5A; KNCE2; ion channel disease; epilepsy; polymorphism; genetic abnormality; genotype; mutation; long QT syndrome; cardiac arrhythmia; hearing loss; sudden infant death syndrome; SIDS; sudden unexpected death in epilepsy; acquired sudden death syndrome; post-myocardial infarction complication; SUDEP; SUDS; ss; sudden unexpected death in sleep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining ion channel disease genotype of an individual, by analyzing nucleic acid sample of individual for a mutation indicating decreased ic channel conductivity resulting in amino acid change of KCNQ1 protein.
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCN5A gene related polymorphism oligonucleotide SEQ ID NO:86.
                                                                                                                                                                              ö
                                                                                                                                     ch 58.4%; Score 14.6; DB 12; Length 34; I Similarity 81.0%; Pred. No. 7.4e+03; 17; Conservative 0; Mismatches 4; Indel8
                                                                                                Seguence 34 BP; 9 A; 9 C; 11 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rienhoff HY;
                                                                                                                                                                                                                   3 GGGCTTCACTTCAGAGGAGAA 23
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                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2002; 2002WO-US026708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001; 2001US-0314331P.
06-MAY-2002; 2002US-0378521P.
                                                                                                                                                                                                                                                                                                                                                         ACC42057 standard; DNA; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curran ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DNAS-) DNA SCI INC.
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                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                    generating
PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-2003
                      because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of
               epilepsy (SUDEP), sudden unexpected death in sleep (SUDS), post-
myocardial infarction complications, and acquired sudden death syndrome,
or the individual is a lineal descendant of an individual who has or is
suspected of having the above diseases. (II) is useful for conducting
clinical trials of drug candidates for ion channel diseases, for
preparing probes or primers for detection of the presence of long OT
genes, and for establishing physical linkage between a genetic locus
associated with a trait of interest and polymorphic markers that are not
locus responsible for the trait of or establishing physical proximity with the genetic
locus responsible for the trait of sequences used in the
ACC42159, ABP96320 and ABP96321 represent sequences used in the
exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toxicologically relevant gene; toxicological response; PCR primer; ss.
sudden unexpected death in
                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kier LD,
                                                                                                                                                                                                                                                                Sequence 41 BP; 7 A; 16 C; 11 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxicologically relevant human PCR primer #1595.
   sudden infant death syndrome (SIDS),
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adkins K, Pickett GG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 351; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                1 CTGGGCTTCACTTCAGAGGAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                     28 CTGGCCTTGGCCTCAGAGGAG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABZ84436 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                       Similarity
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Local Si...
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to a known toxic pharmaceutical or industrial agent, comprising: (a) exposing cells to an agent or isolating cells from a human subject who was exposed to an agent; (b) obtaining the test gene expression profile for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of the agene with a similar function or exposure to other known toxic compounds. The methods are useful for predicting and determining toxicological responses on a cellular, organ or system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a variant of bovine pancreatic desoxyribonuclease I (pancreatic DNase I), by way of amino acid substituted substituted, where at least one different amino acid substitutes for an amino acid residue chosen from Cys173, Cys101, Cys104, Lys117, Arg185, Arg187, I183, Phe82, and Phe128. Bovine pancreatic DNase I is useful for hydrolyzing DNA and subsequently reducing the specific desoxyribonuclease activity of the variant of the enzyme to approximately zero units per mg of procein. The present sequence is a mutagenic primer used to alter the wild-type bovine pancreatic DNase I coding sequence.
                                                                                                                                                                                                                                                                                                                                     Gaps
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amino acid substitutions in bovine pancreatic desoxyribonuclease
increased thermolability and is useful for hydrolyzing DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; PCR; cow; bovine pancreatic DNase I; bovine pancreatic desoxyribonuclease I; DNA hydrolysis; primer;
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                                                                                                                                                                                                                                                                                         Query Match 57.6%; Score 14.4; DB 10; Length 25; Best Local Similarity 75.0%; Pred. No. 8.7e+03; Marches 18; Conservative 0; Mismatches 6; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine pancreatic DNase I mutagenic PCR primer SEQ ID NO: 22
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Engel W;
                                                                                                                                                                                                                                                   Sequence 25 BP; 9 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
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Siedel J, E
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20-JAN-2003; 2003EP-00001214.
21-JAN-2003; 2003US-0441550P.
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Thalhofer J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variant of bovine pancreatic desoxyribonuclease I produced by specific amino acid substitutions in bovine pancreatic desoxyribonuclease I, has increased thermolability and is useful for hydrolyzing DNA.
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                                                                                                                                                           Gaps
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bovine pancreatic desoxyribonuclease I; DNA hydrolysis; primer;
mutagenic.
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                                                                                      57.6%; Score 14.4; DB 12; Length 37; ilarity 75.0%; Pred. No. 9.2e+03; Conservative 0; Mismatches 6; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine pancreatic DNase I mutagenic PCR primer SEQ ID NO:
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                          Seguence 37 BP; 11 A; 10 C; 4 G; 12 T; 0 U; 0 Other;
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Siedel J, Engel W;
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                                                                                                                                                                                                                    2 TGGGCTTCACTTCAGAGAAAA
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21-JAN-2003; 2003US-0441550P.
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Thalhofer J,
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Best Local Similarity 75.0
Matches 18; Conservative
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                                                                                                                       Local Similarity
les 18; Conserv
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1D ADP885.
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AC ADP885.
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MX SS; PC
KW BS; 
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Matches
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EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

15-MAR-2002; 2002US-00098263. 16-MAR-2001; 2001US-0276759P.

US2003104410-A1. Homo sapiens.

05-JUN-2003

(AFFY-) AFFYMETRIX INC.

WPI; 2003-567953/53.

Mittmann MP;

Human microarray DNA oligonucleotide SEQ ID NO 31963,

13-OCT-2003 (first entry)

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The invention relates to human nucleotide reductase 9 (AAMS2683), nucleic acids encoding it (ABA02359), and a method for the recombinant production acids encoding it (ABA02359), and a method for the recombinant production of nucleotide reductase 9. The protein has a molecular weight of 9 kD.

The present invention additionally discloses an antigonist of nucleotide reductase 9 for therapeutic use, and an antibody which specifically binds to nucleotide reductase 9, and nucleotides which encode it may be used for treating a variety of diseases, such as malignant tumours, blood diseases, HIV (human immunodeficiancy virus) infection, immune disorders, inflammatory conditions, disorders of purine and pyrimidine metabolism, and embryonic and growth disorders. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polynucleotide can be used as primer for nucleic acid amplification reactions or as a probe for hybridisation reactions, or in producing gene chips or microarrays. Sequences ABA02364-ABA02365 represent human nucleotide reductase 9 probes
                                                                                                                                                                     Human, nucleotide reductase 9; recombinant production; malignant tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; immune disorder; inflammatory condition; purine; pyrimidine; metabolism disorder; embryonic disorder; growth disorder; gene therapy; cytostatic, anti-HIV; antiinflammatory; immunomodulator; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human reductase nucleotide 9 and encoded polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.4; DB 6; Length 41;
Pred. No. 9.3e+03;
0; Mismatches 6; Indels
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                                                                                                                             Human nucleotide reductase 9 probe, SEQ ID NO:9.
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ABA02365 standard; DNA; 41 BP.
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75.0%;
                                                                                    (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xie Y;
                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation.
                                                                                    22-FEB-2002
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                                          ABA02365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mao Y,
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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 31963; 9pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018 500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 BP; 3 A; 9 C; 7 G; 6 T; 0 U; 0 Other;
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 20
ADP14058/c
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Gaps

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25

2 TGGGCTTCACTTCAGAGAGAAAA

18; Conservative

Matches

15 regerrecacricaerreaacaa 38

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ACI31972 standard; DNA; 25

RESULT 19 ACI31972/ ACI31972;

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ss; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes that are differentially expressed in peripheral blood samples isolated at different stages of progression, development or treatment of RCC and/or other solid tumors. This sequence corresponds to a probe to detect a gene that is differentially expressed and detected by the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having in the peripheral blood sample to reference expression profile of specific genes in the peripheral blood sample to reference expression profile of the blood mononuclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from the conditional RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample (claimed). (M1) is useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trepicchio WL, Dorner A, Stover JA;
Renal cell carcinoma differentially expressed gene probe #462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.8%; Score 14.2; DB 12;
84.2%; Pred. No. 1.1e+04;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 3 A; 6 C; 7 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe for fungal saccharopine dydrogenase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 793; 350pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GGCTTCACTTCAGAGGAGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                    21-NOV-2003; 2003WO-US037481.
                                                                                                                                                                                                                                                                                           21-NOV-2002; 2002US-0427982P. 03-APR-2003; 2003US-0459782P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT31079 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iwine NC, Burczynski ME,
Sloni DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JAN-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                         TWINE N C.
BURCZYNSKI M E
TREPICCHIO W L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-460799/43.
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      DORNER A.
STOVER J A.
SLONI D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention
                                                                                                                                                                  WO2004048933-A2.
                                                                                                                             Homo sapiens
                                                                                                                                                                                                           10-JUN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (DORN/)
(STOV/)
(SLON/)
                                                                                                                                                                                                                                                                                                                                                                                             (BURC/)
(TREP/)
                                                                                                                                                                                                                                                                                                                                                        (AMHP)
                                                                                                                                                                                                                                                                                                                                                                             (LMIN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT31079
  요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes in the peripheral blood sample to reference expressed in peripheral compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample is a whole blood sample (claimed). (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples isolated at different stages of progression, development or treatment of RCC and/or other solid tumors. This sequence corresponds to a probe to detect a gene that is differentially expressed and detected by the method of the invention.
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0
                                                   ss; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing non-blood disease such as solid tumor, involves comparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stover JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
               Renal cell carcinoma differentially expressed gene probe #463.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dorner A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 4 A; 5 C; 6 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trepicchio WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 794; 350pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GGCTTCACTTCAGAGGAGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 GGCCTCACTTCCAAGGAGA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP14057 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                            21-NOV-2002; 2002US-0427982P.
                                                                                                                                                                                                                                                                   21-NOV-2003; 2003WO-US037481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burczynski ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 84.2
Matches 16; Conservative
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TWINE N C.
BURCZYNSKI M E
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STOVER J A.
SLONI D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-460799/43.
                                                                                                                                                                                   WO2004048933-A2
                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differential
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                                                                                                                                                                                                                                                                                                                                                                                             (TWIN/)
(BURC/)
(TREP/)
(DORN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SLOV/)
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ID ADP1405
XX ADP1406
XX DT 26-AUG-
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Gaps

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Length 25; Indels us-10-788-779-5.rng

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16-APR-2002; 2002JP-00113030.
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                                            Sasaki K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ24931;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                      Nishi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mao Y,
                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 24
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                                                                                                                                                                                                                                                                                                                    Nucleic acid sequences derived from polypeptide fragments of Candida albicans saccharopine dehydrogenase and which are conserved in fungi can be used as probes and primers in methods for detecting fungal pathogens. They may be used for the detection of C. albicans, Yarrowia lipolytica, and Cryptococcus neoformans. They mays also be used for the detection of Aspergillus fumigatus and Histoplasma capsulatum, especially in patients suffering from AIDS, those under treatment with immunosuppressive drugs, postoperative patients and other immunocompromised patients. The nucleic acid sequences are described in AAT31079-T31093. The peptide epitopes from which they are derived are described in AAW00483-W00495
                                                                                                                                                                                                                                                      Detecting fungal infection by detection of saccharopine dehydrogenase gene - uses probe, primer or antibody specific to conserved Candida albicans sequences as detection agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
        Probe; primer; fungal pathogen; detection; screening; AIDS; acquired immune deficiency syndrome; Candida albicans; Cryptococcus neoformans; Yarrowia lipolytica; Aspregillus fumigatus; Histoplasma capsulatum; postoperative patients; immunocompromised;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; PCR; primer; ss; transformation; endocrine cell line; expression cloning system; bioactive peptide; GPCR ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.8%; Score 14.2; DB 2; Length 33; 84.2%; Pred. No. 1.1e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer used to amplify human GPR43 DNA (SeqID 182).
                                                                                                                                                                                                                Peery RB;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33 BP; 15 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                               Skatrud PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 54; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 CTTCACTTCAGAGGAGAAA 24
                                                                                                                                                                                                               Bhattacharjee JK, Garrad RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                      95WO-US016684
                                                                                                                                                           94US-00360606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-2003; 2003WO-JP004840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF50502 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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nes 16; Conservative
                                                                                                                                                                              (UYMI-) UNIV MIAMI.
(ELIL ) LILLY & CO ELI.
                                                    immunosuppressed; ss
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                                                                                             WO9619588-A2
                                                                                                                                      20-DEC-1995;
                                                                                                                                                           21-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                 27-JUN-1996
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                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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ADF50502/
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This invention relates to a novel method for obtaining a DNA that encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a peptide acting as agonist, antagonist or inverse agonist on a target receptor. Specifically, it comprises transformation of endocrine cell lines originating from mammalian hypothalamus and pancreatic islets, culturing the transformants and contacting with cells expressing the target receptor. The identification of those cells with a response reaction can be used for selecting a transformant cell line with the appropriate target activity that is expressing the novel transformed DNA. Accordingly, the present invention describes novel cell lines that are applicable in expression cloning systems of bioactive peptide precursor. Genes, and in screening GPCR ligands for use as drugs including agonists antagonists and inverse agonists i.e. activators and inhibitors. Such cell lines can provide a highly sensitive and convenient GPCR ligand assay system. This oligonucleotide sequence is a PCR primer used to amplify human GPCR DNA of the invention.
                                                                                                                                                                                                                                                                                                        pancreatic islet, applicable in expression cloning systems of bioactive peptide precursor genes, and in screening G protein-coupled receptor ligands.
                                                                                   Kunitomo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell division cycle regulatory protein 137.17; tumour; cytostatic; diabetes; cell division; probe; ss.
                                                                                                                                                                                                                                                                 Endocrine cell lines originated from mammalian hypothalamus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.8%; Score 14.2; DB 10; Length 39; 84.2%; Pred. No. 1.1e+04; ive 0; Mismatches 3; Indels (
                                                                               Kishimoto K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell division cycle regulatory protein 137.17 probe #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39 BP; 7 A; 11 C; 12 G; 9 T; 0 U; 0 Other;
                                                                               Yoshizawa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 25; SEQ ID NO 182; 316pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BODE-) BODE GENE DEV CO LTD SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GGGCTTCACTTCAGAGGAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 GGACTTCACTACAGAGTAG 15
                                                                               Saeki S,
(KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-2000; 2000CN-00135176.
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ID ABZ24931 standard; DNA; 41
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les 16; Conservative
                                                                           Miura K,
Obinata M;
                                                                                                                                                                                              WPI; 2003-833737/77.
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Felix CA,
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                                                                                                                                                                                                                     RESULT 26
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  ន្តដ្ឋនូងន
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   confer herbicide resistance activity. Crop plants, such as soybean, cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower, cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower, barley, oat, turf grass, forage grass, sugar cane, pea, field bean, rice, pine, poplar, apple, grape, citrus or nut plants, transformed with a pine, poplar, apple, grape, citrus or nut plants, transformed with a constructed binding protein gene are resistant to the herbicide. Hence, weeds can be selectively controlled in a field of the transformed crops. The plants are substantially resistant or tolerant to herbicides, such as paraquat or diquat, that inhibit photosynthesis by accepting electrons from photosystem I thus generating free radicals which cause lipid peroxidation or by blocking electron transport in photosystem II. The herbicide binding proteins advantageously sequester the herbicide, e.g. at the cell surface or in the vacuoles of a treated plant. Sequestration at the cell surface prevents the entry of the herbicide into the cell so that the herbicide cannot reach its intracellular target and exert any significant cytotoxic effect. The herbicide binding protein inhibits the
                                                                                                                                                                             ö
                                                   present invention relates to cell division cycle regulatory protein 7.17 (see ABP59091). The protein can be used for treating diseases such diabetes and tumours. The present sequence is a probe, which was used
                                                                                                                                                                                                                                                                                                                                                                                                             Paraquat; antibody; light chain; herbicide; resistant; crop plant; weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I; free radical; lipid peroxidation; electron transport; photosystem II; vacuole; cell surface; cytotoxic; sensitive; heavy chain; PQXB1/2; variable region; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                      Paraquat binding antibody PQXB1/2 variable heavy chain PCR primer VH3
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel herbicide binding protein which can
                                                                                                                                                                             ö
                                                                                                                                                 56.8%; Score 14.2; DB 6; Length 41; 84.2%; Pred. No. 1.2e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herbicide binding proteins and related polynucleotides
                                                                                                                       Sequence 41 BP; 13 A; 8 C; 8 G; 12 T; 0 U; 0 Other;
                           Example 7; Page 21 (Disclosure); 38pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 42; 60pp; English.
                                                                                              in an example from the invention
                                                                                                                                                                                                       6 CTTCACTTCAGAGGAGAAA 24
                                                                                                                                                                                                                                  38 circacircedarcada 20
                                                                                                                                                                                                                                                                                                     AAX78849 standard; DNA; 47 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-GB003760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-00026955
 polynucleotide encoding it.
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-405173/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones PG;
                                                                                                                                                              Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9932630-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                           07-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                AAX78849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holt DC,
                                                                                                                                                 Query Match
                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                          RESULT 25
                                                      The |
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The invention relates to amplifying an unknown region that flanks a known region of a cancer-associated DNA sequence comprising providing a cemplate polywincleotide, ligating a loop-forming oligonucleotide to the cemplate polywincleotide, ligating a loop-forming oligonucleotide to the care strand, annealing the loop-forming oligonucleotide to the sense strand, annealing the loop-forming oligonucleotide to the panamadia structure to extension, and subjecting the panamadia structure to proving the persence of a first primer homologous to the second portion, where the unknown region is amplified. In the method of cancer-associated DNA sequence, the template polynucleotide comprises a sense strand, comprising the known and unknown regions. The unknown region is comprises a first or second portion. The first portion is captured than is the second portion. The loop-forming oligonucleotide is complementary to the first portion. The third region
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mobility of the herbicide from the application site to the whole plant preventing the herbicide reaching particularly sensitive organs. Additionally, tolerant plants can be produced against herbicides that have more than one target site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ds; MLL; cancer; AF-4; CDK-6; SEPTIN6; ALL;
acute lymphoblastic leukaemia; AML; acute myeloid leukaemia;
chromosomal break point; chromosome 11q23; ATF; BCR; B cell receptor.
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                  56.8%; Score 14.2; DB 2; Length 47; 84.2%; Pred. No. 1.2e+04; rive 0; Mismatches 3; Indels
                                                                                                                                                                     G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             罚
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human breakpoint region AF-4 #4
                                                                                                                                                                                                                                                                                                                                                                                  4 GGCTTCACTTCAGAGAGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTTACCTTCAGAGGAGA 38
                                                                                                                                                                     Sequence 47 BP; 16 A; 11 C; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0038624P.
97US-0056938P.
97US-0065911P.
98US-00026033.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB73490 standard; DNA; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2003 (first entry)
                                                                                                                                                                                                                                             Query Match 56.8
Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JONE/) JONES D H.
(RAPP/) RAPPAPORT E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FELI/) FELIX C A. (JONE/) JONES D H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003096255-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-1997;
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19-FEB-1998;
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complementary to the second portion is generated at the free end of the loop-forming oligonucleotide. The cancer-associated DNA sequence comprises AFPI (not defined) or BCR (B cell receptor). The method is useful for amplifying an unknown region that flanks a known region of a cancer-associated DNA sequence. Also disclosed as new is the use of the method in the analysis of the breakpoint region of the human MLL gene, where the chromosomal breaks results in gene fusions with AF-4, CDK-6 and SBPTIN6 and are associated with ALL and AML (acute lymphoblastic leukaemia and acute myeloid leukaemia). MLL is located on chromosome 11q23. The present sequence is an MLL breakpoint junction region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a system for detecting gene expression, which gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phillips J;
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte gene expression profiling probe SEQ ID NO 2794.
                                                                                                                                                                                                                                                                 Length 48;
                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                         Sequence 48 BP; 18 A; 11 C; 8 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                 Score 14.2; DB 10;
Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Matcuk G, Altman P, P. Quertermous T, Johnson F;
                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 416; Opp; English.
                                                                                                                                                                                                                                                                                                                                              6 CTTCACTTCAGAGGAGAA 24
                                                                                                                                                                                                                                                                                                                                                                                     20 crecácricadadeccada 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-2001; 2001WO-US047856.
                                                                                                                                                                                                                                                             ch 56.8%;
il Similarity 84.2%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ02803 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wohlgemuth J, Fry K,
Ly N, Woodward R, Q
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                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                              erythropoietin; granulocyte colony stimulating factor;
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                             50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.0%; Score 14; DB 3; Length 29; 60.9%; Pred. No. 1.4e+04; rive 3; Mismatches 6; Indels
                                                       Indels
                             Length
Sequence 50 BP; 15 A; 12 C; 9 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29 BP; 9 A; 5 C; 7 G; 0 T; 7 U; 1 Other;
                           DB 6;
                           Score 14.2; DB 6;
Pred. No. 1.2e+04;
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcswiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGGCTTCACTTCAGAGGAGAAAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACUUCACUGAUGAGNCGAAAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 59; Page 132; 164pp; English.
                                                                                 7 TTCACTTCAGAGGAGAAA 25
                                                                                                             24 rccacrrcacaggaraaaa 42
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                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2000; 2000WO-US009721.
                           56.8%;
84.2%;
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ABA99901/c
ID ABA99901 standard; DNA; 30
XX
AC ABA99901;
                                                                                                                                                                                AAF06504 standard; RNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                        16-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                    Hammerhead ribozyme #3301.
                                                       16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
                                                                                                                                                                                                                                                                                                                interferon alpha; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-647423/62.
                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                Ribozyme;
                                                                                                                                                                                                            AAF06504;
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                                                       Matches
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ID AAF
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The present sequence represents an oligonucleotide used in an example of the present invention. The present invention describes a method for synthesising a selected oligonucleotide (1) having well defined ends. The method comprises: (a) annealing a primer to a single-stranded (ss) circular template to yield a primed circular template, where the template comprises: (i) at least one nucleotide sequence complementary to (1); and (ii) at least one nucleotide effective to produce a cleavage site in the oligonucleotide multimer; (b) combining the primed circular template with at least two types of nucleotide triphosphates and a polymerase enzyme without the addition of auxiliary proteins to yield a ss oligonucleotide multimer complementary to the circular oligonucleotide template,
                                                                                           A nucleic acid-immobilized array useful for detection of a target nucleic
                                                                                                                                                                                                      The invention relates to a novel nucleic acid-immobilised array in which nucleic acids are lined up and immobilised in a predetermined region on a carrier surface and at least two nucleic acids having base sequences at different sites of a same gene are immobilised at a same position. The method of the invention is useful for the preparation of a nucleic acidimmobilised array. The sequences shown in Abili0976-Abili152 represent probes and PCR primers used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthesis, selection, amplification; circular oligonucleotide, rolling circle synthesis; diagnosis; therapeutic agent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                56.0%; Score 14; DB 10; Length 40; ilarity 77.3%; Pred. No. 1.4e+04; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide SEQ ID NO:46 from US5174320 Example 25.
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40 BP; 11 A; 13 C; 6 G; 10 T; 0 U; 0 Other;
                                                                                                                                                          Example 1; SEQ ID NO 18; 52pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGCATTCGCATCAAAGGAGA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGGCTTCACTTCAGAGGAGA
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    (TAKA-) TAKARA BIO KK.
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                                                 WPI; 2003-451501/43.
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les 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 31
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel multiplex amplification reaction for detecting clinically relevant fungal infections by amplifying a region of the 18S RNA gene, where only sequences from pathogenic Candida and Aspergillus species are amplified. The method is quick, simple and sensitive, and can detect all clinically important Candida and Aspergillus species, but generally it does not detect species commonly present in laboratories as contaminants (avoiding false positive results). The detection limit is 3-20 cells/10 ml of blood, depending on the detection method used. This sequence represents a PCR primer used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multiplex amplification for detecting fungal infection, selective for clinically important strains of Candida and Aspergillus, comprises amplifying a region of the 18S RNA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                      18S RNA; muliplex PCR; PCR; primer; detection; amplification;
fungal infection; pathogenic; 8s.
                                            albicans 18S RNA detecting multiplex PCR primer SEQ ID 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14; DB 6; Length 30;
Pred. No. 1.4e+04;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage lambda DNA fragment 1 probe SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 30 BP; 6 A; 8 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenau J, Kirschner P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GGCTTCACTTCAGAGGAGAAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 GACTCCACTTCAGAGCGGAGAA 8
                                                                                                             pathogenic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Page 26; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss; array; Lambda phage; probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      991/c
ADH10991 standard; DNA; 40 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-2001; 2001JP-00142082.
                                                                                                                                                                                                                                                                                             24-SEP-2001; 2001WO-EP011023.
                                                                                                                                                                                                                                                                                                                                           26-SEP-2000; 2000DE-01048009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2001; 2001JP-00142082.
                                                                                                                                                                                                                                                                                                                                                                                     (CYTO-) CYTONET GMBH & CO KG
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 77.3
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-330101/36.
                                                                                                                                                            Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2002330767-A.
                                                                                                                                                                                                      WO200227021-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                  Boettger EC,
17-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-2004
                                                                                                                                                                                                                                                   04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-2002
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Matches

a ò

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Gaps

; 0

3 GGGCTTCACTTCAGAGGAAA 24

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The present sequence represents an oligonuclectide used in an example of the present invention. The present invention describes a method for synthesising a selected oligonuclectide (I) having well defined ends. The method comprises: (a) annealing a primer to a single-stranded (ss) circular template to yield a primed circular template, where the template comprises: (i) at least one nucleotide sequence complementary to (I); and (I) at least one nucleotide effective to produce a cleavage site in the oligonucleotide multimer; (b) combining the primed circular template with at least two types of nucleotide triphosphates and a polymerase enzyme without the addition of auxiliary proteins to yield a ss oligonucleotide wilthout the addition of auxiliary proteins to yield a so oligonucleotide unltimer complementary to the circular oligonucleotide template, comprising multiple copies of (I); and (o) cleaving the oligonucleotide multimer at the cleavage site to produce (I) having well defined ends. The method is used for the large-scale synthesis of DNA and RNA oligomers
                                                                                                                                                                                            ö
comprising multiple copies of (I); and (c) cleaving the oligonucleotide multimer at the cleavage site to produce (I) having well defined ends. The method is used for the large-scale synthesis of DNA and RNA oligomers for use, e.g. as probes and diagnostic agents and/or therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rolling circle synthesis of oligo:nucleotide(s) - using primed circular template to produce oligonucleotide multimer for cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method is used for the large-scale synthesis of DNA and RNA oligome.
use, e.g. as probes and diagnostic agents and/or therapeutic agents
                                                                                                                                                                                            Gaps
                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthesis; selection; amplification; circular oligonucleotide; rolling circle synthesis; diagnosis; therapeutic agent; ss.
                                                                                                                                             56.0%; Score 14; DB 2; Length 49; nilarity 77.3%; Pred. No. 1.5e+04; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide SEQ ID NO:50 from US5174320 Example 25.
                                                                                                      Sequence 49 BP; 9 A; 14 C; 8 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                              3 GGCTTCACTTCAGAGGAGAAA 24
                                                                                                                                                                                                                                                          43 GGCTTTTCTGAAGAGGCGAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 25; Col 63; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-00047860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-00393439
                                                                                                                                                                                                                                                                                                                                                                            AAV12941 standard; RNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYRP ) UNIV ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-144278/13.
                                                                                                                                                                Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5714320-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                  AAV12941;
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kool ET;
                                                                                                                                                                  Best Loc
Matches
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  8X333X8
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The present sequence represents an oligonuclectide used in an example of the present invention. The present invention describes a method for synthesising a selected oligonuclectide (I) having well defined ends. The method comprises: (a) annealing a primer to a single-stranded (ss) circular template to yield a primed circular template, where the template comprises: (i) at least one nuclectide sequence complementary to (I); and (ii) at least one nuclectide effective to produce a cleavage site in the oligonuclectide multimer; (b) combining the primed circular template with a least two types of nuclectide triphosphates and a polymerase enzyme without the addition of auxiliary proteins to yield a so oligonuclectide multimer complementary to the circular oligonuclectide template, comprising multiple copies of (I); and (C) cleaving the oligonuclectide multimer at the cleavage site to produce (I) having well defined ends. The method is used for the large-scale synthesis of DNA and RNA oligomers for use, e.g. as probes and diagnostic agents and/or therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rolling circle synthesis of oligo:nucleotide(s) - using primed circular template to produce oligonucleotide multimer for cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                  Synthesis, selection, amplification, circular oligonucleotide, rolling circle synthesis, diagnosis, therapeutic agent, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.0%; Score 14; DB 2; Length 4>,
                                                                                                                                                                                                    Oligonucleotide SEQ ID NO:47 from US5174320 Example 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
11 GGGCUUUCUGAAGAGGCGAAA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GGGCTTCACTTCAGAGGAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 25; Col 61; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          95US-00393439
                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-00047860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Similarity 63.6%; 14; Conservative
                                                                                             AAV12938 standard; RNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV12939 standard; RNA; 49
                                                                                                                                                                15-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYRP ) UNIV ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-144278/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                          23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-1993;
                                                                                                                                                                                                                                                                                                                                      US5714320-A.
                                                                                                                                                                                                                                                                                                                                                                        03-FEB-1998
                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                 AAV12938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV12939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kool ET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 34
AAV12939
ID AAV12
XX
AC AAV12
          엄
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Gaps

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56.0%; Score 14; DB 2; Length 49; 63.6%; Pred. No. 1.5e+04; ive 3; Mismatches 5; Indels

14; Conservative

Query Match Best Local Similarity Matches 14; Conservat

to 39"

/bound_moiety= "Bound to positions 36 bound_moiety= "Bound to position 49"

*tag=

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Synthesis of oligo:nucleotide(s) - using a single-stranded circular oligo:nucleotide template ribonucleotide tri:phosphate(s) and a polymerase to form multimer(s) which can be cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYRP ) UNIV ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-481202/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1998;
   misc_binding
                                                        misc_binding
                                                                                                         misc_binding
                                                                                                                                                               misc binding
                                                                                                                                                                                                                    misc binding
                                                                                                                                                                                                                                                                       misc_binding
                                                                                                                                                                                                                                                                                                                           misc_binding
                                                                                                                                                                                                                                                                                                                                                                                  misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9838300-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kool ET
   The present sequence represents an oligonucleotide used in an example of the present invention. The present invention describes a method for Synthesising a selected oligonucleotide (I) having well defined ends. The method comprises: (a) annealing a primer to a single-stranded (ss) circular template to yield a primed circular template, where the template comprises: (i) at least one nucleotide sequence complementary to (I); and (ii) at least one nucleotide effective to produce a cleavage site in the oligonucleotide multimer; (b) combining the primed circular template with at least two types of nucleotide triphosphates and a polymerase enzyme at least two types of nucleotide triphosphates and a polymerase enzyme without the addition of auxiliary proteins to yield a ss oligonucleotide wiltimer complementary to the circular oligonucleotide template, comprising multiple copies of (I); and (c) cleaving the oligonucleotide multimer at the cleavage site to produce (I) having well defined ends.

The method is used for the large-scale synthesis of DNA and RNA oligomers from the mathematic formulation of the large-scale synthesis of DNA and RNA oligomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rolling circle synthesis of oligo:nucleotide(s) - using primed circular template to produce oligonucleotide multimer for cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use, e.g. as probes and diagnostic agents and/or therapeutic agents
                                                                   Synthesis, selection, amplification, circular oligonucleotide, rolling circle synthesis; diagnosis; therapeutic agent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.0%; Score 14; DB 2; Length 49; 63.6%; Pred. No. 1.5e+04;
                                   Oligonucleotide SEQ ID NO:48 from US5174320 Example 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 25, Col 61; 38pp; English.
                                                                                                                                                                                                                                                      95US-00393439.
                                                                                                                                                                                                                                                                                        93US-00047860.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 63.69
Local 14; Conservative
                                                                                                                                                                                                                                                                                                                           (UYRP ) UNIV ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-144278/13.
15-MAY-1998
                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                      23-FEB-1995;
                                                                                                                                                                                                                                                                                        15-APR-1993;
                                                                                                                                                                              US5714320-A.
                                                                                                                                                                                                                  03-FEB-1998
                                                                   Synthesis;
                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                               Kool ET;
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/bound_moiety= "Bound to positions 1 and 40"

*tag= i

98WO-US003784.

/*tag= e /bound_moiety= "Bound to positions 26 to 28"

/bound_moiety= "Bound to position 6 to

*tag=

21.

/*tag= f
/bound_moiety= "Bound to positions 19 to

/bound_moiety= "Bound to positions 1 to

p

tag=

36. .39

/bound_moiety= "Bound to position 49"

*tag=

bound moiety= "Bound to positions 12 to 15"

U

*tag=

*tag=

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The oligomer sequence ID No.46 was used in an example of the invention for synthesising an RNA oligonucleotide, comprising combining a singlestranded circular oligonucleotide template comprising combining a single-of a nucleotide sequence complementary to the sequence of the desired RNA oligonucleotide with at least 2 types of ribonucleotide triphosphate and a polymerase enzyme to yield a single-stranded RNA oligonucleotide multimer complementary to the circular oligonucleotide template, where the RNA oligonucleotide multimer comprises multiple copies of the desired RNA oligonucleotide. The methods can be used for producing RNA oligonucleotides having a specific sequence and well defined ends. The RNA oligonucleotides produced can be used as probes, standards and diagnostic or therapeutic agents. They can be used for modifying the structure or function of a target molecule. They can also be used to cleave disease-associated RNA, DNA or protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Revised record issued on 21-OCT-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.0%; Score 14; DB 2; Length 49; 77.3%; Pred. No. 1.5e+04; rive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 49 BP; 9 A; 14 C; 8 G; 18 T; 0 U; 0 Other;
Example 25; Page 67; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 77.3%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent;
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Gaps ; 0

5; Indels

3; Mismatches

11 GGGCUUUUCUGAAGAGGCGAAA 32

g 8

AAV59251 standard; DNA; 49 BP.

RESULT 35 AAV59251,

3 GGGCTTCACTTCAGAGGAGAAA 24

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3 GGGCTTCACTTCAGAGGAGAA 24

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Circular oligomer sequence ID No.46.

circular; cyclic.

Synthetic.

Key

(first entry)

(revised)

21-OCT-2004 14-DEC-1998

AAV59251;

Location/Qualifiers

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misc_structure
                                                                                                                                                                                                                                                                                      14-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                         misc binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1998,
                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                         Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                            AAV59253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stem_loop
                                                                                                                                            ٣
                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EI.
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                                                                                                                                                                                                            RESULT 37
                                                                                                                                                                                                                        AAV59253
  8886666
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                                                                                                                                                                   원
                                                                                                                                                                                                                                                The oligomer sequence ID No.47 was used in an example of the invention for synthesising an RNA oligomucleotide, comprising combining a single-stranded circular oligomucleotide template comprising at least none copy of a nucleotide sequence complementary to the sequence of the desired RNA oligomucleotide with at least 2 types of ribomucleotide triphosphate and multimer complementary to the circular coligomucleotide template, where the RNA oligomucleotide multimer comprises multiple copies of the desired KNA oligomucleotide multimer comprises multiple copies of the desired coligomucleotide. The methods can be used for producing RNA oligomucleotides produced can be used as probes, standards and diagnostic or therapeutic agents. They can be used for modifying the
                                                                                                                                                                              ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthesis of oligo:nucleotide(s) - using a single-stranded circular oligo:nucleotide template ribonucleotide tri:phosphate(s) and a polymerase to form multimer(s) which can be cleaved.
                                                                                                                                                                                                                                                            a
moiety= "Bound to positions 42 to 46"
                                                                                                                                                                                                                                                                                                              to 27"
                                                                                                                                                                                                                                                                                                                                                     20"
                                                                                                                                                                                                                                                                                                                                                                1. .34
*tag= d
bound moiety= "Bound to positions 37 to 40"
                                                                                                                                                                                                                                                                                                                                                                                                                                 positions 31 to 34"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                       to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= g
/bound_moiety= "Bound to positions 6 to
                                                                                                                                                                                                                                                                                                  *tag= b
'bound_moiety= "Bound to positions 25
                                                                                                                                                                                                                                                                                                                                                     bound_moiety= "Bound to positions 18
                                                                                                                                                     multimeric RNA transcript sequence ID No.47.
                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= e
bound moiety= "Bound to
1. .42
                                                                                                                                                                                                                                                                                                                                                                                                                                                         f
"Cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 25; Page 67; 100pp; English.
                                                                                                                                                                                                                                  Location/Qualifiers
22
GGGCTTTTCTGAAGAGGCGAAA
                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00805631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US003784
                                                              AAV59252 standard; RNA; 49
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                 Д
                                                                                                                                                                                                                                                                                                                                         U
                                                                                                                                                                                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .46
                                                                                                                                                                                                                                                                                                                        .27
                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
'note=
                                                                                                                                                                                                                                                           /*tag=
/bound_
                                                                                                                                                                                                                                                                                                                                         tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYRP ) UNIV ROCHESTER
                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-481202/41.
                                                                                                                                                                                                                                             misc_binding
                                                                                                                                                                                                                                                                                    misc binding
                                                                                                                                                                                                                                                                                                                          misc_binding
                                                                                                                                                                                                                                                                                                                                                                misc binding
                                                                                                                                                                                                                                                                                                                                                                                                       misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc binding
                                                                                                             21-OCT-2004
14-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9838300-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-SEP-1998
                                                                                                                                                                                                       Synthetic.
                                                                                       AAV59252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kool ET;
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/note= "Forms double stranded region with bases 1 to 6 of
AAV59254"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for synthesising an RNA oligonucleotide, comprising combining a single-
stranded circular oligonucleotide template comprising at least one copy
of a nucleotide sequence complementary to the sequence of the desired RNA
oligonucleotide with at least 2 types of ribonucleotide triphosphate and
a polymerase enzyme to yield a single-stranded RNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               = "K28 junction in chronic myeloid leukemia" double stranded region with bases 8 to 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The oligomer sequence ID No.48 was used in an example of the invention
                                                                           Revised record issued on 21-OCT-2004 : Correction to feature table key
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthesis of oligo:nucleotide(s) - using a single-stranded circular oligo:nucleotide template ribonucleotide tri:phosphate(s) and a polymerase to form multimer(s) which can be cleaved.
structure or function of a target molecule. They can also be used cleave disease-associated RNA, DNA or protein
                                                                                                                                                                                                                            ;
                                                                                                                                                                DB 2; ... 1.5e+04; 5; Indels
                                                                                                                            49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= b
function= "Catalytic_domain"
                                                                                                                                                                          Score 14; DB 2
Pred. No. 1.5e+3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monomeric ribozyme sequence ID No.48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 25; Page 67; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                          GGGCTTCACTTCAGAGAAA 24
                                                                                                                                                                                                                                                                                                         /bound_moiety= "
/note= "Forms do
                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US003784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-00805631
                                                                                                                                                                          56.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV59253 standard; RNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ъ
                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39. .44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
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                                                                                                                                                                                                    Local Similarity
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Page 18

us-10-788-779-5.rng

24

GGGCTTCACTTCAGAGGAGAAA

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multimer complementary to the circular oligonucleotide template, where the RNA oligonucleotide multimer comprises multiple copies of the desired RNA oligonucleotide. The methods can be used for producing RNA oligonucleotides having a specific sequence and well defined ends. The RNA oligonucleotides produced can be used as probes, standards and diagnostic or therapeutic agents. They can be used for modifying the structure or function of a target molecule. They can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              multimer, comprising multiple contiguous copies of a repeated oligonucleotides. The detectably labelled oligonucleotide multimer is useful for detecting a target molecule. Oligonucleotide multimers may be produced in sufficient quantity to be useful for diagnostic and medical applications. The multimers are useful for affinity labelling of proteins, and for signal amplification in highly sensitive affinity a faster, cheaper and sequence identification applications. The method provides a faster, cheaper and simpler way for large-scale production of DNA and RNA oligomers and multimers. The incorporation of labels enables the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligonucleotide multimers to be useful in diagnostics and medicine. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence represents an oligonucleotide used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New detectably labelled oligonucleotide multimer, comprising multiple contiguous copies of a repeated oligonucleotide - useful for detecting target molecules in diagnosis and medicinal applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes a detectably labelled oligonucleotide
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multimer; probe; diagnosis; synthesis; detection; polymerase; ss.
                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                       Score 14; DB 2; Length 49;
Pred. No. 1.5e+04;
                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                   Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
                                                                                                                              cleave disease-associated RNA, DNA or protein
                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 25; Page 70; 103pp; English
                                                                                                                                                                                                                                                                                                    11 GGGCUUUCUGAAGAGGCGAAA 32
                                                                                                                                                                                                                                                                               3 GGGCTTCACTTCAGAGGAGAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA oligonucleotide SEQ ID NO:50.
                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                       56.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US016776,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-00910632.
                                                                                                                                                                                                                                                                                                                                                                                                        AAX30039 standard; RNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYRP ) UNIV ROCHESTER
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-181062/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9909216-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX30039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kool ET;
                                                                                                                                                                                                                                                                                                                                                                       RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The 1
                                                                                                                                                                                                                                                                                                                                                                                        AAX30039
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The invention relates to a method for synthesising an RNA cligonuclectide template with at least two types of ribonuclectide template with at least two types of ribonuclectide template with at least two types of ribonuclectide triphosphate and a polymerase enzyme to yield a single-stranded RNA cligonuclectide multimer complementary to the circular oligonuclectide RNA oligonuclectide multimer comprises multiple copies of the desired RNA oligonuclectide with well-defined ends. The method is useful for synthesising an RNA oligonuclectide with well-defined ends. The circular oligonuclectide is introduced into the cell using direct injection, allocation cation-mediated delivery. The method is useful for treating bacterial and/or viral infections in mammals, particularly drug resistant infections and for producing double stranded DNA oligomers. The method is performed in the absence of an oligonuclectide primer, or without the addition of auxiliary proteins. This sequence represents an
                                                                                                                                                                                                                                                     RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase; electroporation; calcium phosphate treatment; lipid-mediated delivery; cation-mediated delivery; bacterial infection; viral infection; drug resistant infection; double stranded DNA oligomer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthesizing RNA oligonucleotide involves combining single-stranded circular oligonucleotide, ribonucleotide triphosphate and polymerase enzyme to yield desired RNA complementary to circular oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.0%; Score 14; DB 10; Length 49; 63.6%; Pred. No. 1.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         addition of auxiliary proteins. This sequence repres oligonucleotide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 25; SEQ ID NO 47; 78pp; English.
GGGCUUUCUGAAGAGGCGAAA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGGCTTCACTTCAGAGGAGAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-00047860.
95US-00393439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2000; 2000US-00569344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00805631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-2001; 2001US-00997931
                                                                                                        ADC65914 standard; RNA; 49
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
                                                                                                                                                                                                                     RNA oligonucleotide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYRP ) UNIV ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-755141/71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 JS2003087241-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1993;
23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1997;
                                                                                                                                                                                 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                            ADC65914;
             11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         template.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kool
                                                                      RESULT 39
                                                                                         ADC65914
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GGCCUUUUCUGAAGAGGCGAAA 24

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Gaps

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56.0%; Score 14; DB 2; Length 49; 63.6%; Pred. No. 1.5e+04; ive 3; Mismatches 5; Indels

63.68;

Query Match Best Local Similarity 63.6°

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oligonuclectide, comprising combining a single-stranded circular cligonuclectide, comprising combining a single-stranded circular cligonuclectide template with at least two types of ribonuclectide template with at least two types of ribonuclectide cripopal polymerase enzyme to yield a single-stranded RNA oligonuclectide multimer comprises multiple complementary to the circular oligonuclectide multimer comprises multiple copies of the desired RNA oligonuclectide. The method is useful for copies of the desired RNA oligonuclectide with well-defined ends. The circular oligonuclectide is introduced into the cell using direct injection, calcitum phosphate treatment, lipid-mediated delivery, or cation-mediated delivery. The method is useful for treating bacterial and/or viral infections in mammals, particularly drug resistant infections, and for producing double stranded DNA oligoners. The method is performed in the absence of an oligonucleotide primer, or without the addition of auxiliary proteins. This sequence represents an cligonucleotide used in the method of the invention.
                                                                                                                                                                                                 RNA oligonucleotide synthesis, ribonucleotide triphosphate; polymerase, electropozation; calcium phosphate treatment; lipid-mediated delivery; cation-mediated delivery; bacterial infection; viral infection; drug resistant infection; double stranded DNA oligomer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthesizing RNA oligonucleotide involves combining single-stranded circular oligonucleotide, ribonucleotide triphosphate and polymerase enzyme to yield desired RNA complementary to circular oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.0%; Score 14; DB 10; Length 49; 63.6%; Pred. No. 1.5e+04; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for synthesising an RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 25; SEQ ID NO 48; 78pp; English
                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-1993; 93US-00047860.
23-FEB-1995; 95US-0033439.
26-FEB-1997; 97US-00805631.
11-MAY-2000; 2000US-00569344.
                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-2001; 2001US-00997931.
                                       ADC65915 standard; RNA; 49
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.6
Matches 14; Conservative
                                                                                                                                                            RNA oligonucleotide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYRP ) UNIV ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-755141/71
                                                                                                                                                                                                                                                                                                                                             US2003087241-A1.
                                                                                                                  18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2003
                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                             ADC65915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kool ET;
RESULT 40
                    ADC65915
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3 GGGCTTCACTTCAGAGAAA 24 11 GGGCUUUUCUGAAGAGGCGAAA 32 ઠે

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Gaps

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Search completed: November 18, 2005, 11:52:27 Job time : 174.148 secs

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AZ792764 2M0045N21 CG72173 1119075A1 BX563109 BX5650109 AIS97737 UU91b01.09 BX664190 Arabidops BX664190 Arabidops AZ776620 2M0010823 CG784583 RRR727 Ba AI446300 U131805.X BH629703 1007075E0 BH911440 SALK 0687 AU105888 AU105888 AZ992198 2M0276E17 BI562246 603254963 BZ663146 SALK 0266 AIS72884 WF545065.X AZ392172 BALK 0266 AZ392172 AM0214114 AAS3777 mq76409.R

Title: Perfect score:

Sequence:

nucleic

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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AF039758 Human Homo sapiens genomic clone ET27.9, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 50).

Whitmore, S.A., Crawford, J., Apostolou, S., Eyre, H., Baker, E., Lower, K.M., Settasatian, C., Goldup, S., Seshadri, R., Gibson, R.A., Mathew, C.G., Cleton-Jansen, A.M., Savoia, A., Pronk, J.C., Auchbarland, A.D., Doggett, N.A., Sutherland, G.R. and Callen, D.F. Construction of a high-resolution physical and transcription map of chromosome 16q24.3: A region of frequent loss of heterozygosity in sporadic breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 King William Rd, North Adelaide, SA 5006, Australia Email: swhitmor@pulse.mad.adelaide.edu.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Cytogenetics and Molecular Genetics Womens and Childrens Hospital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.4; DB 8;
Pred. No. 2.7e+04;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .50
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
AZ818575
CN488991
CN44938
AZ792764
CG723173
AIS54190
AIS64190
AZ764190
AZ76
                                                                                                                                                                                                                           AU105888
AZ992198
BI562246
BZ663146
AI973284
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/clone="ET27.9"
/clone_lib="Human"
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                                               8054668648848
   Class: unknown.
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BH853060 SALK 0759
CL656736 PRIDÎZ7D
AA074188 2182902.7
AA076656.6 Seg6d66.8
BE379892 SALK 1141
BF322803 maa33h03.
AA479970 VU18b11.8
BH809976 SALK 0368
BH840479 KOU1991-3
AU105696 AU105696
WB8034 M£6804.11
CL214736 MO73D06 G
BZ289408 SALK 0228
AU107432 AU107432
AU107433 AU107434
CU4889991 MÄGW20181
BI388654 BST-CD34N
BI38864 SALK 0228
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AU247370 AU247370
BZ353192 SALK_1199
                                                                                                November 18, 2005, 11:22:09; Search time 1195.82 Seconds (without alignments) 795.779 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                        34239544 segs, 19032134700 residues
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AA074188
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BH840479
AU105696
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AU247370
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Gapop 10.0 , Gapext 1.0
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gb_htc:;
gb_est4:;
gb_est4:;
gb_est6:;
gb_gss1:;
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seq length: 50
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No. Result

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/clone="IMACE:383474"
/lab_host="DH10B (ampicillin resistant)"
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/db_xref="GDB:1291731"
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Matches 18; Conservative
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                                                                    BH853060 40 bp DNA linear GSS 13-JUN-2002 SALK 075945.23.15.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 075945.23.15.x, genomic
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/clone="SALK 075945.23.15.x"
/clone="lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                      Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Wagnoliophyta; eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.

(bases 1 to 40)
Alonso,J.M., Leisse,T.J., Barasias,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Bcker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 49)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g30890.
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Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis Genome
Unpublished (2001)
Contact: Oseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: TDNA tagged.
Location/Qualifiers
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CL656736
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CL656736/c
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The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty.
Fossible reversed clone: similarity on wrong strand
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:54126"
/clone lib="Mixed stage fosmid library of P. pacificus
var. Cālifornia"
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Control of the contro
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Hillier,L. Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strāin="California"
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Homo sapiens
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Best Local Similarity
Matches 18; Conserv
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Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center.
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 25
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 35 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
AW246497 35 bp mRNA linear EST 07-JAN-2000 2821639.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821639 3',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 35)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 281639.5prime
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 56.0%; Score 14; DB 1; Length 43; Best Local Similarity 77.3%; Pred. No. 1.2e+05; Matches 17; Conservative 0; Mismatches 5; Indels
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/tissue type="small cell carcinoma"
/cell line="MGC3"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Homo sapiens"
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High quality sequence stop: 25.
Location/Qualifiers
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GGCTTCACTTCAGAGGAGAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGTACACTCCGGATGAGAA 22
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AW246497/c
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AA908626 46 bp mRNA linear EST 24-AUG-1998 og86d06.81 NCI_CGAP_Ov8 Homo sapiens cDNA clone IMAGE:1455179 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="serous adenocarcinoma"
/lab host="NH10B"
/clone lib="NCI CGAP_Ov8"
/note="Organ: ovary; Vector: pCMV-SPORT4; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Life Technologies catalog #:
insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis it (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea Lo 46) Lorda http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                             Length 35;
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Unpublished (1997)
Contect: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Trace considered overall poor quality
Insert Length: 696 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                          55.2%; Score 13.8; DB 2; 72.0%; Pred. No. 1.4e+05; ive 0; Mismatches 7;

    .46
    /organism="Homo sapiens"

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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                              CTGGGCTTCACTTCAGAGAAAA 25
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BZ379892
BZ379892.1 GI:25472195
GSS.
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                                                                                                                                                                          Query Match
Best Local Similarity 72.09
Matches 18; Conservative
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/sex="female"
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                                                                    MGI:1455092
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AUTHORS
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AA479970
LOCUS
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Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF322803 1 NCI_CGAP_LilO Mus musculus cDNA clone IMAGE:3812980 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="SALK_114176.40.35.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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              Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicacea; Arabidopsis.

1 (bases 1 to 46)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                   Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Arabidopsis thaliana"
Arabidopsis thaliana (thale cress)
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Other ESTs: maa33h03.y1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic_DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: TDNA tagged.
Location/Qualifiers
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AA479970 31 bp mRNA linear EST 08-AUG-1997 zv18b11.gl Soares NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753981 3' similar to SW:CAIH_HUWAN P39060 COLLAGEN ALPHA 1(XVIII) CHAIN ;,
                                                                                                                                                                                                                                                                                                                                                                        /dev stage="10 weeks"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Li10"
/note="Organ: līver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Library constructed by Life
Technologies."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mamalais; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dasas 1 to 31)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Kacaba,T., Lacy,M., Leh,N., Lehnon,G., Marra,M., Martin,J.,

Moore, B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,

White,Y., Wylie,T., Waterston,R. and Wilson,R.

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:753981"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab host="Math.08"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: esc@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL ; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.5e+05;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 55.2%; Score 13.8; DB 2; Best Local Similarity 72.0%; Pred. No. 1.5e+05; Matches 18; Conservative 0; Mismatches 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5976854"
                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3812980"
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                                                                                                                            Seg primer: -40UP from Gibco.
Location/Qualifiers
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Query Match

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ORIGIN

RESULT 10 BH809976/c DEFINITION

ORGANISM

REFERENCE

JOURNAL

COMMENT

TITLE

FEATURES

ACCESSION VERSION KEYWORDS SOURCE

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BH840479 29 bp DNA linear GSS 30-MAY-2002 KG01991-3prime Drosophila melanogaster P{SUPor-P} P element insertion lines Drosophila melanogaster genomic Sequence recovered Erom 3' end of P element, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insertion lines"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P{SUPOR-P} P-element transposon insertion. The resultant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://www.fruitfly.org/about/methods/inverse.pcr.html."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
| fmol_trype="genomics DNA"
| db xref="texon:7227"
| clone_lib="Drosophila melanogaster P{SUPor-P} P element
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The P element insertion position is base 1 in the 29 bases. This insertion position refers to the first base of the 8 base target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levis, R., Hoskins, R., Liao, G., Mozden, N., Tsang, G., He, Y., Karpen, G., Bellen, H., Rubin, G. and Spradling, A.
The Berkeley Drosophila Genome Project Gene Disruption Project Unpublished (2001)
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
University of California, Berkeley
Fax: 5106439947
                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Mecazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
(bases 1 to 29)
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Pred. No. 2.1e+05;
0; Mismatches 6;
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Location/Qualifiers
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       34 CTTAACTTAAGAGCACAAAA 15
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73.9%;
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KEYWORDS
SOURCE
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHW, pregnant uterus NbHPU, and fetal heart NbHHJ9W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools 340488-345479, and 484488-489479."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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dadtinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is single pass sequence recovered from the left border of
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                                                                                                                                                                                                                                                                                                                                    54.4%; Score 13.6; DB 1; Length 31; 80.0%; Pred. No. 1.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 6379
Email: ecker@salk.edu
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/mol_type="genomic DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Location/Qualifiers
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Best Local Similarity 80.0
Matches 16; Conservative
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Gaps

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6 CTTCACTTCAGAGGAGAAAA 25

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organism="Mus musculus"
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Best Local Similarity 76.2<sup>†</sup>
Matches 16; Conservative
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                                                                                                                                                                                                Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Basil: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Orar, T. Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO. Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W88034 mf68d04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:419431 5' similar to SW:AGRI_RAT P25304 AGRIN
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
Unpublished (1996)
Contact: Marxa M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Cloubs574"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.6%; Score 13.4; DB 1; Length 50; 93.3%; Pred. No. 2.3e+05; ive 0; Mismatches 1; Indels
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Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 93.3
Matches 14; Conservative
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/clone lib="Scares mouse embryo NbME13.5 14.5"
/clone lib="Scares mouse embryo NbME13.5 14.5"
/noce="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site=1: Not 1; Site=2: Eco R1; Ist strand cDNA
was primed with a Not 1 - oligo(dr) primer [5'
rgrrAccaarcrgaAgragGagGcGcGcGGGAAATTTTTTTTTTTTTTTTTT
T 31; on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [tcotal RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco R1 adaptors (Pharmacia), adgested with Not I and
cloned into the Not I and Eco R1 sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M. Fatima Bonaldo.
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'http://genetrap.gsf.de/project/web new/database/result clone.html?
clone.id=M073D06' Es cell line harboring insertion mutation of target gene is available at:
'http://genetrap.gsf.de/project/web new/order_clones/howtoorder.html'.Inhouse Sequence Identifier: 09460
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47 bp mRNA linear GSS 30-JUN-2004 M073D06 GGTC Gene Trap Library GV04C04 Mus musculus cDNA clone CL214736
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Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F., Arnold,H.H., Schnutgen,F., Murst,W., Von Melchner,H. and Ruiz,P. A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
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                                                                                                                                                       tissue type="embryo"
/dev stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
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/clone="M073D06"
                                                              /db xref="taxon:10090"
/clone="IMAGE:419431"
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/mol_type="mRNA"
/strain="C57BL/6J"
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/strain="129 Sv"
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                                                                                                                                   sex="unknown"
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ORIGIN

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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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AU107433 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNG14512, mRNA sequence.
50 bp mRNA linear EST 28-JAN-2004
AU107432 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNG1157, mRNA sequence.
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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1 (bases 1 to 50).

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

BERO Rep. 2 (5), 388-393 (2001)
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Department of Virology
Institute of Medical Science, University of Tokyo
A-6-1, Shirokanda, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukidins.u-cokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
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/db_xref="texon:9606"
/dbone="th911157"
/clone=lib="Sugano Homo sapiens cDNA library"
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/organism="Homo sapiens"
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[ bases 1 to 48]
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="SALK 022805.55.00.x"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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                  /cell_type="Embryonic stem cell"
/cell_line="ES cells 12952 (formerly 129/SvPas)"
/clol=lih="GGTC Gene Trap Library GV04C04"
/note="Vector: ROSAbetageo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Joseph R. Bcker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Flat: 858 453 4100 x1752
Fax: 858 558 658 659
Email: ecker@salk.edu
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                                                                                                                                                                         Score 13; DB 9; Length 47;
Pred. No. 3.5e+05;
0; Mismatches 5; Indels
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/ecotype="Col-0"
/db_xref="taxon:3702"
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Location/Qualifiers
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1 Similarity 76.2%;
16; Conservative
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Unpublished (2001)
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Local Similarity 76.2.
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RESULT 16 AU107432/c

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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yeuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitcom-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a S.-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CN488991 50 bp mRNA linear EST 24-MAY-2004 Mdfw2018i03.yl Mdfw Malus x domestica cDNA clone Mdfw2018i03 5',
Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
ENERG Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                            1. .50
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/mol_type="mRNA"
/mol_traxon:9606"
/clone="LNG14512"
/clone="LNG14512"
/clone_lib="Sugano Homo sapiens cDNA library"
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Pred. No. 3.5e+05;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                          46 GGGCTTCCCTGGTGCGGAGAA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNG15774, mRNA sequence.
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Best Local Similarity 76.2
Matches 16; Conservative
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Matches 16; Conserv
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| 1. .41 | /organism="Arabidopsis thaliana" | /organism="Arabidopsis thaliana" | /organism="Arabidopsis thaliana" | /organism="Col-0" | /organism="State" | /organism=
        BZ288847 linear GSS 24-OCT-2002 SALK 022237.36.30.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 022237.36.30.x, genomic
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Ablonso,J.W., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
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adatrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At1916100 and 300 bases of the 5' end of At1916110. Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute Genomic Analysis Laboratory (SIGnAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 678 678
Email: ecker@salk.edu
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                                                                                                                                                                                                                                                                             thaliana (thale cress)
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Unpublished (2001)
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                            between the single-stranded library and the PCR products as carried out for 44 hours at 30°C. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DHIOB cells to generate the normalized library. The total number of clones with insert was 9x10°6 cfu.

Background of empty clones was less than 1%"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST-CD34NN-022 cDNA Library from human CD34+ stem/progenitor cells Homo sapiens cDNA 3', mRNA sequence.
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/cell_type="CD34+ stem/progenitor cells"
/clone_lib="cDNA Library from human CD34+ stem/progenitor
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m GLGI} method"
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1 (Dases 1 to 35)
Zhou,G., Chen,J., Lee,S., Terry,C., Rowley,J.D. and Wang,S.M.
The pattern of gene expression in human hematopoietic CD34+
stem/progenitor cells
Unpublished (2001)
were used as a driver for normalization. Hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Chicago Medical Center
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Tel: 773-702-6788
Fax: 773-702-3002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.2%; Score 12.8; DB 4; Length 35; 70.8%; Pred. No. 4e+05; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.0%; Score 13; DB 7; Length 50; Best Local Similarity 76.2%; Pred. No. 3.5e+05; Matches 16; Conservative 0; Mismatches 5; Indels
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 GCTTCTCCTCAGATGTGATAA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Best Local Similarity
Matches 17; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL

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DEFINITION BI388654/c

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ORIGIN

FEATURES

AUTHORS

RESULT 21 BZ288847

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Length 41;

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AZ818575 48 bp DNA linear GSS 20-FEB-2001 2M0088M10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0088M10 R, genomic survey sequence.
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/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana TDNA insertion lines ach of was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                GSS 14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases i to 47)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Salonso,J.M., Zimmerman,J. and Ecker,J.R.
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                            SALK 119906.25.15.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_119906.25.15.x, genomic survey sequence.
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m TDNA}.
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                                                                     Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Joseph R. Bcker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute fer Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Fax: 858 558 6379
                                                                                                                        Indels
                                                                     51.2%; Score 12.8; DB 1;
87.5%; Pred. No. 4.2e+05;
iive 0; Mismatches 2;

    .47
    /organism="Arabidopsis thaliana"

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/ecotype="Col-0"
/db_xref="taxon:3702"
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/clone_lib="FL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BZ353192.1 GI:24944054
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                                                                                                                                                                                                                     ACTTCGGAGGAAAAA 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: TDNA tagged
                                                                                                                                                                            10 ACTTCAGAGGAGAAAA
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                                                                                                                        Conservative
                                                                                            Best Local Similarity
Matches 14; Conserv
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KEYWORDS
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AUTHORS
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/clone="SALK 02393.41.95.x"
/clone="SALK 02393.41.95.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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contact:Tadashi Takamizo (takamizo@affrc.go.jp)
National Institute of Livestock and Grassland Science, Nishinasuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poeae; Lolium.
1 (bases 1 to 44)
                                                                Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 858 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
This is single pass sequence lies within 300 bases of the 5' end of
Atlgl6100 and 300 bases of the 5' end of Atlgl6110.
Class: TDNA tagged.
Location/Qualifiers
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AU247370 FL Lolium multiflorum CDNA clone FL031A04-5, mRNA
A Sequence-Indexed Library of Insertion Mutations in the
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Higasiakada 388-5, Nishinasuno, Tochigi 329-2742, Japan Tel: 81-287-37-6755
Fax: 81-287-37-6755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2004)
Contact: Seishi Ikeda
Japan Grassland Farming Forage Seed Association (JFSA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.2%; Score 12.8; DB 8; Length 41; 70.8%; Pred. No. 4.2e+05; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/ecotype="Col-0"
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Lolium multiflorum
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/db_xref="taxon:4521"
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Location/Qualifiers
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AU247370
AU247370.1 GI:46504639
                         Arabidopsis Genome
Unpublished (2001)
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Best Local &
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CN488991.1 GI:46602340
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. (bases 1 to 48)

E. (bases 1 to 48)

S. Dum, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

E. Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0088 row: M column: 10
Seq.primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
High quality sequence stop: 48.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="UUGC2M0088M10"
                                                                                 Mus musculus (house mouse)
                               AZ818575.1 GI:12988483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                Mus musculus
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Matches 14; Conserv
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CN488991 50 bp mRNA linear EST 24-MAY-2004 Mdfw2018i03.yl Mdfw Malus x domestica cDNA clone Mdfw2018i03 5', mRNA sequence.

LOCUS

CN488991

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//doing lib="Mdfw"
//doing lib="Mdfw]
//doing lib="
                                                                                                                                                                                                            1 (bases 1 to 50)
Korban, S., Vodkin, L., Liu, L., Gasic, K., Gonzales, O., Hernandez, A., Aldwinckle, H., Mannoy, M., Carroll, N., Goldsbrough, P., Orvis, K., Clifton, S., Pape, D., Marra, M., Hillier, L., Martin, J., Wylle, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Ronko, I., Asgazreishvili, R., Kennedy, S., Waterston, R. and Wilson, R. Thoublished (2004)
                                 Malus x domestica
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Rosales, Rosaceae, Maloideae, Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
Library materials provided by: Schuyler S. Korban Library
constructed by: A. Hernandez / K. Gasic Library sequenced by:
Washington University Genome Sequencing Center
WashU EST name: aaf69e02.y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B ampicillin resistant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Schuyler S. Korban
Apple Functional Genomics grant - NSF 0321702
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="Mdfw2018i03"
Malus x domestica (cultivated apple)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 50.
Location/Qualifiers
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LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL COMMENT

FEATURES

REFERENCE

CR449386/c

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Laboratory Mouse DNA Resources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared but was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                         Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
Musculla, Lobases 1 to 24)
Dunn, D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longarere,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.,
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 0045 row: N column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0045N21"
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Location/Qualifiers
                                                                                     Mus musculus (house mouse)
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                             AZ792764.1 GI:12937031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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between the single-stranded library and the PCR products was carried out for 44 hours at 30C. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B cells to generate the normalized library. The total number of clones with insert was 9x10<sup>6</sup> of cfu. Background of empty clones was less than 1%"
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/dev stage="tailbud (stage 28-30)"
/lab_host="Escherichia coli DH10B."
/clone=lib="XGC-tailbud"
/note="Vector: pCS107; Site 1: ECORI; Site 2: NotI; cDNA
was oligo dT primed from sug of poly A+ RNA from tailbud.
ECORI-NotI cut cDNA was then ligated into pCS107 with
ECORI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CR449386 CC-tailbud Xenopus tropicalis cDNA clone TTbA045i16 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 50)
Crohing, M.D.R., Ashurst, J.L., Taylor, R., Garrett, N. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (2004)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TTDA045i16.plkSP6
This sequence is from a Xenopus Gene Collection (XGC) library
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
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CR449386.1 GI:48974973
                                                                                                                                                                                                                                                                                                                                                                      8 TCACTTCAGAGGAGAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                           19 rcacarcreaddadaa 34
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                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 14; Conserv
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DEFINITION

RESULT 28 AZ792764

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ORIGIN

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Ph.D., CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WI-GAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIS97737 10 CGAP Gas4 Homo sapiens CDNA clone IMAGE:2258377 3' similar to TR:Q08805 Q08805 SALIVARY PROLINE-RICH PROTEIN L ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="country: Zimbabwe; EST from adult gut infected with
                                                                                                                                                                                                                                                                                                                                                        'n
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Tse97el0_qlc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans adult infected
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                    University of Wales,
Bangor LL57 2UW
All clones with suffix glc are reverse primer reads starting at
end of the cDNA all plc reads are from
the 3' end.
          putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                  Trust Genome Campus
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                                                                                                                            Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome C
Hinzton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
       norsitans morsitans and expression analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12.6; DB 5
Pred. No. 5e+05;
); Mismatches
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Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualiffers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/sub_species="morsitans"
                                 response genes
Genome Biol. 4 (10), R63 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'db_xref="taxon:37546"
                                                                                                                                                                                                                                                        Prof. M.J.Lehane
School of Biological Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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78.9%;
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Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pBlueScript backbone); Site_I: BamHI; Site_2: BgIII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AAA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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                                                                                                                                                                                                                                              Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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1. (bases 1 to 34)

1. (bases 1 to 34)

Lehane,M.J., Asoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina
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SA bp mRNA linear EST 14-OCT-200
BX569109 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse97e10_glc, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence. Plate: 1119075 row: A column: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mod_type="genomic DNA"
/mod_type="genomic DNA"
/mod_type="genomic DNA"
/db_xref="taxon:457"
/db_xref="leaf"
/dev stage="leaf"
/dev stage="adult"
/lab_nost="DHIDB"
/note="Organ: leaf; Vector: RescueMu (engines)
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                                                                                                                                                                                                                                                                                                                                                                          855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                         Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Zea mays"
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BX569109.1 GI:33437048
                            GI:37758756
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                         CG723173.1
                                                                             Zea mays
                                                                                                       Zea mays
     CG723173
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BX569109/c
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Arabidopsis thaliana (thale cress)
                                                                 /mol_type="genomic_DNA"
/strain="Columbia 0"
Location/Qualifiers
                                                                                                                                                                            /ecotype="Col-0"
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Matches 15; Conserv
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Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plank Mol. Biol. 53 (1-2), 247-259 (2003)
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Arabidopsis thaliana T-DNA flanking sequence GK-598D09-021211,
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                                                                                                                                                 /lab_host="DHIOB"
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/clone_lib="NCI_CGAP_Gas4"
/note="Corgan: stomach; Vector: pCWV-SPORT6, Site 1: Sal1;
Site_2: Not!; Cloned unidirectionally. Primer: Öligo dT: Average insert size 1.69 kb. Life Technologies catalog #:
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
                                                                                    /clone="IMAGE:2258377"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
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12874060
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                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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BX654190.1 GI:37610578
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Best Local Similarity 78.9
Matches 15; Conservative
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Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Kocln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g21990. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.
                                                                                                                                                                                                                                                                            /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AN537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion.
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Arabidopsis thaliana T-DNA flanking sequence GK-598D09-021211,
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                                                                                                                    /db xref="taxon:3702"
/clone="GK-598D09-021211"
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'organism="Arabidopsis thaliana"
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2M0010E23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0010E23 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
                                                                                                                                                                                                     /clone="GK-598D09-021211"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Wouse 10kb plasmid UUGC1M library"
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Pred. No. 5.1e+05;
0; Mismatches 4; Indels
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                              organism="Arabidopsis thaliana"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 $td Brror: 0.00
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Seq primer: CGTTGTAAAACGACGCCAGT
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                                                                                                                                   /mol_type="genomic_DNA"
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/db xref="taxon:3702"
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/strain="C57BL/6J"
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High quality sequence stop: 40.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gilfalfalgalfalpal2072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://baygenomics.ucsf.edu/
Unpublished (2001)
On Mar 1, 2004 this sequence version replaced gi:38157143.
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
Generation ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=RRR727
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Library pGTOLxf Mus musculus cDNA,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/note="Vector: pGT0Lxf"
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Pred. No. 5.1e+05;
); Mismatches 4;
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RRR727 BayGenomics Gene Trap
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/strain="129 ola"
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1 Similarity 78.9%;
15; Conservative (
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Matches 15; Conserv
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/laminost-incorp.
/clone lib="1007" - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.isatate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII; and ligated to form circular plasmids. DH108 cells were transformed and then screened on LB plates with ampicillin."
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Alonso J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Mrabidopsis Genome
Unpublished (2001)
Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                         Department of Bloiogical Sciences
Stanford University
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Bmail: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007075 column: 36
Class: transposon-tagged.
Location/Qualifiers
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Pax: 858 558 6379
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Mou_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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/dev_stage="adult"
/lab_host="DH10B"
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BH911440
LOCUS
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Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         рньду/03
1007075E03.2EL xl 1007 - RescueMu Grid H Zea mays genomic, genomic
survey sequence.
                                                                                                                                                                                                                                   AI446300 46 bp mRNA linear EST 09-MAR-1999 tj31g05.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2143160 3' similar to gb:M5937I TYROSINE-PROTEIN KINASE RECEPTOR ECK PRECURSOR
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/tissue_type="adenocarcinoma"
/lab host="DH10B"
/clone_lib="NCI_CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sal1; Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to /bases 1 to /bases 1 to /base 1 to /b
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Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
      24
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                                                              CTTCCCATCTGAGGAGGAA 22
                                                                                                                                                                                                                                                                                                                                 (HUMAN);, mRNA sequence.
AI446300
AI446300.1 GI:4294243
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          CTTCACTTCAGAGGAGAAA
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Matches 15, Conservative
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AZ992198 27-APR-2001
2M0276E17R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0276E17 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (basea I to 20)

Dunn, D., Aoyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Lengdri. 10000 Std Error: 0.00
Plate: 0276 row: E column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:10090"
/clone="UUGC2M0276E17"
                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
  43 GGGTGTCTTCAGAGCAG 25
                                                                                                                                                                                                                                              AZ992198.1 GI:13863425
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                       Mus musculus
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                              g
                                                                                                                                  /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecorype="Col-0"
/db xref="taxon:3702"
/db xref="taxon:3702"
/clone="SALK 068707.30.80.x"
/clone="SALK 068707.30.80.x"
/clone="Farabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.htm!"
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU105888 Sugano Homo sapiens CDNA library Homo sapiens cDNA clone
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S., Okubo,K.,
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                      This is single pass sequence recovered from the left border of TDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/db_xref="taxon:9606"
/clone="CAS03170"
/clone_lib="&ugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.4%; Score 12.6; DB 8; Length 47; Best Local Similarity 78.9%; Pred. No. 5.3e+05; Matches 15; Conservative 0; Mismatches 4; Indels
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    .50
    /organism="Homo sapiens"

                                                                   Class: TDNA tagged.
Location/Qualifiers
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AU105888.1 GI:13555409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yutaka Suzuki
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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Best Local Similarity 78.9%
warches 15; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil #4732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
/sex="Female" | Jab host-"B. coli strain XL10-Gold, T1-resistant, F-" | Jab host-"B. coli strain XL10-Gold, T1-resistant, F-" | /clone lib="Mouse 10kb plasmid UUGC2M library" | /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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3 GGGCTTCACTTCAGAGGAG 21

Search completed: November 18, 2005, 21:12:46 Job time : 1198.82 secs

a

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CTGGGCTTCACTTCAGAGGAGAAAA
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                                                                            November 18, 2005, 00:26:13; Search time 48.5741 Seconds (without alignments) 842.154 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 4
Sequence 4
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-396-196G-50969
US-09-396-196G-52946
US-09-396-117350
PCT-US96-11445-19
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US-09-396-1966-113292
US-08-353-372A-28
US-08-353-372A-28
US-08-350-430A-19
US-08-316-246
US-08-910-632-48
US-08-910-632-48
US-08-910-632-48
US-08-910-632-48
US-08-910-631-48
US-08-805-631A-47
US-08-805-631A-48
US-08-805-631A-48
US-08-805-631A-48
US-09-569-344-47
US-09-569-344-47
US-09-569-344-48
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US-08-388-029A-60
US-08-659-251-19
                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                   1202784 segs, 818138359 residues
                                                                                                                                  US-10-788-779-5
25
1 CTGGGCTTCACTTCAGAGGAGAAAA 25
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Maximum Match 100%
Listing first 45 summaries
                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0 Maximum DB seq length: 50
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                                                     OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                   Searched:
                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
No.
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Appli App App App Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Appl Ap		0;
22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		Gaps
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US-09-230-288-5 US-08-943-731-239 US-08-943-731-239 US-09-396-1966-1967-13674 US-09-396-1966-64443 US-09-396-1966-64443 US-08-396-1966-64567 US-08-160-670A-19 US-08-160-670A-19 US-08-546-969-36 US-09-547-267-36 US-09-331-260-58 US-09-331-260-58 US-09-331-260-58 US-09-142-138-3 US-09-582-660-3	ALIGNMENTS US/07989160 CHRISTINE JOHN HUGH HUGH HUGH DISEASE-ASSOCIATED MUTATIONS SS: & COCKFIELD STREET, Suite 510 ST	Score 25; DB 1; Pred. No. 0.0075; 0; Mismatches 0;
W W W W W W W W W W W W W W W W W W W	Ation US/07989160 NN: NMAN, CHRISTINE NMAN, JOHN KINS, HUGH STAWEIG, ANTHONY CON: DISEASE-ASS COND: DISEASE-ASS ADDRESS: 10 DISEASE-ASS HIVE & COCKFIELD TATE STREET, SUIT CHOUSE OF COMPANIES AND DATA: 11 DISC-1993 TIN DATA: TON DATA: TO	100.0%; 100.0%; tive
######################################	NO N	100 Similarity 100 5; Conservative
	SULT 1 Sequence 5, Applicat Patent No. 542923 GENERAL INFORMATION APPLICANT: SEIDM APPLICANT: RESEDM APPLICANT: RATKI APPLICANT: ROSEN TITLE OF INVENTION TITLE OF INVENTION WHEBER OF SEQUENC CORRESPONDENCE AD ADDRESSEE: LAH STREET: 60 STA CITY: BOSTON STATE: MASSACH CONFUTER: MASSACH COMPUTER: LAH STATE: MASSACH COMPUTER: LAH STELEY APPLICATION TITLE OF INVENTION COMPUTER: LAH ACTORNEY ASCI CURRENT APPLICATION FILING DATE: 1 CLASSIFICATION NUM FILING DATE: 1 CLASSIFICATION NUM FILING DATE: 1 CLASSIFICATION TELEFAX: (617) INFORMATION FOR SEQ SEQUENCE CHARACTE LENGTH: 25 DASS TYPE: MOLECULE TYPE: COPPLICATION TELEFAX: (617) INFORMATION FOR SEQ SEQUENCE CHARACTE LENGTH: 25 DASS TYPE: MOLECULE TYPE: CION-100-100-100-100-100-100-100-100-100-10	atch Sal
00000000000000000000000000000000000000	RESULT 1 US-07-989-: Sequence Patent N GENERAL APPLIC APPL	Query Ma Best Loc Matches
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1 CTGGGCTTCACTTCAGAGGAGAAA 24
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Breitling, Frank
Seehaus, Thomas
Dubel, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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Dubel, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-353-372A-28
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US-08-057-430A-19
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APPLICANT:
APPLICANT:
                      APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                          Sequence 113292, Application US/09396196G;
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
APPLICANT: Affymetrix, Inc.
APPLICANT: Affymetrix, Inc.
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
ATTLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: 00/106,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRASESQ for Windows Version 4.0
SEQ ID NO 113292
LENGTH: 25
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APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
ITILE OF INVENTION: Methods of Genetic Analysis
FILE REPRENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SSOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.2%; Scor.
90.0%; Pred. No. ...
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1 CTGGGCTTCACTTCAGAGGAGAAAA 25
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US-08-353-372A-28
Sequence 28, Application US/08353372A
Patent No. 5840479
GENERAL INFORMATION:
APPLICANT: Little, Melvyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TGGGCTTCACTTCAGAGGAGA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA; CRGANISM: mus musculus
US-09-396-196G-113292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: mus musculus
                                                             RESULT 2
US-09-396-196G-113292
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US-09-396-196G-90079
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APPLICANT: Klewinghaus, Iris
TITLE OF INVENTION: Preparation and Use of Gene Banks of
TITLE OF INVENTION: Synthetic Human Antibodies ("Synthetic Human-Antibody
TITLE OF INVENTION: Libraries")
NUMBER OF SEQUENCES: 39
CORRESSED: DADRESS:
ADDRESSEE: Dunner
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                                                                                                                                                                                                                                                                                   COUNTRY: U.C.

COUNTRY: U.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,372A

FILING DATE: 02-DEC-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/247,393

FILING DATE: 23-MAY-1994

CLASSIFICATION NUMBER: 07/654,207

FILING DATE: 30-JAN-1991

CLASSIFICATION NUMBER: DE P 40 02 897.6

FILING DATE: 01-FEB-1990

PRIOR APPLICATION NUMBER: DE P 40 3880.7

FILING DATE: 01-FEB-1990

PRIOR APPLICATION NUMBER: DE P 40 03 880.7

FILING DATE: 09-FEB-1990

ATTONINY/AGENT INFORMATION:

ANAME: DECENT ON NUMBER: DE P 40 03 880.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

57.6%; Score 14.4; DB 2;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REPERENCE/DOCKET NUMBER: 0552.1032-02000
TELEPHONE: (202) 408-4000
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                               STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
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GENERAL INFORMATION:

APPLICANT: KOOL, ERIC T.

TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
FILE REFERENCE: 220,0010130
CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER FILING DATE: 1997-02-26
EARLIER FILING DATE: 1995-02-23
EARLIER FILING DATE: 1995-02-23
EARLIER FILING DATE: 1995-04-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PATENTIN UMBER: 08/047,860
SOFTWARE: PATENTING DATE: 1995-04-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.2; DB 2;
Pred. No. 1.5e+03;
0; Mismatches 3;
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Pred. No. 2.1e
0; Mismatches
              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD 7.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION TOWNER: US/00360,606B
FILING DATE: December 21, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BARGISTRATION NUMBER: 30,243
REGISTRATION NUMBER: 30,243
REFERENCE/DOCKET NUMBER: 94,319
TELECHONE: (312)913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: coding DNA circle US-08-910-632-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
US-08-100-632-46/c
Fequence 46, Application US/08910632B
; Patent No. 6077668
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84.2%;
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                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity 77.3;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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            TITLE OF INVENTION: PREPARATION AND USE OF GENE BANKS OF TITLE OF INVENTION: HUMAN ANTIBODIES ("HUMAN-ANTIBODY LIBRARIES") NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Junanendra K. Bhattacharjee
APPLICANT: Richard C. Garrad
APPLICANT: Richard C. Garrad
APPLICANT: Robert P. Peery
TITLE OF INVENTION: Methods and Reagents for
TITLE OF INVENTION: Detecting Fungal Pathogens in a
TITLE OF INVENTION: Biological Sample
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive Suite 3200
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & ADDRESSEE: DUNNER, LLP
ADDRESSEE: DUNNER, LLP
CITY: Washington
STATE: DC
                                                                                                                                                                                                                 CUUNTRY: UGA

21P: 20005-3315

COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/057,430A
FILING DATE: 06-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648,522
FILING DATE: 30-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 02 898.4
FILING DATE: 01-PEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 03 881.5
FILING DATE: 09-PEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE P 40 03 881.5
FILING DATE: 09-PEB-1990
RECEISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552.1033-01000
TELECOMMUNICATION: NUMBER: 05552.1033-01000
TELEBERONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.4; DB 3;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 30 base pairs TYPE: nucleic acid STRANDEDNESS: single
APPLICANT: Klewinghaus, Iris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.6%;
Best Local Similarity 75.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-057-430A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-360-606B-14
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Gaps

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RESULT

Gaps

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OTHER INFORMATION: monomeric ribozyme
US-08-910-632-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                        TYPE: RNA ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                           APPLICANT: KOOL, ERIC T.

TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
FILE REFERENCE: 220.0010130
CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT PILING DATE: 1997-08-13
FARLIER PLLING DATE: 1997-02-26
EARLIER FILING DATE: 1997-02-26
EARLIER FILING DATE: 1995-02-26
EARLIER FILING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PATENTING DATE: 1993-04-15
SOFTWARE: PATENTING DATE: 1993-04-15
SOFTWARE: PATENTING DATE: 1993-04-15
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INPORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT PILING DATE: 1997-08-13
EARLIER FILING DATE: 1997-02-26
EARLIER FILING DATE: 1997-02-26
EARLIER FILING DATE: 1995-02-33
EARLIER FILING DATE: 1995-02-33
EARLIER FILING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.0%; Score 14; DB 3; Length 49; 63.6%; Pred. No. 2.1e+03; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 56.0%; Score 14; DB 3; Length 49; Best Local Similarity 63.6%; Pred. No. 2.1e+03; Matches 14; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: multimeric RNA transcript US-08-910-632-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: momomeric ribozyme
US-08-910-632-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48, Application US/08910632B Patent No. 6077668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
18-08-910-632-50
'Sequence 50, Application US/08910632B
'Patent No. 6077668
Sequence 47, Application US/08910632B
Patent No. 6077668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGGCUUUUCUGAAGAGGCGAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GGCTTCACTTCAGAGGAGAA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GGGCTTCACTTCAGAGGAGAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.0
Best Local Similarity 63.6
Matches 14; Conservative
                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-910-632-48
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APPLICANT: KOOL, ERIC T.

TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES FILE REFERENCE: 220.001013 US/08/910,632B
CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT FILING DATE: 1997-08-13
EARLIER PILING DATE: 1997-02-26
EARLIER FILING DATE: 1995-02-26
EARLIER FILING DATE: 1995-02-23
EARLIER FILING DATE: 1995-04-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PATENTIN Ver. 2.0
ESEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46, Application US/08805631A

Patent No. 609680

GENERAL INFORMATION

TITLE OF INVENTION: DNA

TITLE OF INVENTION: DNA

TITLE OF INVENTION: DNA

CORRESPONDENCE: 72

CORRESPONDENCE: 72

ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.

STREET: 119 No. 6096880th Fourth Street, Suite 201

CUTY: Minneapolis

STATE: Minneapolis

COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.0%; Score 14; DB 3; Length 49; Best Local Similarity 63.6%; Pred. No. 2.1e+03; Matches 14; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPACIEM: Limb PC COMPACIDATE
COMPACIEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,631A
FILING DATE: 26-FEB-97
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 13-APR-1993
ATORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REGISTRATION NUMBER: 41,287
REGISTRATION NUMBER: 41,287
REGISTRATION NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear
                       GENERAL INFORMATION:
APPLICANT: UNIVER
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                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
TITLE OF INVENTION: DAA
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6096880th Fourth Street, Suite 201
                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                   Query Match 56.0%; Score 14; DB 3; Length 49; Best Local Similarity 77.3%; Pred. No. 2.1e+03; Matches 17; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.0%; Score 14; DB 3; Length 49; 63.6%; Pred. No. 2.18+03; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,631A
FILING DATE: 26-FEB-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-FEB-97
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                Sequence 47, Application US/08805631A Patent No. 6096880
                                                                                                                                                                                        3 GGGCTTCACTTCAGAGGAGAAA 24
                                                                                                                                                                                                                             43 GGGCTTTCTGAAGAGGCGAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GGGCTTCACTTCAGAGGAGAAA 24
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                   ; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-805-631A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.0
Best Local Similarity 63.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Minneapolis
STATE: Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55401
                                                                                                                                                                                                                                                                                                               US-08-805-631A-47
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US-08-805-631A-48
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APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
TITLE OF INVENTION: DNA
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS: 72
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6096880th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minneapolis
CITY: Minneapolis
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-805-631A-50

Sequence 50, Application US/08805631A

Patent No. 6096880

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF ROCHESTER

TITLE OF INVENTION:

TITLE OF INVENTION: DNA

TUMBER OF SEQUENCES:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUSTING, RAASCH & GEBHARDT, P.A.
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STREET: 119 No. 6096880th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesora
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/805,631A
FLING DATE: 26-FEB-97
CLASSIFICATION 536
PRIOR APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
PRIOR APPLICATION NUMBER: US 08/393,439
FILING DATE: 13-FEB-1995
RIOR APPLICATION NUMBER: US 08/393,439
FILING DATE: 13-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 2.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220.00010140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Minnear-
CITY: Minnear-
STATE: Minneact
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"MPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GGGCTTCACTTCAGAGGAGAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 GGGCUUUCUGAAGAGGCGAAA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: SANDBERG, VICTORIA A. REGISTRATION NUMBER: 41,287 REFERENCE/DOCKET NUMBER: 22 TELECOMMUNICATION INFORMATION: 512-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Gaps

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APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 119 No. 6368802th Fourth Street, Suite 201 CITY: Minneapolis
                                                                                                                                                                                                                                                                         Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 49;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
                                                                                                                                                                                                                                                    Score 14; DB 3; Ler
Pred. No. 2.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14; DB 3; I
Pred. No. 2.1e+03;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-May-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                     TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-569-344-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                  3 GGGCTTCACTTCAGAGGAGAA 24
                                                                                                                                                                                                                                                                                                                                                                                                            43 GGGCTTTCTGAAGAGGCGAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 47, Application US/09569344
Patent No. 6368802
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 612-305-1226
  TELEPHONE: 612-305-1226
                       TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612-305-1228
                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.0%;
                                                                                                                                                                                                                                                                      Query Match 56.0%;
Best Local Similarity 77.3%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 47
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Best Local Similarity 63.64
....has 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Minnesota
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-569-344-47
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) Sequence 46, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
FILING DATE: 28-FEB-195
APPLICATION NUMBER: US 08/393,439
FILING DATE: 28-FEB-199
FILING DATE: 15-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
PatentIn Release #1.0, Version #1.30
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NAME: SANDBERG, VICTORIA A.
REGISTRATION UNDRER: 41,287
REFERNCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                      PILING DATE: 26-FEB-97
CLASSIFICATION: 536
PIOOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
PILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATYONEY/ASET INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEFRANCE: 612-305-1226
TELEFRANCE: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 S6.0%; Score 14; DB ilarity 63.6%; Pred. No. 2.16 Conservative 3; Mismatches
                                   UMBER: US/08/805,631A
26-FEB-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 GGCUUUCUGAAGAGGCGAAA 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear _ MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 55401
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Minnesota
COUNTRY: USA
                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
...rhes 14; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-805-631A-50
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55.2%; Score 13.8; DB 4; Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: mus musculus
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US-09-396-196G-113293
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                                                                                                                                                Sequence 48, Application US/09569344
Patent No. 6368802
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50, Application US/09569344
Sequence 50, Application US/09569344
Patent No. 6368802
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER KEAUABLE FURNT

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OSOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/569,344

FILING DATE: 11-May-2000

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/805,631

FILING DATE: 26-FEB-97

APPLICATION NUMBER: US 08/39,439

FILING DATE: 26-FEB-1995

APPLICATION NUMBER: US 08/047,860

FILING DATE: 15-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG, VICTORIA A.

REGISTRATION NUMBER: 220.00010140

TELECOMUNICATION INDRER: 220.00010140
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: WUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.0%; Score 14; DB 3; Length 49; Best Local Similarity 63.6%; Pred. No. 2.1e+03; Matches 14; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: RNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                         3 GGGCUUUCUGAAGAGGCGAAA 24
GGGCTTCACTTCAGAGGAGAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GGGCTTCACTTCAGAGGAGAA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 49 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 55401
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Minnesota
COUNTRY: USA
                                                                                                                               US-09-569-344-48
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minnespolis
STATE: Minnesota
COUNTRY: USA
                                                                                                                                                              ZIP: 55401
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-May-2000
CLASSIFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/33,439
FILING DATE: 28-FEB-193
APPLICATION NUMBER: US 08/47,860
FILING DATE: 15-APPL193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFRENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ TWARE: Fasteseq for Windows Version 4.0
SEQ ID NO 113293
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 113293, Application US/09396196G Patent No. 6821724
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Sequence 19, Application US/09256490

Sequence 19, Application US/09256490

Patent No. 6235881

GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie
APPLICANT: Talbott, Rands,
TITLE OF INVENTION: Isolation of No. 6235881el HIV-2 Proviruses
INVMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "GR72 (outside, left) primer for HIV-2KR env"
                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TEM PC Compatible
COMPUTER: TEM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659_251
FILING DATE: No. 5883081 yet assigned
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 60/001,441
FILING DATE: 26-01-1995
ATTORNEY/AGENT INFORMATION:
NAME: Garret-Wackowski, Eugenia
REGISTRATION NUMBER: 02307B-056410US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: MOCHAICA COINGER: SINGle
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.6; DB 2;
Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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80.0%;
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Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: -
LOCATION: 1..25
OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
USA
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MOLECULE TYPE: I
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-256-490-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-659-251-19
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                          Gaps
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Patent No. 5883081
GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie
APPLICANT: Talbott, Randy
APPLICANT: Talbott, Randy
APPLICANT: Isolation of No. 5883081e1 HIV-2 Proviruses
NUMBER OF SEQUENCES: 50
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0
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                                                                                                                                                                                                Sequence 60, Application US/08388029A

Patent No. 6116665
GENERAL INFORMATION:
APPLICANT: FENGER, CLARA K.
APPLICANT: GAJADHAR, ALVIN R.
TITLE OF INVENTION: SARCOCYSTIS NEURONA DIAGNOSTIC PRIMER NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSER: LOWE, PRICE, LEBLANC & BECKER
88.2%; Pred. No. 2.2e+03;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: ...
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,029A
FILING DATE: 14-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PRICE, ROBERT I.
REFERENCE/DOCKET NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 22,685
TELEPHONE: 703-684-1111
TELEPHONE: 703-684-1124
                                                                                                                                                                                                                                                                                                                                                                                                   E: LOWE, PRICE, LEBLANC & BECKER
99 CANAL CENTER PLAZA, SUITE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 TTCACTTCAGAGGAGAAAA 25
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                                                               4 GGCTTCACTTCAGAGGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: AMERPAT
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                        15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: US
    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
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US-08-388-029A-60
                                                                                                                                                                      RESULT 20
US-08-388-029A-60
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CITY: AL
                        Matches
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Gaps

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Length 25; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                    APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.;
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT PILING DATE: 1999-09-15
PRIOR PELICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NO 50969
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | FACERIL NO. 0521/24|
| FACERIL NO. 0521/24|
| APPLICANT: Michael Mittmann | APPLICANT: Michael Mittmann | APPLICANT: David Mack |
| APPLICANT: David Lockhart |
| APPLICANT: Affymetrix, Inc. |
| TILLE OF INVENTION: Methods of Genetic Analysis |
| FILE REPRENCE: 310.1. |
| CURRENT APPLICATION NUMBER: US/09/396,196G |
| FILE REPRENCE: 1910.1 |
| CURRENT FILING DATE: 1999-09-15 |
| PRIOR FILING DATE: 1998-09-17 |
| NUMBER OF SEQ ID NOS: 127806 |
| SOFTWARE: FASELSEQ for Windows Version 4.0 |
| SEQ ID NO 52946 |
| LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 26
US-09-396-117350/c
; Sequence 117350, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 54.4%; Score 13.6; DB 4;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-396-196G-52946/c
; Sequence 52946, Application US/09396196G
; Patent No. 6821724
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Best Local Similarity 80.09
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: mus musculus
US-09-396-196G-50969
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; ORGANISM: mus musculus
US-09-396-196G-52946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.4%; Score 13.6; DB 3; Length 25; 80.0%; Pred. No. 2.8e+03; live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.4%; Score 13.6; DB 4; Length 25; 80.0%; Pred. No. 2.8e+03; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50968 Application US/09396196G; Patent No. 6821724; GENERAL INFORMATION: Michael Mittmann; APPLICANT: Michael Mittmann; APPLICANT: David Mack, APPLICANT: David Lockhart; APPLICANT: David Lockhart; APPLICANT: Affymetrix, Inc.; APPLICANT: Pavid Nochhart; APPLICANT: Affymetrix, Inc.; TITLE OF INVENTION: Methods of Genetic Analysis; FILE REFERENCE: 310.1
                                                      PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/659,251
PTLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackcowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 02307B-056410US
TELEFORMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STREET COMMUNICATION:
SEGUENCE CHARACTERISTICS:
SEGUENCE CH
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CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 50968
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 24
US-09-396-196G-50969
; Sequence 50969, Application US/09396196G
; Parent No. 6821724
; GENERAL INFORMATION:
APPLICATION NUMBER: US/09/256,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GGCTTCACTTCAGAGGAGAA 23
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Best Local Similarity 80.0%
Matches 16; Conservative
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Best Local Similarity 80.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 1..25
; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-256-490-19
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; ORGANISM: mus musculus
US-09-396-196G-50968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-09-396-196G-50968
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RESULT 29
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; Sequence 19, Application PC/TUS9611445
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Isolation of Novel HIV-2 Proviruses
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
                                                                                                                                                                               54.4%; Score 13.6; DB 4; Length 25; 80.0%; Pred. No. 2.8e+03; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.4%; Score 13.6; DB 5; Length 25; 80.0%; Pred. No. 2.8e+03; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTE: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11445
FILING DATE:
CLASSIFICATION:
NAME: Berliner, Robert
REGISTRATION: NUMBER: 25.5199C1
TELEPANE: (213) 977-1001
TELEPANE: (213) 977-1001
TELEPANE: (213) 977-1001
TELEPANE: (213) 977-1003
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: MUCLeic acid
STRANDEDNESS: single
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 117350
LENGTH: 25
                                                                                                                                                                                                                                                         2 TGGGCTTCACTTCAGAGGAG 21
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Bast Local Similarity 80.v.
Past Local Similarity 10.v.
                                                                                                                                                                                                Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                  TYPE: DNA ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA
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RESULT 28 US-09-230-288-5/c

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KORKKO, JARMO
ALA-KOKKO, LEENA, et al.
VIENTION: COMPOSITIONS AND METHODS FOR DETECTING
COMPOSITION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
EQUENCES: 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                         COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/230,288
FILING DATE: 07-Sep-1999
CLASS:PICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/AU97/00473
FILING DATE: 29-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: NEINMERK, Sheridan
REGISTRATION NUMBER: 20,520
REFERENCE/DOCKET NUMBER: SCHNEIDER=2
TELEPHONE: 202-625-570
                                                    APPLICANT: SCHNEIDER, Rene
VANCOV, Tony
UTRY, Azen
TITLE OF INVENTION: BIOSENSORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
STREET: 624 Ninth Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-230-288-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROCKOP, DARWIN J.
SPOTILA, LORETTA D.
DELTAS, CONSTANTINOS D.
SEREDA, LARISA
LARSON, ANDREA W.
PACK, MICHAEL
COLIGE, ALAIN
EARLY, JAMES
KORKKO, JARMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 239, Application US/08943731; Patent No. 6265157; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 5, Application US/09230288 Patent No. 6329160 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-943-731-239
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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Query Match 53.6%; Score 13.4; DB 4; Length 25; Best Local Similarity 73.9%; Pred. No. 3.5e+03; Matches 17; Conservative 0; Mismatches 6; Indels
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                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                           US-09-396-196G-56218/C

Sequence 56218 Application US/09396196G

Patent No. 682124

GENERAL INPORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Mack
APPLICANT: ALIVE OF 1909-109-15
AURENT FILING DATE: 1998-09-17
AURENTH: 25
AURITH: 25
AURITH: 25
AURITH: 25
AURITH: 25
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Sequence 64443, Application US/09396196G

Sequence 64443, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mitmann

APPLICANT: David Lockhart

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REPREBENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NOS 127806
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              73.9%; Pred. No. 3.5e+03; ive 0; Mismatches 6
                                                                                                                        TGGGCTTCACTTCAGAGGAGAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTGGGCTTCACTTCAGAGGAGAA 23
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                                                                                                                                                                                      25 redcarreactreadareadaaa 3
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          Best Local Similarity 73.9%
Matches 17; Conservative
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Best Local Similarity 73.5%
The 17; Conservative
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US-09-396-196G-64443
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                                    ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
                                                                                                                                                                                              CUUNTRY: USA

ZIP: 19103-7086

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHALIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 08/212,322
PILING DATE: 14-MAR-1994
PRIOR APPLICATION NUMBER: 050/803,628
FILING DATE: 13-DEC-1991
ATPONEY/AGENT INFORMATION:
REGISTRADION NUMBER: 36,317
REGISTRADION NUMBER: 36,317
REGISTRADION NUMBER: 36,317
RELEPRANT SISSEMENCE/DOCKET NUMBER: 36,317
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATIO
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US-09-396-196G-13674/C

Sequence 13674, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann
APPLICANT: David Mack

APPLICANT: David Mack

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REPERRNCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1998-09-15

PRIOR PILING DATE: 1998-09-15

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEC ID NOS: 127806

SEC ID NO 13674

LENTH: 25
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US-08-943-731-239
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH S
                                                                                                                                          PHILADELPHIA
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RESULT 33

53.6%; Score 13.4; DB 4; Length 25;

TYPE: DNA ORGANISM: Mus musculus

US-09-396-196G-13674 Query Match

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                                                                                                                 11 UĞĞĞTİTTCİİÇTĞAĞĞTAĞA 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 340 Kingsland Street CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 53.6%;
Best Local Similarity 73.9%;
Matches 17; Conservative
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.6%; Score 13.4; DB 4; Length 25; Best Local Similarity 73.9%; Pred. No. 3.5e+03; Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us-ub-160-670A-19
; Sequence 19, Application US/08160670A
; Patent No. 5449758
; GENERAL INFORMATION:
APPLICAMT: Hartley, James L.
TITLE OF INVENTION: Protein Size Marker Ladder
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CLASSIFICATION NUMBER: US/08/160,670A
FILING DATE: 12/2/93
CLASSIFICATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 31-2600
TELEFORMURICATION INFORMATION:
TELEFEHONICATION INFORMATION:
US-09-396-196G-64567
; Sequence 64567, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Mack
; APPLICANT: David Mack
; APPLICANT: David Mack
; APPLICANT: David Mack
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FRStSEQ for Windows Version 4.0
; SEQ ID NO 64567
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
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Best Local Similarity 69.6
Matches 16; Conservative
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US-08-160-670A-19
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US-08-160-670A-19
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US-08-660-645A-36/c

Sequence 36, Application US/08660645A

Sequence 36, Application US/08660645A

GENERAL INFORMATION:

APPLICANT: Hohman, Hans-Peter
APPLICANT: Tessier, Michel

APPLICANT: van Loon, Adolphus

TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 42;
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| Sequence 36, Application US/09298718
| Patent No. 6124113
| GENERAL INFORMATION:
| APPLICANT: Pasamontes, Luis
| APPLICANT: Passier, Michel
| APPLICANT: Passier, Michel
| APPLICANT: Pessier, Michel
| APPLICANT: Pessier, Michel
| APPLICANT: Pessier, Michel
| APPLICANT: Pessier, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: COMPACTORY
COMPUTER: IBM PC compatible
COMPACTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,645A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: EP 95108688.9
FILING DATE: 09-JUN-1995
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.4; DB 3;
Pred. No. 3.9e+03;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Pokras, Bruce A. REGISTRATION VINDER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
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Gaps
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US-08-980-832-15
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Batent No. 6291204

GENERAL INFORMATION:

APPLICANT: Pasamontes, Luis

APPLICANT: Tsygankov, Yuri

TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentive Carotenoid

CURRENT APPLICATION NUMBER: US/08/980,832B

CURRENT FILING DATE: 1997-12-01

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.6%; Score 13.4; DB 3; Length 42; Best Local Similarity 73.9%; Pred. No. 3.9e+03; Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: PERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.6%; Score 13.4; DB 3; 73.9%; Pred. No. 3.9e+03; tive 0; Mismatches 6;
                                                           ATTORNEY/AGENT INFORMATION:
NAME: POKTAS, Bruce A.
REGISTRATION NUMBER: 32,748
REGISTRATION NUMBER: 32,748
REPRENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2363
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTGGGCTTCACTTCAGAGGAGAA 23
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                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/09547267; Patent No. 6613543
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 73.9 Matches 17; Conservative
                                                                                                                                                                                                                                                                                        LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-09-546-969-36
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US-08-980-832-15/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Passier, Michel
APPLICANT: Tessier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,969
FILING DATE:
                                                                                                                                                                   COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.6%; Score 13.4; DB 3; 73.9%; Pred. No. 3.9e+03; tive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POKras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCS/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 chéccercechicanaceaea 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/09546969
Patent No. 6207409
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 73.9°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                            COUNTRY: USA
ZIP: 07110
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US-09-298-718-36
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US-09-546-969-36/c
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STATE: NJ
                                                                                                         STATE: N. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 53.6%; Score 13.4; DB 4; Length 42; Best Local Similarity 73.9%; Pred. No. 3.9e+03; Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 40

US-09-920-923B-15/c

Sequence 15, Application US/09920923B

Patent No. 6677134

GENERAL INFORMATION:
APPLICANT: Pasamones, Luis
APPLICANT: Pasamones, Luis
TITLE OF INVENTION: Fermentative Carotenoid Production
FILE REFERENCE: 15464 US (C38435/125944)

CURRENT APPLICATION NUMBER: US/09/920,923B

CURRENT APPLICATION NUMBER: 08/980,832

PRIOR APPLICATION NUMBER: 08/980,832

PRIOR FILING DATE: 1997-12-01

WUMBER OF SEQ ID NOS: 66

SOFTWARE: Patentin version 3.1

SEQ ID NO 15

LENGTH: 42
                                                                                                          ZONDONIA
ZIP: 0710
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/547,267
                                                                                                                                                                                                                                                                                      APELICATION
FILING DATA:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POACEAS, BACE A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELEPHONE: (201) 235-2801
TELEPHONE: (201) 235-2801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 Dase pairs
ADDRESSEE: Hoffmann-La Roche Inc. STREET: 340 Kingsland Street CITY: Nutley STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTGGGCTTCACTTCAGAGGAGAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 criciccorcectronanicani 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-547-267-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Primer MUT6
US-09-920-923B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial
                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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1 CTGGGCTTCACTTCAGAGGAA 23

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Db 32 CTGGCCGTCGCTTGAAAGGAGGA 10
Search completed: November 18, 2005, 11:22:00
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Search completed: November 18, 2005, 11:22:00 Job time : 49.5741 secs

100259, 633439, 64997, 970185, 970186, 261669, 482864, 243899, 419911, 311977, 209513,

Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Scoring table:

Searched:

Database

Title: Perfect score:

Sequence:

nucleic

Run on:

Sequence Sequence Sequence

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RESULT 1
US-08-469-172-5
US-08-469-172-5
Sequence 5, Application US/08469172
Sequence 5, Application US/08469172
Publication No. US20030054343A1
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOSH
APPLICANT: WATKINS, HUGH
APPLICANT: ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A BETHOD FOR DETECTING
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
US-10-809-189-113292
US-11-036-317-100259
US-11-036-317-100259
US-11-036-317-764997
US-10-719-900-970185
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US-10-719-906-261669
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US-10-719-900-978130
US-11-036-317-366190
US-11-036-317-366249
US-11-036-317-9266-62957
US-11-036-317-9266-62957
US-11-036-317-9266-62957
US-11-036-317-9266-629974
US-11-036-317-9266-63934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,172
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
    STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
   BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
CITY: BO
   16.8
116.8
116.6
116.6
116.2
116.2
                                                                                                                                                                                                                               Sequence 5, Appli
Sequence 593102,
Sequence 978129,
Sequence 424739,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Appli
                                                                                                  November 18, 2005, 06:36:48; Search time 336.027 Seconds (without alignments) 615.265 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications NA:*

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20: /cgn2_6/ptodata/1/pubpna/US0
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-788-779-5
US-10-719-900-593102
US-10-719-900-978129
US-10-719-900-424739
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           9794790 segs, 4134909567 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-469-172-5
                                                                                                                                                                                               1 CTGGGCTTCACTTCAGAGGAGAAAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        - nucleic search, using sw model
                                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 50
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Match
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100.0
68.8
68.0
67.2
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Score

Result No.

25 25 17.2 17

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182301, 424738, 823343, 826249, 9865, Ap 629374, 633436,

Sequence

Sequence Sequence Sequence

Sequence

430286, 828846,

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

823363, 823363, 430473, 430473, 866704, 788701, 287762, 387762, 387762, 387762, 379510, 315928, 315928, 316190, 978130,

Sequence Sequence Sequence Sequence

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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-593102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus
US-10-719-900-978129
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                           US-10-719-900-593102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULI 2
US-10-18-779-5
Sequence 5, Application US/10788779
Publication No. US20040152121A1
GENERAL INFORMATION:
APPLICANT: SEIDMAN, CHRISTINE
SEIDMAN, JOHN
MATKINS, HUGH
ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
DISEASE-ASSOCIATED MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
FILING DATE: 27-Reb-2004
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/469,172
FILING DATE: «Unknown»
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTATION NUMBER: 33,565
REFERENCE/DOCKET NUMBER: GML-111
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 227-740
TELEFAN: (617) 227-740
TELEFAN: (617) 227-740
TELEFAN: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: BOSTON
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-469-172-5
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US-10-719-900-978129/C

Sequence 978129, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITILE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

FRIOR FILING DATE: 2002-11 20

NUMBER OF SEQ ID NOS: 982914

SOOFWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 978129

TERGITH: 25

TERGITH: 25
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                                                                                           Score 25; DB 20; Length 25; Pred. No. 0.052;
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
FILE REPERENCE: 3528.1
CURRENT PAPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11.20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTHARE: MICROARTAY Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.0%; Score 17; DB 22; Length 25; 80.0%; Pred. No. 4e+02;
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Best Local Similarity 86.4%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 3;
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0; Mismatches
                                                                                                                                        0; Mismatches
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
                                                                                                                                                                                       1 CTGGGCTTCACTTCAGAGGAGAAAA 25
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) MOLECULE TYPE: CDNA
) SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-788-779-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 creeccrirararcecaecreaaa 1
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                                                                                         100.0%;
ilarity 100.0%;
Conservative 0
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Best Local Similarity 80.09
Matches 20, Conservative
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-100259
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US-11-036-317-764997
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Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION UMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                  APPLICANT SWENTION: Methods of Genetic Analysis of Mouse TITLE OF INVENTION: Methods of Genetic Analysis of Mouse FILE REFERENCE: 35.28.1
CURRENT APPLICATION NUMBER: US/10/719,900
PRIOR PILING DATE: 2003-11-20
PRIOR PILING DATE: 2002-11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 424739
LENGTH: 25
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0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 113292, Application US/10809189
Publication No. US20050048531A1
BEBERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affayetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/809,189;
CURRENT FILING DATE: 2004-03-25;
PRIOR APPLICATION NUMBER: US/09/396,196;
PRIOR FILING DATE: 1990-09-15;
PRIOR APPLICATION NUMBER: 60/100,678;
PRIOR FILING DATE: 1998-09-17;
NUMBER OF SEQ ID NOS: 127806;
SOFTWARE: PSECSEQ for Windows Version 4.0;
SEQ ID NO 113292;
LENGTH: 25
                        Sequence 424739, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
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Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus
US-10-719-900-424739
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CORGANISM: mus musculus
US-10-809-189-113292
US-10-719-900-424739/c
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT TRING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 63439
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 764997, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Williams, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3664.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US/01/036,639
FRIOR APPLICATION NUMBER: US 60/536,639
FRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARR: Microarray Probe Sequence Listing Generator V 1.1
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PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 100259
LENGTH: 25
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                                                                                                                                                                                                                   Score 16.8; DB 26;
Pred. No. 5.1e+02;
0; Mismatches 2;
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90.0%; Pred. No. 5.1e+02;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-11-036-317-633439/c
; Sequence 633439, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
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Best Local Similarity 90.0'
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Best Local Similarity 90.0
Matches 18; Conservative
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Best Local Similarity 90.0
Matches 18; Conservative
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 261669
LENGTH: 25
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85.7%;
                                                                                                                                                                                  TYPE: DNA
CRGANISM: Rattus norvegicus
US-10-719-956-261669
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; ORGANISM: Mus musculus
US-10-719-900-482864
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Best Local Similarity
Matches 18; Conserv
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; Sequence 970186, Application US/10719900
; Publication No. US20050026164A1
; GRNERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
; CURRENT PAPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR PILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 970186
; LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.4%; Score 16.6; DB 22; Length 25; 82.6%; Pred. No. 6.3e+02; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                       APPLICANT CONTINUED TO THE APPLICANT CONTINUED OF THE APPLICANT SALE MET APPLICANTON: Methods of Genetic Analysis of Mouse FILE REFERENCE: 35.20 CURENT APPLICANTON NUMBER: US/10/719,900 CURRENT FILING DATE: 2003-11-20 PRIOR PILING DATE: 2002-11-20 PRIOR FILING DATE: 2002-11-20 NUMBER OF SEQ ID NOS: 982914 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 970185 LENGTH: 25
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Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITULE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
                                                                                                                                                                           US-10-719-900-970185/c
; Sequence 970185, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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                                   25
                                                                               24 CCTCACTTCGGAGGAGAAA 5
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Best Local Similarity 82.6
Matches 19; Conservative
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ORGANISM: Mus musculus
US-10-719-900-970186
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; ORGANISM: Mus musculus
US-10-719-900-970185
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US-10-719-900-970186/c
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US-10-719-956-261669/c
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US-10-719-956-243899/C
is Sequence 243899/C
is Sequence 243899/C
is Sequence 243899/C
is Publication No. US20040146910A1
is GENERAL INFORMATION:
is APPLICANT: Xue Mei Zhou
is TITLE OF INVENTION: Methods of Genetic Analysis of Rat
is FILE REFERENCE: 357.1
is CURRENT APPLICATION NUMBER: US/10/719,956
is CURRENT PILING DATE: 2003-11-20
is PRIOR FILING DATE: 2002-11-20
is PRIOR FILING DATE: 2002-11-20
is NUMBER: OF SEQ ID NOS: 699466
is SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
is ENGHH: 25
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; Sequence 482864, Application US/10719900
; Publication No. US2050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT APPLICATION NUMBER: 60/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11.20
; NUMBER OF SEQ ID NOS: 982914
; SEQ ID NO 482864
; LENGTH: 25

**LENGTH: 25
Query Match 65.6%; Score 16.4; DB 24; Length 25; Best Local Similarity 94.4%; Pred. No. 7.9e+02; Matches 17; Conservative 0; Mismatches 1; Indels C
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Best Local Similarity 85.7%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 3;
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Pred. No. 9.9e+02;
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPRENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT PILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 8: 991174
SEQ ID NO 8: 23362
LENGTH: 25
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APPLICANT: Williams, John
APPLICANT: Blume, John
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
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                                                                                                                                                                                                                                                                                 Length 25;
                     PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: 201513
LENGTH: 25
LENGTH: 25
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SEQ ID NO 366428
LENGTH: 25
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64.0%; Score 16; DB 26;
Best Local Similarity 79.2%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5.
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; Sequence 882362, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
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     2005-01-13
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79.2%;
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Best Local Similarity 79.24
Matches 19; Conservative
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CORGANISM: Mus musculus
US-11-036-317-366428
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US-11-036-317-209513
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CORGANISM: Mus musculus
US-11-036-317-823362
     CURRENT FILING DATE:
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Best Local Similarity
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                                                                                                                                                                                TYPE: DNA
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANTON: UUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: UUCLEIC AM 101081)
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 311797
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APPLICANT: Williams, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 419911
LENOTH: 25
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Best Local Similarity 79.2%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                     Sequence 419911, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR FILING DATE: 2003-11-20
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Publication No. US20050214823A1
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CTGGGCTTCACTTCAGAGGAG 21
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                            22 CTGGGCTCCACTCCAGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-419911
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                                                                                                                         RESULT 15
US-10-719-956-419911/c
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TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-866704
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CORGANISM: Mus musculus
US-10-719-900-430473
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CORGANISM: Mus musculus
US-11-036-317-788701
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LENGTH: 25
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APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3664.
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 823363
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
    TITLE OF INVENTION:
    FILE REFERENCE: 3528.1
    CURRENT FILING DATE: 2003-11-20
    PRIOR FILING DATE: 2003-11-20
    PRIOR FILING DATE: 2002 11 20
    PRIOR FILING DATE: 2002 11 20
    NUMBER OF SEQ ID NOS: 982914
    SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
    SEQ ID NO 383306
    LENGTH: 25
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79.2%; Pred. No. 1.2e+03;
ive 0; Mismatches 5; Indels
    5; Indels
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; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
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Pred. No. 1.5e+03;
0; Mismatches 2;
0; Mismatches
                                                                                                                                         RESULT 20
US-11-036-317-823363
; Sequence 823363, Application US/11036317
; Publication No. US20050214823A1
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
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                                        2 TGGGCTTCACTTCAGAGGAGAAA 25
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
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Best Local Similarity 79.2
Matches 19; Conservative
19; Conservative
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; ORGANISM: Mus musculus
US-10-719-900-383306
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US-10-719-900-383306/c
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APPLICANT: Williams, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
FRICA APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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j Sequence 866704, Application US/10719900

j Edublication No. US20050026164A1

GENERAL INFORMATION:

j APPLICANT: Xue Mei Zhou

j TITLE OP INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

j CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

prior FILING DATE: 2002-11-20

prior APPLICATION NUMBER: 60/427,808

j PRIOR PILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 982914

s SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

j. FROM NO 866704
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CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Pred. No. 1.5e+03;
0; Mismatches 2;
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Pred. No. 1.5e+03;
0; Mismatches 2;
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Publication No. US20050214823A1
GENERAL INFORMATION:
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5%;
Matches 17; Conservative (
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SEQ ID NO 279510
LENGTH: 25
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LENGTH: 25
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                                                                                                                                                                                  Sequence 248480, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: We Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT PILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2003-11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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Fublication No. US20050026164A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3520.1
CURRENT FILING DATE: 2003-11-20
FILE REPLICATION NUMBER: 60/427,808
FRIOR APPLICATION NUMBER: 60/427,808
FRIOR PELLING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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US-10-719-900-593103
; Sequence 593103, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.4%; Score 15.6; DB 22;
81.8%; Pred. No. 1.9e+03;
tive 0; Mismatches 4;
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81.8%; Pred. No. 1.9e+03;
tive 0; Mismatches 4;
 89.5%; Pred. No. 1.5e+03;
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                     17; Conservative
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; ORGANISM: Mus musculus
US-10-719-900-248480
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Matches 18; Conserv
Best Local Similarity
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Best Local Similarity
Matches 18; Conserv
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US-10-719-900-248480/c
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US-10-719-900-387762
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LENGTH: 25
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APPLICANT: Wyeth
APPLICANT: Wounte, William
APPLICANT: Wounte, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PALENTIN VETSION 3.2
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: UCCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: UCCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOAPTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031996-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
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CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Pred. No. 1.9e+03;
); Mismatches 4;
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Pred. No. 1.9e+03;
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Pred. No. 1.9e+03;
0; Mismatches 4;
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81.8%;
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Best Local Similarity 81.8°
Matches 18; Conservative
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Best Local Similarity 81.8
Matches 18; Conservative
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US-10-956-157-279510
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US-10-956-157-315928
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; ORGANISM: Mus musculus
US-10-719-900-593103
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Best Local Similarity
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Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT FILING DATE: 2005-01-13

CURRENT FILING DATE: 2005-01-13

PRIOR PLILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 366190
                                                                                                                                                                             Sequence 270365, Application US/11036317
Sequence 270365, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
FRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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4; Indels
0; Mismatches
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Publication No. US20050214823A1
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                                       2 TGGGCTTCACTTCAGAGGAGA 23
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18; Conservative
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                                                                                                                                          RESULT 30
US-11-036-317-270365/c
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US-11-036-317-423606
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US-11-036-317-270365
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Matches
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 423606
LENGTH: 25
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Sequence 978130.

Sequence 978130.

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

HAPPLICATHY: Xue Met Zhou

TITLE OF INFORMATION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT APPLICATION NUMBER: 00/427,808

PRIOR FILING DATE: 2002 11.20

PRIOR FILING DATE: 2002 11.20

NUMBER OF SEQ ID NOS: 982914

SEQ ID NO 978130

LENGTH: 25
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Publication No. US20040146910A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT APPLICATION NUMBER: 00/427,836

PRIOR FILING DATE: 2002 11 20

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Pred. No. 2.4e+03;
0; Mismatches 6;
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Best Local Similarity 76.0%;
Matches 19; Conservative (
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CORGANISM: Mus musculus
US-10-719-900-978130
                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-423606
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APPLICANT: Williams, Alan
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                                           Gaps
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US-10-719-956-439125/c
Sequence 439125, Application US/10719956
Publication No. US20040146910A1
GENERAL INPORMATION:
APPLICANT: Xue Mei Zhou
ITILE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPRENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR PILING DATE: 2002 11 20
PRIOR FILING DATE: 2002 11 20
NUMBER: OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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LENGHIALS
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     Length 25;
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LENGTH: 25
                                         Indels
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61.6%; Score 15.4; DB 24;
94.1%; Pred. No. 2.4e+03;
live 0; Mismatches 1;
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US-11-036-317-430286/c
| Sequence 430286, Application US/11036317
| Publication No. US20050214823A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 828846, Application US/11036317; Publication No. US20050214823A1; GENERAL INFORMATION:
                                                                             4 GGCTTCACTTCAGAGGA 20
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                   Best Local Similarity 94.1
Matches 16; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-430286
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US-11-036-317-828846/c
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APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT APPLICATION NUMBER: US/11/060,756
NUMBER OF SEQ ID NOS: 301284
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.11
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 828846
LENGTH: 25
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; Sequence 424738, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US/10/719,900
; PRIOR PILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 424738
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Publication No. US20050221354A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mus musculus
US-11-036-317-828846
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Matches 16, Conserv
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Best Local Similarity
Matches 19; Conserv
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US-11-060-756-182301
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US-10-719-900-823343
; Sequence 823343, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 05/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; RIGHT FLING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SEQ ID NO 823343
; LENGTH: 25
Query Match 60.8%; Score 15.2; DB 22; Length 25; Best Local Similarity 85.0%; Pred. No. 3e+03; Matches 17; Conservative 0; Mismatches 3; Indels (
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                                                                                       5 GCTTCACTTCAGAGGAGAA 24
                                                                                                                 TYPE: DNA ORGANISM: MUS musculus
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Search completed: November 18, 2005, 15:41:06 Job time : 337.027 secs

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6 CTTCACATCAGAGAAGCAAA 25

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Run on:

Sequence:

Searched:

Database

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120147 Sequence 10
120149 Sequence 10
AR340325 Sequence 10
AR340327 Sequence
AJ010898 Homo sapi
A59897 Sequence 15
C0006450 Sequence 15
A58695 Sequence 2
A58603 Sequence 2
BD016942 Plant pro
AX669192 Sequence
E59198 Method for
E54179 Process of
AX781258 Sequence
AX781258 Sequence
190211 Sequence 37
190210 Sequence 37
AR124176 Sequence
AR442783 Sequence
AR036016 Sequence
AR161840 Sequence
185694 Sequence 43
BD000197 Viral vec
AR035911 Sequence
AR035913 Sequence
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    /organism="unknown"
    /mol_type="unassigned DNA"

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Location/Qualifiers
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1 (bases 1 to 26)
Shi,Y. and Ruben,S.M.
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A72867 Sequence 11
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AR410131 Sequence
AR410131 Sequence
AR410135 Oligomucleo
AR410135 Oligomucleo
AR41035 Oligomucleo
AR57316 Sequence
AR57316 Sequence
AR68955 Sequence
AR659855 Sequence
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Bovenberg, R.A., Koekman, B.P., Hoekema, A., Van, D.L. and Verweij, J.
PROCESS FOR THE EFFICIENT PRODUCTION OF 7-ADCA VIA
3-(CARBOXVETHYLITHO) PROPIONY1-7-ADCA
Patent: WO 9504149-A 11 09-FEB-1995;
GIST BROCADES NV (NL)
Other publication PL 312747 960513
Other publication CA 2168004 950209.
                                                                                                                                      Gaps
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Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 26)
Shi, Y. and Ruben,S.M.
Polymucleotides encoding a novel interleukin receptor termed interleukin-17 receptor-like protein
Patent: US 6635443-A 9 21-OCT-2003;
Location/Qualifiers
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                                                                                                         Query Match 60.7%; Score 18.2; DB 6; Length 26; Best Local Similarity 87.0%; Pred. No. 1.2e+04; Matches 20; Conservative 0; Mismatches 3; Indels
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Interleukin 17-like receptor protein
Patent: US 6482923-A 9 19-NOV-2002;
Location/Qualifiers
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Sequence 11 from Patent WO9504149.
A42996.
A42996.1 GI:2298440
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Sequence 9 from patent US 6635443.
AR410127
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/mol_type="unassigned DN/
/db_xref="taxon:32644"
                                                                    /mol_type≂"genomic DNA"
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DB 6; Length 48;

55.3%; Score 16.6;

Query Match

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1 (Dases 1 to 48)

1 (Dases 1 to 48)

Bovenberg, R.Ary Lans, Koekman, B.Pieter., Hoekema, A., Van Der Laan, J.Meteke., Verweij, J. and De Vroom, E.

Process for the efficient production of 7-ADCA via Patent: US 5795733-A 11 18-AUG-1998;
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                        Indels
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BOVGEDS PA, and Koekman, B.P.
BOVGESS POR THE EFFICIENT PRODUCTION OF 7-1
2- (CARBOXYETHYLTHIO) ACETYL-7-ADCA AND
3- (CARBOXYMETHYLTHIO) PROPIONYL-7-ADCA
PATENT: WO 9504148-A 11 09-FEB-1995;
GIST BROCADES NV (NL); BOVENBERG ROELOF ARY
LOCATION/QUALIFIES
                        4.
82.6%; Pred. No. 5e+04; ative 0; Mismatches
                                                                                                                                                                                                    DNA
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/organism="unidentified"
/mol_type="unassigned DNA"
/isolate="OligoNUCLEOTIDE 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR023759 48 bp E
Sequence 11 from patent US 5795733.
AR023759. GI:3977053
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                                                                                                                                                                                            48 bp
Sequence 11 from Patent WO9504148.
A72867
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                                                              6 ACCCCAGCAGCCCGGCCTTGAAG 28
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Best Local Similarity 82.6%;
Matches 19; Conservative
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                        Conservative
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unidentified
unclassified.
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Best Local Similarity
Matches 19; Conserv
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Gaps

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PAT 20-DEC-2002

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 7

ORGANISM

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ORIGIN

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FEATURES

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Unknow...
Unclassified.
1 (bases 1 to 28)
Shi,Y. and Ruben,S.M.
Shi,Y. and Ruben,S.M.
Polynucleotides encoding a novel interleukin receptor termed interleukin-17 receptor-like protein Patent: US 6635443-A 11 21-OCT-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.0%; Score 16.2; DB 6; Length 28; larity 85.7%; Pred. No. 7.5e+04; Conservative 0; Mismatches 3; Indels
                                                                                                                                   Score 16.2; DB 6; Length 28;
Pred. No. 7.5e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Untrivent.
Unclassified.
1 (Bases 1 to 28)
Shi,Y. and Ruben,S.M.
Interleukin 17-like receptor protein
Patent: US 6482923-A 13 19-NOV-2002;
Location/Qualifiers
                                                                                                                       54.0%; Scc...
85.7%; Pred. No. ...
0; Mismatches
Interleukin 17-like receptor protein
Patent: US 6482923-A 11 19-NOV-2002;
Location/Qualifiers
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AR410129
AR410129.1 GI:40161306
                                                                                                                                                                                                                                                                                                             28 bp 1
Sequence 13 from patent US 6482923.
AR256117
                                                    1. .28
/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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Matches 18; Conserv
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Matches 18; Conserv
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AR256117
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Bovenberg, R.Ary. Lans., Koekman, B. Pieter., Hoekema, A., Van Der Laan, J. Metske., Verweij, J. and De Vroom, E.

Process for the efficient production of 7-ADCA via
2-(carboxyethylthio) acetyl-7-ADCA and
3-(carboxymethylthio) propionyl-7-ADCA
Patent: US 5726032-A 11 10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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1 (bases 1 to 30)
Weissmann,C., Bueler,H., Aguet,M., Fischer,M. and Sailer,A.
Weissmann,C., Bueler,H., Aguet,M., Fischer,M. and Sailer,A.
Transgenic animals lacking prion proteins
Patent: US 5698763-A 1 16-DEC-1997;
Location/Qualifiers
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Pred. No. 6.2e+04;
0; Mismatches 6;
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AR256115
AR256115.1 GI:27305505
                                                                                                                                                                                                                                                                                                            /organism="unknown"
/mol_type="unassigned DNA"
                                 191791 48 bp
Sequence 11 from patent US 5726032.
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/mol_type="unassigned DNA"
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Sequence 1 from patent US 5698763.
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76.9%;
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Unclassified.
1 (bases 1 to 28)
Shi,Y. and Ruben,S.M.
                                                                                191791.1 GI:3936261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:3205551
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Best Local Similarity 76.9
Matches 20; Conservative
                                                                                                                                 Unknown.
Unclassified.
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                                                                   191791
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ACCESSION
VERSION
KEYWORDS
SOURCE
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ORGANISM

RESULT 8 I85833/c

8

REFERENCE AUTHORS

TITLE JOURNAL FEATURES

ORIGIN

DEFINITION

ACCESSION VERSION

KEYWORDS

SOURCE

RESULT 9 AR256115 LOCUS

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Gaps

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PAT 18-DEC-2003

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PAT 22-JUN-2001

source

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FEATURES

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AR410131

ACCESSION VERSION KEYWORDS

ORGANISM

AUTHORS

TITLE

REFERENCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets, R.A. and Leach, M. Nucleic acids containing single nucleotide polymorphisms and
               Luiten, R.G.M., Quax, W.J., Schuurhuizen, P.W. and Mrabet, N. Novel glucose isomerase enzymes and their use Patent: EP 0351029-A 8 17-JAN-1990; GIST-BROCADES N.V.; PLANT GENETIC SYSTEMS, N.V Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimkets, R.A. and Leach, M.

Nucleic acids containing single nucleotide polymorphisms methods of use thereof

Patent: WO 0140521-A 644 07-UUN-2001;

Curagen Corporation (US)
                                                                                                                                                                                                                   Score 16.2; DB 6; Length 33; Pred. No. 7.4e+04; 0; Mismatches 8; Indels
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/organism="Homo sapiens"
/mol rype="unassigned DNA"
/db_xref="taxon:9606"
25..26
/note="Nucleotide deleted between bases 25
Accession number cg20705188"
                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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79.2%; Pred. No. 8.7e+04;
tive 0; Mismatches 5; Indels
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                                                                                                                             /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 6994 from Patent WO0147944.
CQ008354
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Sequence 644 from Patent WO0140521.
AX157316.1 GI:14538647
                                                                                                                                                                                                                                                                                               2 CGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                                                         32 CGCGACTCCATCTCGACCTTCAAGAA 4
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Location/Qualifiers
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ilarity 72.4%;
Conservative (
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Best Local Similarity 79.28
Matches 19, Conservative
   1 (bases 1 to 33)
                                                                                                                1. .33
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Matches 21; Conserv
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                                                                                                                                                                                          Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 28)
Shi,Y. and Ruben,S.M.
Polymucleotides encoding a novel interleukin receptor termed interleukin-17 receptor-like protein
Patent: US 6635443-A 13 21-OCT-2003;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          54.0%; Score 16.2; DB 6; Length 28; 85.7%; Pred. No. 7.5e+04; ive 0; Mismatches 3; Indels
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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other sequences; artificial sequences.
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other sequences; artificial sequences.
1 (bases 1 to 33)
                                                                                         AR410131
Sequence 13 from patent US 6635443.
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A10235
A10235.1 GI:490665
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A06417
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Matches 18; Conserv
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DEFINITION

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ACCESSION

RESULT 13 A06417/c

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ORGANISM

VERSION KEYWORDS SOURCE

TITLE JOURNAL FEATURES

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PAT 16-JAN-2004

SOURCE ORGANISM

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A10235/c LOCUS

RESULT 14

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ACCESSION VERSION

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52.0%; Score 15.6; DB 6; Length 32;
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ilarity 62.5%;
Conservative
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FEATURES
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1 (bases 1 to 32)
Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 32)
Blanc, V., Blanche, F., Crouzet, J., Jacques, N., Lacroix, P.,
                                                                                                                                                                       25._.26
/note="Nucleotide deleted between bases 25 and
Accession number cg41501665"
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Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                          Score 15.8; DB 6
Pred. No. 1e+05;
0; Mismatches
methods of use thereof
Patent: WO 0147944.4, 6994 05-JUL-2001;
Curagen Corporation (US)
Location/Qualifiers
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                                                                            1.50 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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Sequence 43 from patent US 5891695.
AR069895
AR069895.1 GI:7220783
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Sequence 27 from Patent W09408014.
A37857
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/db_xref="taxon:32644"
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62.5%;
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89.5%;
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AR069895/c
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Thibaut, D., Zagorec, M., Debussche, L. and De Crecy-Lagard, V. Polypeptides involved in the biosynthesis of streptogramins, nuclectide sequences coding for these polypeptides and their use Patent: US 5891695-A 43 06-APR-1999;
Location/Qualifiers
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I (Dases 1 to 32)

Blanc, V., Blanche, F., Crouzet, J., Jacques, N., LaCroix, P.,
Thibaut, D., Zagorec, M., DeBussche, L. and De Crecy-Lagard, V.
Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
Patent: US 6171846-A 43 09-UNN-2001,
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Blanc, V., Blanche, F., Crouzet, J., Jacques, N., Lacroix, P.,
Thibaut, D., Zagorec, M., Debussche, L. and De Crecy-Lagard, V.
Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
Patent: US 6077699-A $2 20-UUN-2000;
Location/Qualifiers
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                                                                                                                                                                                                                                                                 Score 15.6; DB 6;
Pred. No. 1.3e+05;
5; Mismatches 4;
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Sequence 43 from patent US 6171846.
AR124176.1 GI:14109537
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/mol_type="unassigned DNA"
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Sequence 45 from patent US 6077699.
AR099999
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CGGTACCASAGSAGSGGSGGCTTS
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27 bp
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                                                                                                                   Location/Qualifiers
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/organism="unknown"
     AR161840.1 GI:16228821
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                                                    Unclassified.
1 (bases 1 to 43)
Huse, W.D.
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BD000197
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I85694/c
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Blanc, V., Blanche, F., Crouzet, J., Jacques, N., Lacroix, P.,
Blanc, V., Blanche, F., Crouzet, J., Jacques, N., Lacroix, P.,
Hibaut, D., Zagorec, M., Debussche, L. and De Crecy-Lagard, V.
Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
Patent: US 6670157-A 43 30-DEC-2003;
Location/Qualifiers
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Patent: US 5871974-A 43 16 FEB-1999;
Location/Qualifiers
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62.5%; Pred. .v.
tive 5; Mismatches
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Sequence 43 from patent US 6670157.
AR442783
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AR036016
AR036016.1 GI:5952684
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/organism≃"unknown"
/mol_type="unassigned DNA"
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Sequence 42 from patent US 6258530.
AR161840
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/organism="unknown"
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Best Local Similarity 70.0°
Matches 21; Conservative
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Best Local Similarity 62.5
Matches 15; Conservative
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Unclassified.
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AR161840/c
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AR036016/c
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AR442783/c
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Surface expression libraries of randomized peptides Patent: US 6258530-A 42 10-JUL-2001;
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Best Local Similarity 70.0%; Pred. No. 1.30+05;
Matches 21; Conservative 0; Mismatches 9;
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Patent: JP 2000279178-A 10 10-OCT-2000;
JAPANESE FOUNDATION FOR CANCER RESEARCH
OS Attificial Sequence
PN JP 2000279178-A/10
PD 10-OCT-2000
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JP 2000279178-A/10.
Synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 27)
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/organism="unknown"
/mol_type="unassigned DNA"
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                                                                                                        /mol_type="unassigned DNA"
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Gaps

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Unknown.
Unclassified.

1 (bases 1 to 40)

Bukh,J., Miller,R.H. and Purcell,R.H.

Bukh,J., Miller,R.H. and sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods and vaccines

Fatent: US 5514539-A 104 07-MAY-1996;

Location/Qualifiers
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Bukh, d., Miller,R.H. and Purcell,R.H.
Bukh,d., Miller,R.H. and Purcell,R.H.
Wicleotide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods and vaccines
Patent: US 5514339-A 106 07-MAY-1996;
Location/Qualifiers
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Best Local Similarity 76.0%; Pred. No. 1.5e+05;
Matches 19; Conservative 0; Mismatches 6;
                                                                                                    Score 15.4; DB 6;
Pred. No. 1.5e+05;
0; Mismatches 6;
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Sequence 104 from patent US 5514539.
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/wol_type="unassigned DNA"
                                                     /mol_type="unassigned DNA"
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Bukh,J., Miller,R.H. and Purcell,R.H.

Buch,J., Miller,R.H. and Purcell,R.H.

Nucleotide and deduced amino acid sequences of the envelope 1 gene

of 51 isolates of hepatitis C virus and the use of reagents derived

from these sequences in diagnostic methods

Patent: US 5871962-A 104 16-FEB-1999;

Location/Qualifiers
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Bukh,J., Miller,R.H. and Purcell,R.H.
Bukh,J., Miller,R.H. and Purcell,R.H.
Nucleotide and deduced amino acid sequences of the envelope 1 gene
of 51 isolates of hepatitis C virus and the use of reagents derived
from these sequences in diagnostic methods
Patent: US 5871962-A 106 16-FEB-1999;
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            C12N15/09,A61K31/00,A61K31/70,A61K38/00,A61K39/235,A61K48/00,
C07K14/075,
                                               C07K14/52, C07K14/68, C07K14/72, C12N7/00, C12N9/12, C12N9/80, PC
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                                                                                                                                                /organism='Artificial Sequence'. Location/Qualifiers
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Pred. No. 1.6e+05;
                                                                                                                    Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 104 from patent US 5871962. AR035911
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                                                                                                                                                                                                                                                                                                                          0; Mismatches
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/mol_type="unassigned DNA"
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Best Local Similarity 76.0
Matches 19; Conservative
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Unclassified.
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AR035911/c
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PAT 06-MAR-1998
                                                                                                                                              The memory cytotoxic T-lymphocyte (CTL) response to human cytomegalovirus infection contains individual peptide-specific CTL clones that have undergone extensive expansion in vivo 9 Virol. 73 (3), 2099-2108 (1999)
                     Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 42)
Weekes,M.P., Wills,M.R., Mynard,K., Carmichael,A.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="cytotoxic T-lymphocyte clones"
/tissue_type="blood"
1. .42
/product="TCRBV782BJ181 junctional region"
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MAP KINASE PHOSPHATNES GENE AND USES THEREOF
PATENT: WO 9706245-A 15 20-FEB-1997;
MEDICAL RES COUNCIL (GB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.4; DB 9;
Pred. No. 1.5e+05;
     beta-chain; T-cell receptor; VDJC region
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/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mkNk"
/db_xref="taxon:9606"
/clone="07/97 Clone 2"
/haplotype="A3 A3 B7 B7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 DP
Sequence 15 from Patent WO9706245.
A59897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="TCRBJ1S1 START"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .43
/organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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76.0%;
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Best Local Similarity 76.0°
Matches 19; Conservative
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Bukh, J., Miller, R.H. and Purcell, R.H.
Nuclectide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods and vaccines patent: US 6572864-A 106 03-JUN-2003;
Location/Qualifiers
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Bukh, J., Miller,R.H. and Purcell,R.H.
Bukh,J., Miller,R.H. and Purcell,R.H.
Nucleotide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods and vaccines
Patent: US 6572864-A 104 03-UNN-2003;
Location/Qualifiers
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                                                                                                            AR340325 40 bp D) Sequence 104 from patent US 6572864.
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
/mol_type="genomic DNA"
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27 GGCACATCAATAGCACGGCCTTGAA 3
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AR340325.1 GI:33731797
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AJ010898.1 GI:3559921
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AR340327/c
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AR340325/c
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PAT 06-MAR-1998

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Davison, A.R., Duckworth, G.S., Rao, V., Brown, T. and Mcclean, J.P. Labelling and detection of nucleic acids
Patent: EP 0754700-A 2 22-JAN-1997;
CRUACHEM ITD (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davison, A.R., Duckworth, G.S., Rao, V., Brown, T. and Mcclean, J.P. Labelling and detection of nucleic acids
Patent: EP 0754700-A 9 22-JAN-1997;
CRUACHEM LID (GB)
Location/Qualifiers
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BD016942.
BD016942.1 GI:2258118
JP 200125858-A/4.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 28)
Yoshida,M., Yanai,Y. and Takahasi,S.
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                                                                                                                                                                                                                                                                                  /mol_type="unassigned DNA"
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 44 bp
Sequence 2 from Patent EP0754700.
A58596
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Sequence 9 from Patent EP0754700.
A58603
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                                                  A58596.1 GI:3714176
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: EP 0754700-A 1 22-JAN-1997;
CRUACHEM LTD (GB)
Location/Qualifiers
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Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

Datent: WO 014794-A 5090 05-JUL-2001;

Curagen Corporation (US)

Location/Qualifiers
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/mol_txpe="unassigned DNA"
/mb_xref="taxon:9606"
25. .26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg43958634"
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Sequence 5090 from Patent WO0147944.
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    .40
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RESULT 34 CQ006450

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ACCESSION VERSION

PAT 06-MAR-1998

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HARUO SETO,
TOMOHISA KUZUYAMA,SHUNJI TAKAHASHI
C12N15/09,A01N57/12,C12N1/21,C12N9/00,C12P23/00,C12Q1/18//
2N1/21,C12R1:18),(C12P23/00,C12R1:19),(C12P23/00,C12R1:18),
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PN JP 2000300257-A/18
PD 31-OCT-2000
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1 (bases 1 to 32)

Miyake,K., Hashimoto,S., Motoyama,H., Ozaki,A., Set,H., Kuzuyama,T. and Takahashi,S.
Method for searching antibacterial or herbicidally active compound Patent: JP 2000300257-A 18 31-OCT-2000;
                                                                                                                                                                                                                    Description of
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S Artificial Sequence

B J2-20125858-A/4

PD 22-SEP-2000 JP 2000075781

PF 17-MAR-2000 JP 2000075781

PF MASANORI YOSHIDA, YUKTHIRO YANAI, SHIGERU TAKAHASI PC

C12015/09, A01H5/00, C12N5/10, C12N15/00, C12N5/00 CC

Artificial Sequence oligo nucleotide primer FH Key

Location/Qualifiers.
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Patent: JP 2001258558-A 4 25-SEP-2001;
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

November 18, 2005, 05:29:23 ; Search time 206.578 Seconds Run on:

(without alignments)
859.686 Million cell updates/sec

US-10-788-779-6 30 Perfect score: Title:

1 GCGGTACCCCAGCCCGGCCTTGAAGAA 30 Sequence:

IDENTITY NUC Scoring table: 4390206 seqs, 2959870667 residues Searched:

Gapop 10.0 , Gapext 1.0

4167226 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 50 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseg 16Dec04:* geneseqn1980s:* Database

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genesequ2002as:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2003as:* geneseqn2003bs:* geneseqn2004bs: geneseqn1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Adr05302 Human bet Aaz35752 Human IL1 Aaz52041 3'primer Aaa75767 PCR prime Aaq84993 Expandase Aaq82717 P. chryso Aci28074 Human mic Aci41032 Human III Aaz25756 Human III Aaz25063 3'primer Aaa75771 PCR prime Adc75771 PCR prime Adc93853 Human int Adc93851 Human int Adt93849 Human int Acf36917 Human alp Acf36933 Human alp Aaq91126 Beta-card Aca63116 Human bet Description SUMMARIES ACA63116 ADR05302 ADT93853 ADT93851 ADT93849 ACF36933 AAQ84993 AAQ82717 ACI28074 AAZ35752 AAZ52041 ACI41032 AAZ35754 AAZ35756 AAZ52043 ACF36917 AAA75767 AAA75771 13 6 5 Query Match Length DB 60 60 57 55 55 54 Score Result Š.

16.2 54.0 38 10 ADF72771 16.2 54.0 38 12 ADH34521 16 53.3 29 6 ARK49653 15 8 52.7 19 9 ACD82439 15.8 52.7 19 9 ACD82439 15.8 52.7 39 10 ACF29513 15.8 52.7 41 6 ARM86094 15.6 52.0 43 2 AAX13627 15.4 51.3 27 3 AAA93897 15.4 51.3 40 2 AAX18692 15.4 51.3 40 2 AAX18691 15.4 51.3 40 2 AAX1882 15.4 51.3 40 2 AAX1882 15.4 51.3 40 2 AAX1882 15.4 51.3 40 2 AAX1882 15.4 51.3 40 2 AAX1882 15.5 50.7 25 11 ADL6717 15.2 50.7 33 10 AD72409 15.2 50.7 44 2 AAX5819	Adf72771 Fusarium Adh34521 PCR prime Abk49653 Human int
44 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0 ADF72771 2 ADH34521 ABK49653
	38 1 38 1 29 6
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ALIGNMENTS

Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy; diagnosis; primer; mutation; detection; ss. Beta-cardiac myosin heavy chain PCR primer D. AAQ91126 standard; cDNA; 30 BP 92US-00989160 92US-00989160 19-FEB-1996 (first entry) 11-DEC-1992; 11-DEC-1992; US5429923-A. 04-JUL-1995. Synthetic. AAQ91126; RESULT 1 AAQ91126

(GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA (HARD) HARVARD COLLEGE. (BGHM) BRIGHAM & WOMENS HOSPITAL

Ä Rosenzweig Watkins H, Seidman J, Seidman C,

WPI; 1995-245715/32.

Non-invasive method for diagnosis of hypertrophic cardio-myopathy useful for testing asymptomatic individual(s).

Example 1; Col 10; 22pp; English.

AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-sasociated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain

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asymptomatic individuals suspected of having the disease. The method has a broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B. Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease and phenylketonuria
                                                                                                                                                                                                                                                                                                                                                    Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
phenylketonuria; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting a presence or absence of a mutation associated with hypertrophic cardiomypathy, useful for diagnosing cystic fibrosis or hemophilia, by detecting a mutation in an amplified product of a beta cardiac myosin heavy-chain DNA.
                                                                                                                                 Gaps
                                                                                                                                 ;
0
                                                                                                       Length 30;
                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                               Human beta cardiac myosin heavy chain PCR primer D.
                                                                             Sequence 30 BP; 7 A; 11 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosenzweig A;
                                                                                                     DB 2;
0.022;
                                                                                                                               0; Mismatches
                                                                                                                                                                     1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                         1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                     Score 30;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watkins H,
                                                                                                     100.0%;
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                                                                                                                                                                                                                                                 ACA63116 standard; DNA; 30
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                   Query Match
Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seidman C, Seidman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROSE/) ROSENZWEIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-512374/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SEID/) SEIDMAN C.
(SEID/) SEIDMAN J.
(WATK/) WATKINS H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003054343-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-1992;
                                                                                                                                                                                                                                                                                                      28-AUG-2003
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                                                                                                                                                                                                                                                                           ACA63116;
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DNA. The method is useful for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. This method is especially useful for diagnosing SHC and FHC, as well as for determining the estimated the life expectancy of a person with familial hypertrophic cardiomyopathy. In particular, the method is useful for determining an individual's genetic information, and diagnosing e.g. Gaucher's disease, haemophilia, buchenne's muscular dystrophy, sickle cell ansemia, Tay-Sachs disease, phenylketonuria or cystic fibrosis. The present sequence is a PCR primer used to amplify a region of the beta cardiac myosin heavy chain cDNA containing an FHC-associated mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (familial or sporadic, FHC, SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy, comprising amplifying beta-cardiac myosin heavy-chain DNA forming an amplified product, and detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy in the amplified product, thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also included are a set of DNA oligonucleotide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting mutations associated with hypertrophic cardiomyopathy to diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac myosin heavy-chain DNA and detecting the mutation in the amplified
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, beta cardiac myosin, heavy chain, PCR, primer, ss, FHC, SHC,
familial hypertrophic cardiomyopathy,
sporadic hypertrophic cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta cardiac myosin heavy chain mutation detection primer D.
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                                                                                                                                                                                                                                                             100.0%; Score 30; DB 9; Length 30; 100.0%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                          Sequence 30 BP; 7 A; 11 C; 9 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                                                                       1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-00989160.
95US-00469172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2004; 2004US-00788779,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR05302 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-2004 (first entry)
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Marches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seidman J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-592586/57.
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SEIDMAN J.
WATKINS H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004152121-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1995;
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                                                                                                                                                                                                                                                               Query Match
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(SEID/)
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(ROSE/)
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The invention relates to detecting the presence or absence of a mutation and secoidated with hypertrophic cardiomyopathy (sporadic or familial, SHC and FHC) comprises detecting a mutation associated with hypertrophic cardiomyopathy in an amplified product of a beta cardiac myosin heavy chain DNA. The mutations associated with SHC/FHC are detected in the myosin gene isolated from blood, by detecting mis-matched areas in RNA-DNA hybrid double strands (RNA from the normal gene, DNA from the suspect determine life expectancy in affected individuals e.g. using a Kaplan-Meier curve for the classified type of FHC causing point mutation. Also included are an RNA probe comprising ribonucleotides arranged in a sequence which is complementary to at least a portion of beta-cardiac myosin heavy-chain DNA and a set of DNA oligonucleotide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

Example 1; Page 5; 22pp; English.

oligonucleotide primers being useful for facilitating the diagnosis of hypertrophic cardiomyopathy by being capable of detecting a hypertrophic cardiomyopathy (comprising the diagnosis of hypertrophic cardiomyopathy (comprising a first container holding an RNA probe completely hybridisable to the beta-cardiac myosin heavy chain DNA, where the RNA probe is capable of detecting a hypertrophic cardiomyopathy associated mutation, a second container holding primers for amplifying beta-cardiac myosin heavy-chain DNA and instructions for using the components of the kit to detect the presence or absence of a hypertrophic cardiomyopathy-associated mutation in amplified beta-cardiac myosin heavy-chain DNA). The method is used for amplified beta-cardiac myosin heavy-chain DNA). The method is used for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. Presently, the diagnosis of individuals hypertrophic cardiomyopathy relies on the presence of typical clinical symptoms and the demonstration of unexplained ventricular hypertrophy. The present invention is non-invasive and based, at least in bart, on the discovery that hypertrophic cardiomyopathy is caused by point mutations in the beta cardiac myosin heavy-chain gene. Prior art reveals that there are no extensive studies involving a large number of families which established that this particular disease or disorder was caused by point mutations in the beta cardiac myosin heavy-chain gene. The present sequence is a PCR primer used to amplify a region of the beta cardiac myosin heavy chain having a disease-related point mutation. which amplify beta-cardiac myosin heavy-chain DNA (the set of 88888888888888888888888888888888888

Sequence 30 BP; 7 A; 11 C; 9 G; 3 T; 0 U; 0 Other;

Gaps ; 0 100.0%; Score 30; DB 13; Length 30; 100.0%; Pred. No. 0.022; or Mismatches 0; Indels GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30 1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30 30; Conservative Query Match Best Local Similarity Matches 30; Conserv ઠે 셤

AAZ35752

AAZ35752 standard; DNA; 26 AAZ35752;

ВЪ

(first entry) 01-FEB-2000

Human IL17RLP PCR 3' primer SEQ ID NO:9.

Human; interleukin 17 receptor like protein; IL17RLP; IL-17; diagnosis; detection; immune system related disorder; haemostasis; cellular activation; angiogenesis; tumour metastasis; ovulation; cellular migration; neurogenesis; infection; T-cell proliferation; autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation; sepsis; tumour; cancer; interstitial lung disease; arthritis; lymphoma; immunosuppression; immunity; inflammatory bowel disease; myelo suppression; PCR primer; ss.

Homo sapiens Synthetic

WO9914240-A1

25-MAR-1999.

16-SEP-1998;

98WO-US019121.

97US-0059133P. 17-SEP-1997; (HUMA-) HUMAN GENOME SCI INC.

Ruben SM; Shi Y,

WPI; 2000-061918/05

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The present invention describes nument interferent, it is tereptor, its present invention describes nument interferent, its tereptor, its protein (ILITRLP), isolated from a CDNA library of human adult pulmonary tissue. The present sequence represents a PCR primer for human ILITRLP. ILITRLP and its agonists can be used to treat disorders relating to cellular activation, haemostasis, angiogenesis, tumour metastasis, cellular activation and ovulation, and neurogenesis. They can also be used to enhance host defences against resistant chronic and acute infections, cellular migration and ovulation of the attraction and acute infections, cellular microbial leukocytes. ILITRLP may also be used to increase T-cell mcdiated autoimmune diseases and lymphocytic leukaemias, to cregulate haematopoiesis by regulating the activation and differentiation of T-cell mcdiated autoimmune diseases and lymphocytic leukaemias, to combilisation or to treat sepsis repedicts cells, e.g. to release mature cleukocytes from the bone marrow following chemotherapy, i.e. in stem cell eukocytes from the bone marrow following chemotherapy, i.e. in stem cell disgnosis or treatment of immune system related disorders e.g. tumours, cancers, interstitial lung disease, and any disregulation of immunity, humoral immunity, inflammatory bowel
New human interleukin-17 receptor like protein, e.g. to treat disorders relating to cellular activation.
                                                                                                                                                           The present invention describes human interleukin 17 receptor like
                                                                                                 Example 2; Page 95; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease, or myelo suppression
   ##X#XDDDDDDDDDDDDDXX8
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Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;

Gaps ö Score 18.2; DB 3; Length 26; Pred. No. 1.1e+03; 0; Mismatches 3; Indels , 0 60.7%; Query Match
Best Local Similarity 87.0*

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RESULT 5 AAZ52041

AAZ52041 standard; DNA; 26

AAZ52041;

09-AUG-2000 (first entry)

3'primer for amplification of IL-17RLP leader sequence.

Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor; resistant chronic infection; acute infection; mycobacterial infection; T-cell proliferation; IL-2 biosythesis; lymphocytic leukaemia; T-cell mediated autoimmune disease; hemacopoiesis; sepsis; hybridoma; IL-6 expression; myeloma; plasmacytoma; Lennert's Lymphoma; cytostatic, hematopoietic, proliferative, Immunoprotective; cytostatic; }
antibacterial; PCR primer; 88.

Homo sapiens

WO200015759-A1.

23-MAR-2000.

99WO-US021048 15-SEP-1999;

99US-00268311 98WO-US019121 16-SEP-1998; 16-SEP-1998; 16-MAR-1999; (HUMA-) HUMAN GENOME SCI INC

Ruben SM, Shi Y;

WPI; 2000-271403/23

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The patent relates to novel interleukin-17-like receptor protein (IL-17RLP) IL-17RLP is a homologue of the IL-17 receptor and has a wide range of cytokine receptor-like activities. IL-17RLP or its agonists may be used to enhance host defenses against resistant chronic and acute infections, e.g. mycobacterial infections, via the attraction and cetivation of microbicidal leukcytes. It may also be used to increase T-cell proliferation by stimulating IL-2 hosynthesis, for the treatment of T-cell mediated autoimmune diseases and lymphocytic leukaemias. IL-17RLP may also be used to regulate hematopoiesis and to treat sepsis.

Traple agonists and antagonists can also be used to modulate IL-6. TYRLP agonists and intreatment of cancers such as myelomas, carracellular intreatment of cancers such as myelomas, but seful in treatment of cancers such as myelomas.

Sequession, useful in treatment of cancers such as myelomas, so the side of the 3 PCR primer used for the amplification of IL-17RLP leader is the 3 PCR primer used in the cloning and expression of IL-17RLP protein
Novel polynucleotides encoding interleukin-17-like receptor protein, useful for diagnosis and treatment of immune system-related disorders, e.g. sepsis and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                      Example 2; Page 98; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a baculovirus expression system
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60.7%; Score 18.2; DB 3; Length 26; larity 87.0%; Pred. No. 1.1e+03; Conservative 0; Mismatches 3; Indels
                                                                        1 GCGGTACCCCAGCAGCCCGGCCT 23
                                                                                                        24
                                                                                                        GCGGTACCCCAGCCTCCCGGCTT
                  Local Similarity
ses 20; Conserv
   Query Match
                                  Matches
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Gaps

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Bb AAA75767 standard; DNA; 26 (first entry) 22-JAN-2001 AAA75767; RESULT 6 AAA75767

Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis; cellular activation; haemostasis; angiogenesis; tumour metastasis; cellular migration; ovulation; neurogenesis; arthritis; autoimmune disorder; systemic lupus erythromatosus; PCR primer; ss. PCR primer for a human interleukin 17 receptor-like cDNA fragment.

09-MAR-2004; 2004AU-00200961. 09-MAR-2004; 2004AU-00200961.

AU2004200961-A1

01-APR-2004,

(HUMA-) HUMAN GENOME SCI INC

Shi Y, Ruben SM;

Homo sapiens,

WO200055204-A1

21-SEP-2000

06-MAR-2000; 2000WO-US005759

99US-00268311.

16-MAR-1999;

(HUMA-) HUMAN GENOME SCI INC

Ruben SM; Shi Y, WPI; 2000-647065/62.

Novel gene encoding a polypeptide of the interleukin-17 receptor family, and an antagonist and agonist of the polypeptide, useful for treating, and an antagonist and agonist of the polypeptide, useful for treating, diagnosing, detecting and/or preventing immune system related disorders.

Example 2; Page 179; 247pp; English.

'R primers AAA75766-67 were used to amplify a fragment of cDNA encoding human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP

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                                                                                                                                                                                                                                                                                                                                            ss; antiinflammatory; cytostatic; gastrointestinal; immunosuppressive; interleukia 17-receptor-like protein; ILJYRLP; callular activation; hemostasis; angiogenesis; tunor metastasis; cellular migration; ovulation; neurogenesis; immune-related disorder; Crohn's disease; tumor;
polypeptide is useful for screening for agonists and antagonists. These antagonists and agonists are useful for treating, diagnosing, detecting and or preventing disorders related to cellular activation, haemostasis, angiogenesis, tumour metastasis, cellular migration, ovulation or neurogenesis, such as osteoporosis, arthritis and autoimmune disorders e.g. systemic lupus erythromatosus
                                                                                                                                                                                                                                                                                                                                                                                             inflammatory bowel disease, autoimmune disease, lymphocytic leukemia, graft versus host disease, chromosomal identification, primer, PCR.
                                                                                                                                                                                                                                                                                                                     Human interleukin 17 receptor-like protein cDNA expression 3' primer.
                                                                                                                                       Gaps
                                                                                                                                      ;
0
                                                                                                          Score 18.2; DB 3; Length 26;
Pred. No. 1.1e+03;
); Mismatches 3; Indels
                                                                                      Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                             23
                                                                                                                                                                           GCGGTACCCCAGCCTCCCGGCTT 24
                                                                                                                                                             1 GCGGTACCCCAGCAGCCCGGCCT
                                                                                                                                      -
0
                                                                                                            60.7%;
87.0%;
                                                                                               Query Match
Best Local Similarity 87.2

Best Local Similarity 87.2
                                                                                                                                                                                                                                               ADT93849 standard; DNA; 26
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                              16-DEC-2004
                                                                                                                                                                                                                                                                       ADT93849;
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                                                                                                                                                                                                                                    ADT93849
ID ADT9
                                                                                                                                                                                                                        RESULT 7
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immune-related disorders e.g., Crohn's disease, tumor, inflammatory bowel disease, autoimmune diseases, lymphocytic leukemias, or graft versus host Novel isolated interleukin 17-receptor-like protein useful for treating WPI; 2004-662639/65. disease

Example 2; SEQ ID NO 9; 145pp; English.

The invention relates to an isolated interleukin 17-receptor-like protein (IL17RLP) (I) comprising an amino acid sequence that is 95% or more identical to a sequence e.g., sequence having amino acids from positions 19-407 of a fully defined sequence (SI) of 436 amino acids as given in the specification, sequence having amino acids from positions 18-407 of (SI) that comprises N-terminal methionine or sequence having amino acids from positions 1-407 of (SI). (I) is useful for treating amino acids related to cellular activation, hemostasis, angiogenesis, tumor metastasis, cellular migration, ovulation or neurogenesis. (I) is useful for treating immune-related disorders e.g., Crohn's disease, tumor inflammatory bowel disease, autoimmune diseases, lymphocytic leukemias, or graft versus host disease. (II) is useful for chromosomal cidentification. (I) exhibits enhanced activity, solubility and stability, and is produced in large quantities. This sequence corresponds to a PCR primer to amplify the extracellular region DNA from the human IL17RLP

88333

RESULT 8 ACF36917 ID ACF3

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New fusion protein comprising a stem region of fucosyltransferase VI and a catalytic domain of fucosyltransferase VII, useful for enzymatically synthesizing glycoproteins, glycolipids, and oligosaccharide moieties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer; amplify; PCR; expandase gene; cefE; Nicordia lactamdurans; Streptomyces clavuligarus; expression cassette; acyltransferaes; fungus; Penicillin chrysogenum; hybrid promoter; Aspergillus nidulans; 7-ADCA; 7-amino-desacetoxycephalosporanic acid; cephalosporin; antibiotic; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a fusion protein comprising a stem region of human fucosyltransferase VI and a catalytic domain of fucosyltransferase VII, where the fusion protein has high enzymatic activity, and catalyses the transfer of fucose residue from a donor substrate to an acceptor substrate. The fusion protein is useful for enzymatically synthesising glycoproteins, glycolipids, and oligosaccharide moieties. The present sequence is a PCR primer used to isolate a coding sequence in the exemplification of the invention
                                                                                                                          Alphal, 3 fucosyltransferase; FT; glycosyltransferase; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expandase gene amplification primer #11 for expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.2; DB 12; Length 37;
Pred. No. 2.8e+03;
0; Mismatches 3; Indels (
                                                                                   Human alpha1,3 fucosyltransferase VII plasmid PCR primer #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37 BP; 7 A; 18 C; 10 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCGGTACCCCAGCAGCCCGGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GCGGTACCCCGCACCCCAGCC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 81; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                        (NEOS-) NEOSE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                         05-MAY-2003; 2003WO-US014235.
                                                                                                                                                                                                                                                                                                                                                03-MAY-2002; 2002US-0377730P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.3%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ84993 standard; DNA; 48
                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Conservative
                                                                                                                                             enzyme, PCR, primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                               Bayer RJ, Mendoza G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-053043/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                          WO2003093448-A2.
                                                                                                                                                                                      Homo sapiens.
                                             15-APR-2004
                                                                                                                                                                                                                                                                 13-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9504148-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
04-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ84993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
      ACF36933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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      à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New fusion protein comprising a stem region of fucosyltransferase VI and a catalytic domain of fucosyltransferase VII, useful for enzymatically synthesizing glycoproteins, glycolipids, and oligosaccharide moieties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a fusion protein comprising a stem region of human fucosyltransferase VI and a catalytic domain of fucosyltransferase VII, where the fusion protein has high enzymatic activity, and catalyses the transfer of fucose residue from a donor substrate to an acceptor substrate. The fusion protein is useful for enzymatically synthesising glycoproteins, glycollyids, and enzymatically synthesising glycoproteins, glycollyids, and oligosaccharide moieties. The present sequence is a PCR primer used to isolate a coding sequence in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alphal, 3 fucosyltransferase; FT; glycosyltransferase; fusion protein;
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
cDNA sequence (ADT93841) for expression in a baculovirus expression
                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human alphal, 3 fucosyltransferase VII plasmid PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.2; DB 12; Length 24; Pred. No. 2.7e+03;
                                                                                                   Length
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                        Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                               th 60.7%; Score 18.2; DB 13; Similarity 87.0%; Pred. No. 1.1e+03; 20; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 4 A; 13 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                              1 GCGGTACCCCAGCAGCCCGGCCT 23
                                                                                                                                                                                                       GCGGTACCCCAGCCTCCCGGCTT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGGTACCCCGCCACCCCAGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCGGTACCCCAGCCAGCCCGGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 72; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-2003; 2003WO-US014235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.3%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAY-2002; 2002US-0377730P
                                                                                                                                                                                                                                                                                                                       ACF36917 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACF36933 standard; DNA; 37
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mendoza G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-053043/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003093448-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bayer RJ,
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                                                                                                 Query Match
                                                                                                                      Best Loca
Matches
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ACF36933 ID ACF RESULT 9

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Gaps

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sapiens
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                                                                                                                                                                                                                                                                                                                                                   AC128074;
                                                                                                                                                                                                                                                                       18
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ношо
                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                  AC128074
                                                                                                                                                                                                                                                                                                                               원
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                                                                                                                                                                           Primers (AAQ84983-95) were used to amplify the expandase gene (cefE) from either Nicordia lactamdurans or Streptomyces clavuligerus. The resultant sequences were placed in an expression cassette for simultaneous expression of the cefE gene and the gene encoding an acyltransferas expression cassette is placed in the fungus Penicillin chrysogenum. Expression of the genes in the cassette is driven either by a trp-lac hybrid promoter or the promoter from the Aspergillus nidulans gpdA gene. The terminator is the 3'-end of the p.chrysogenum penDE gene. The primers AAQ84991-3 were used to amplify a 0.5 kb region containing the
                                                                                                                       7-amino-desacetoxy-cephalosporanic acid prodn. in Penicillium chrysogenum
                                                                                                                                                                                                                                                                                                                desacetoxycephalosporanic acid (7-ADCA), an intermediate in the production of cephalosporin antibiotics. Note: the sequences shown in this patent are identical to those in patent WO 95/04149. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                P.chrysogenum penDE (acyltransferase gene) terminator sequence. This sequence was linked by PCR to the 3' end of the N.lactamdurans cefE gene. The cassette is used in the production of 7-amino-
                                                                             Verweij J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Verweij J;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps

    P. chrysogenum cefE gene expression cassette construction oligo.

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0
                                                                                                                                   by simultaneous expression of expandase and acyl-transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N. lactamdurans; S. clavuligerus; P. chrysogenum; cefE gene; expression cassette; 7-amino-desacetoxy-cephalosporanic acid;
                                                                                                                                                                                                                                                                                                                                                                                               Score 16.6; DB 2; Length 48; Pred. No. 5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Der Laan JM,
                                                                            Van Der Laan JM,
                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                         Sequence 48 BP; 11 A; 18 C; 11 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expandase gene; cephalosporin antibiotics; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoekema A,
                                                                           Bovenberg RAL, Koekman BP, Hoekema A,
                                                                                                                                                                                                                                                                                                                                                                                                                                           6 ACCCCAGCAGCCCGGCCTTGAAG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 Accececececececerricas 40
                                                                                                                                                       Example 1; Page 14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ82717 standard; DNA; 48 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93EP-00202260.
93EP-00203695.
94WO-EP002543
                   93EP-00202259
                                                                                                                                                                                                                                                                                                                                                                                               55.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovenberg RAL, Koekman BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KONN ) GIST-BROCADES NV.
                                                                                                                                                                                                                                                                                                                                                                                                                     19; Conservative
                                                      (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                 WPI; 1995-082231/11.
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
29-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9504149-A1
                   30-JUL-1993;
                               24-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ82717;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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                                                                               7-amino-desacetoxy-cephalosporanic acid prodn. in Penicillium chrysogenum - transformed with expandase gene, using 3,3'-thiodi:propionic acid as side chain precursor and deacylation of intermediate.
                                                                                                                                                                                                                                                                                                                                        AAQ82707-082719 are oligonuclectides used in the construction of P. chrysogenum expression cassettes for the N. lactamdurans and S. clavuligerus ceff (expandase) gene. The transformed P. chrysogenum can now be used for 7-amino-desacetoxy-cephalosporanic acid prodn. an intermediate for cephalosporin antibiotics. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 55.3%; Score 16.6; DB 2; Length 48; Local Similarity 82.6%; Pred. No. 5e+03; nes 19; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human microarray DNA oligonucleotide SEQ ID NO 28065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 48 BP; 11 A; 18 C; 11 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 28065; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ACCCCAGCAGCCCGGCCTTGAAG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accecceccecceccicaring 40
                                                                                                                                                                                                                                                                      Example 1; Page 14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2002; 2002US-00098263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACI28074 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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WPI; 1995-082232/11.
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gene expression levels, identifying biallelic markers or polymorphisms or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid brobes is useful in in situ hybridisation, in Southern, Northern or dothor hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termin of many molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at segdence.html
probes are attached to a solid support. The analysis comprises monitoring
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Score 16.2; DB 9; Length 25; Pred. No. 6.8e+03; 3; Indels Sequence 25 BP; 3 A; 9 C; 8 G; 5 T; 0 U; 0 Other; 0; Mismatches 22 2 CGGTACCCCAGCAGCCCGGCC 54.0%; 85.7%; Query Match
Best Local Similarity 85.77
Matches 18, Conservative

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Gaps

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4 CGGTACCCTAGGAGCCCGGTC 24 BP ACI41032 standard; DNA; 25 ACI41032; RESULT 13 ACI41032 g 8

(first entry) 13-OCT-2003

Human microarray DNA oligonucleotide SEQ ID NO 41023.

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

98WO-US019121. 97US-0059133P

16-SEP-1998;

25-MAR-1999.

WO9914240-A1

Homo sapiens

Synthetic.

(HUMA-) HUMAN GENOME SCI INC.

17-SEP-1997;

WPI; 2000-061918/05 Shi Y, Ruben SM;

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 41023; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms,

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or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; interleukin 17 receptor like protein; IL17RLP; IL-17; diagnosis; detection; immune system related disorder; haemostasis; cellular activation; angiogenesis; tumour metastasis; ovulation; cellular migration; neurogenesis; infection; T-cell proliferation; autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation; sepsis; tumour; cancer; interstitial lung disease; arthritis; lymphoma; immunosuppression; immunity; inflammatory bowel disease; myelo suppression; PCR primer; ss.
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0
                                                                                                                                                                                                                         Score 16.2; DB 9; Length 25;
Pred. No. 6.8e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                             Sequence 25 BP; 3 A; 9 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IL17RLP PCR 3' primer SEQ ID NO:11.
                                                                                                                                                                                                                                                                                          2 CGGTACCCCAGCAGCCCGGCC 22
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85.7%;
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Best Local Similarity 85.7
Matches 18; Conservative
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New human interleukin-17 receptor like protein, e.g. to treat disorders Example 3; Page 100; 133pp; English. relating to cellular activation.

The present invention describes human interleukin 17 receptor like protein (IL17RLP), isolated from a CDNA library of human adult pulmonary tissue. The present sequence represents a PCR primer for human IL1RLP. IL17RLP and its agonists can be used to treat disorders relating to cellular activation, haemostasis, angiogenesis, tumour metastasis, cellular migration and ovulation, and neurogenesis. They can also be used to enhance host defences against resistant chronic and acute infections, e.g. mycobacterial infections via the attraction and activation of microbial leukocytes. IL17RLP may also be used to increase T-cell

proliferation by the stimulation of IL-2 biosynthesis for the treatment

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proliferation by the stimulation of IL-2 biosynthesis for the treatment of T-cell mediated autoimmune diseases and lymphocytic leukaemias, to regulate haematopolesis by regulating the activation and differentiation of various haematopolesic progenitor cells, e.g. to release mature leukocytes from the bone marrow following chemotherapy, i.e. in stem cell mobilisation or to treat sepsis. The products can also be used for the diagnosis or treatment of immune system related disorders e.g. tumours, cancers, interstitial lung disease, and any disregulation of immune cell function including autoimmunity, arthritis, leukaemias, lymphomas, immunosuppression, immunity, humoral immunity, inflammatory bowel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; immune system related disorder; haemostasis; cellular activation; angiogenesis; tumour metastasis; ovulation; cellular migration; neurogenesis; infection; T-cell proliferation; autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation; sepsis; tumour; cancer; interstitial lung disease; arthritis; lymphoma; immunosuppression; immunity; inflammatory bowel disease; arthritis; lymphoma; myelo suppression; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; interleukin 17 receptor like protein; IL17RLP; IL-17; diagnosis;
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                                                                                                                                                                                                                                                                                      54.0%; Score 16.2; DB 3; Length 28; 85.7%; Pred. No. 6.9e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                              Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human IL17RLP PCR primer SEQ ID NO:13.
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                                                                                                                                                                                                                                                                                                                                                                                                                 GGTACCCCAGCCTCCCGGCTT
                                                                                                                                                                                                            disease, or myelo suppression
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Best Local Similarity 85.7
Matches 18; Conservative
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            of T-cell mediated autoimmune diseases and lymphocytic leukaemias, to regulate haematopoiesis by regulating the activation and differentiation of various haematopoietic progenitor cells, e.g. to release mature leukocytes from the bone marrow following chemotherapy, i.e. in stem mobilisation or to treat sepsis. The products can also be used for the diagnosis or treatment of immune system related disorders e.g. tumours, cancers, interstitial lung disease, and any disregulation of immune cell function including autoimmunity, arthritis, lenkaemias, lymphomas, immunosuppression, immunity, humoral immunity, inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor; resistent chronic infection; acute infection; wycobacterial infection; T-cell proliferation; IL-2 biosynthesis; lymphocytic leukaemia; T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL-6 expression; myeloma; plasmacytoma; Lennert's Lymphoma;
Immunoprotective; cytostatic; hematopoietic; proliferative;
antibacterial; PCR primer; ss.
                                                                                                                                                                                                                                Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3'primer for amplification of IL-17RLP cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                         6 GGTACCCCAGCCTCCCGGCTT 26
                                                                                                                                                                                           disease, or myelo suppression
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Best Local Similarity 85...
And 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200015759-A1.
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16-MAR-1999;
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may also be used to regulate hematopoiesis and to treat sepsis.

Extracellular IL-17RLP domains may be used as antagonists of IL-17RLP. IL-17RLP and antagonists can also be used to modulate IL-6 expression, useful in treatment of cancers such as myelomas, plasmacytomas and hybridomas and Lennert's Lymphoma. The present sequence is the 3' PCR primer used for the amplification of IL-17RLP cDNA. This primer comprises Aspil8 and 17 of nucleotides complementary to the 3'coding region immediately before the stop codon. This is used in the construction of vectors for expression in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primers AAA75768-69 were used to amplify a fragment of cDNA encoding a human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP polypeptide is useful for screening for agonists and antagonists. These antagonists and agonists are useful for treating, diagnosing, detecting and or preventing disorders related to cellular activation, hemostasis, angiogenesis, tumour metastasis, cellular migration, ovulation or neurogenesis, such as osteoporosis, arthritis and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel gene encoding a polypeptide of the interleukin-17 receptor family, and an antagonist and agonist of the polypeptide, useful for treating, diagnosing, detecting and/or preventing immune system related disorders.
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellular activation; haemostasis; angiogenesis; tumour metastasis; cellular migration; ovulation; neurogenesis; arthritis; autoimmune disorder; systemic lupus erythromatosus; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer for a human interleukin 17 receptor-like cDNA fragment.
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                                                                                                                                                                                                                                                 Score 16.2; DB 3; Length 28;
Pred. No. 6.9e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                           Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;
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Best Local Similarity 85.7%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 17
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PCR primers AAA75770-71 were used to amplify a fragment of DNA encoding a human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP polypeptide is useful for screening for agonists and antagonists. These antagonists and agonists are useful for treating, diagnosing, detecting and or preventing disorders related to cellular activation, haemostasis, ampiogenesis, thuour metragens, cellular migration, ovulation or neurogenesis, such as osteoporosis, arthritis and autoimmune disorders e.g. systemic lupus erythromatosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel gene encoding a polypeptide of the interleukin-17 receptor family, and an antagonist and agonist of the polypeptide, useful for treating, diagnosing, detecting and/or preventing immune system related disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                       cellular activation; haemostasis; angiogenesis; tumour metastasis; cellular migration; ovulation; neurogenesis; arthritis; autoimmune disorder; systemic lupus erythromatosus; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                       PCR primer for a human interleukin 17 receptor-like DNA fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3b; Page 185; 247pp; English.
23
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                               6 GGTACCCCAGCCTCCCGGCTT
3 GGTACCCCAGCAGCCCGGCCT
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                                                                                                                                                                                                                                                                                                   22-JAN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-647065/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200055204-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2000
                                                                                                                                                                                                                                                AAA75771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADT93853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Gaps

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Query Match 54.0%; Score 16.2; DB 3; Length 28; Best Local Similarity 85.7%; Pred. No. 6.9e+03; Matches 18; Conservative 0; Mismatches 3; Indels

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interleukin 17-receptor-like protein; IL17RLP; cellular activation; hemostasis; angiogenesis; tumor metastasis; cellular migration; ovulation; neurogenesis; immune-related disorder; Crohn's disease; tumor; inflammatory bowel disease; autcimmune disease; lymphocytic leukemia; graft versus host disease; chromosomal identification; primer; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      se; antiinflammatory; cytostatic; gastrointestinal; immunosuppressive; interleukin 17-receptor-like protein; IL17RLP; cellular activation; hemostasis; angiogenesis; tumor metastasis; cellular migration; ovulation; neurogenesis; immune-related disorder; Crohn's disease; tumor; inflammatory bowel disease; autoimmune disease; lymphocytic leukemia; graft versus host disease; chromosomal identification; primer; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated interleukin 17-receptor-like protein useful for treating immune-related disorders e.g., Crohn's disease, tumor, inflammatory bowel disease, autoimmune diseases, lymphocytic leukemias, or graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer to amplify the extracellular domain from the human IL17RLP cDNA sequence (ADT93841) for expression in Chinese Hamster Ovary (CHO) cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human interleukin 17 receptor-like protein extracellular domain primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; SEQ ID NO 13; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GGTACCCCAGCAGCCCGGCCT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTACCCCAGCCTCCCGGCTT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADT93851 standard; DNA; 28 BP
                                                                                                                                                                                                                                                                                                                          09-MAR-2004; 2004AU-00200961.
                                                                                                                                                                                                                                                                             09-MAR-2004; 2004AU-00200961.
                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-662639/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               Shi Y, Ruben SM;
                                                                                                                                                                                 AU2004200961-A1.
                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-2004
                                                                                                                                                                                                                                01-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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The invention relates to an isolated interleukin 17-receptor-like protein (ILIRIP) (I) comprising an amino acid sequence that is 95% or more identical to a sequence e.g., sequence having amino acids from positions 19-407 of a fully defined sequence (SI) of 426 amino acids as given in the specification, sequence having amino acids from positions 18-407 of (SI) that comprises N-terminal methionine or sequence having amino acids from positions 1-407 of (SI). (I) is useful for treating amino acids related to cellular activation, hemostasis, angiogenesis, tumor metastasis, callular migration, ovulation or neurogenesis. (I) is useful for treating immune-related disorders e.g., Crohn's disease, tumor, inflammatory bowel disease, autoimmune diseases, lymphocytic leukemias, or graft versus host disease. (II) is useful for chromosomal cidentification. (I) exhibits enhanced activity, solubility and stability, and is produced in large quantities. This sequence corresponds to a PCR primer to amplify the extracellular domain from the human ILITRLP CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                           Novel isolated interleukin 17-receptor-like protein useful for treating immune-related disorders e.g., Crohn's disease, tumor, inflammatory bowel disease, autoimmune diseases, lymphocytic leukemias, or graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immobilizing; functional organic molecule; predetermined density; mixed monolayer surface; MMS; reducing end; peracetylated sugar; chemoselective; ss; primer; cutinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.0%; Score 16.2; DB 13; Length 28; 85.7%; Pred. No. 6.9e+03; ive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusarium solani cutinase gene primer, ExonlB.
                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 11; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTACCCCAGCAGCCCGGCCT 23
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                                                                                                                            09-MAR-2004; 2004AU-00200961.
                                                                                                                                                                09-MAR-2004; 2004AU-00200961
                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence (ADT93841).
                                                                                                                                                                                                                                                                          WPI; 2004-662639/65.
                                                                                                                                                                                                                                      Shi Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusarium solani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003018854-A2.
                                                      AU2004200961-A1
                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAR-2003.
                                                                                        01-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF72771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e
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Matches
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ID ABK
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                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel method for immobilizing a functional organic molecule in a predetermined density on a mixed monolayer surface (MMS). The novel method comprises a first monolayer moiety (MMI) having a covalent bond forming reactive group and a second monolayer moiety (MMZ) covalent bond forming reactive group and a second monolayer moiety (MMZ) thaving an inert group. The method involves contacting MMS with the functional organic molecule to form a covalent bond between the contactional organic molecule and MMI to immobilize the functional organic molecule in a predetermined density on a mixed concluder, the novel method of the invention is useful for immobilizing a functional organic molecule in a predetermined density on a mixed conjugopetides, peptides, polypeptides, oligonucleocides, nucleocides, oligonucleosides, carbohydrates, proteins, nucleosides, uncleotides, oligonucleosides, and small molecules, but preferably a carbohydrate. The carbohydrate comprises a reducing an n-pentenyl group. This polymcleotide converses a primer used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                    Immobilizing functional organic molecule in a predetermined density on a mixed monolayer surface, by contacting the surface with the organic molecule to form a covalent bond and to immobilize the organic molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alkanethiol, reactant ligand, substrate, protein chip, polypeptide immobilisation, enzyme activity, antibody detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.0%; Score 16.2; DB 10; Length 38; 72.4%; Pred. No. 7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                          Wang E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38 BP; 5 A; 14 C; 10 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer #2 for Fusarium solani cutinase gene.
                                                                                                                                        Duffy D, Agosto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGTACCCAAGTTGCCCCGTCTCTGTTGAA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                   Example 6; SEQ ID NO 2; 234pp; English.
                               2001US-0315544P.
2002US-0356765P.
2002US-0358412P.
2002US-0357136P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                          26-APR-2002; 2002US-0380259P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-2001; 2001US-00923760.
27-AUG-2002; 2002WO-US027195
                                                                               2002US-0375023P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH34521 standard; DNA; 38
                                                                                                                                        Hodneland C, Campbell S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide immobilisation cutinase; PCR; primer; ss.
                                                                                                                 (SURF-) SURFACE LOGIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 72.4
                                                                                                                                                              WPI; 2003-393250/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003119054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusarium solani.
                                                        15-FEB-2002;
                                 28-AUG-2001;
15-FEB-2002;
                                                                               20-FEB-2002;
                                                                     19-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
ADH34521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to alkanethiols substituted with a reactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid sequences encoding novel mammalian nonerythroid Rh type C and glycoproteins which have a characteristic twelve transmembrane domain
                                                                                                                                                                                                                                                                                                 New alkanethiols substituted with a reactant ligand useful for immobilizing polypeptides on gold surfaces, e.g. for determining enzyme activity or detecting antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RhCG: mouse; human; non-erythroid Rh type C glycoprotein; ss; intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.2; DB 12; Length 38; Pred. No. 7e+03; 0; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38 BP; 5 A; 14 C; 10 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 cécraccaságraccicércrerentas 30
                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; SEQ ID NO 2; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human intron 1 3' acceptor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NYBL-) NEW YORK BLOOD CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example, Fig 6, 53pp, English
07-AUG-2001; 2001US-00923760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.0%;
72.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK49653 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
                                                                                                                                                                  ΰ
                                                                                                                                                              Mrksich M, Hodneland
                                                        (MRKS/) MRKSICH M.
(HODN/) HODNELAND C.
                                                                                                                                                                                                                                 WPI; 2004-080248/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-351774/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200220719-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK49653;
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AAM53114 to AAM5329 represent peptides related to human polymorphic polymucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. For example, (I) may be used to treat disorders by rectifying mutations or beletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (I) and its complementary
            This invention relates to the nucleic acid and protein sequences of novel human and mouse non-erythroid Rh type C glycoprotein (RhCG). The RhCG protein and the mouse homologue (rhcg) have a characteristic 12 transmembrane domain structure and are expressed in kidneys and testis. The invention also comprises a method for antibody that specifically binds an epitope of the glycoprotein and a method for detecting the protein using this antibody. The antibodies of the invention may be used in Western blots, enzyme linked immunosorbent assays (BLISA) or immunohistochemical assays to identify the non-erythroid tissues, particularly kidney and testis, that express the RhCG or Rhcg glycoproteins. The methods are used for detecting an Rhcg or and Rhcg glycoprotein in a sample. The present sequence represents the intronic sequence at an intron/exon splice site of the rhcg gene of the invention
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, single nucleotide polymorphism; SNP; genome; gene therapy; protein therapy; vaccine; probe; diagnostic assay; detection; quantitation; restorative therapy; polymorphic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic nucleic acid sequences, useful in genetic testing and
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                                                                                                                                                                                                                                                                                                                                  53.3%; Score 16; DB 6; Length 29; 79.2%; Pred. No. 8.3e+03;
                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                           Sequence 29 BP; 5 A; 11 C; 10 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP containing nucleic acid SEQ:644.
                                                                                                                                                                                                                                                                                                                                                     8.3e+03;
                                                                                                                                                                                                                                                                                                                                                 79.2%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                3 GGTACCCCAGCAGCCCGGCCTTGA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 251; 2653pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI73703 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-2000; 2000WO-US032758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1999; 99US-0168138P.
29-NOV-2000; 2000US-00726173.
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                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-356160/37.
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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Matches
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AAI73703/
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sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar mucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic
                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                      53.3%; Score 16; DB 4; Length 50;
79.2%; Pred. No. 8.6e+03;
tive 0; Mismatches 5; Indels
                                                                                                                                                                                                          Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid cloning associated adaptor molecule #140.
                                                                                                                                                                     Sequence 50 BP; 4 A; 14 C; 15 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 2 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.8; DB 9;
Pred. No. 9.6e+03;
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                                                                                                                                                                                                                                                                                                                     3 GGTACCCCAGCAGCCCGGCCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Fig 3; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                   ACD82439 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                               Conservative
                                                                                                                                  polypeptides in samples
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-521745/49.
                                                                                                                                                                                                                          Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
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                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                       38
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Matches

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The present sequence is that of a primer used, with the primer given in ACF79912, for the PCR amplification of cDNA encoding the human Her-2 protein Cytoplasmic kinase domain. The PCR product was used in the construction of a fusion protein comprising the Her-2 kinase domain and a modified (W687F mutant) chitin binding domain (CBD) of Bacillus circulans PL-12 chitchase Al. The modified CBD acted as an affinity tag for purification of the Her-2 kinase domain, allowing protein elution under non-denaturing conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                 (mutant) chitin binding domain capable of reversibly binding a chitin bstrate under a selected non-denaturing condition, useful for producing d purifying a target protein molecule.
                                                                            Human; Her-2; chitin binding domain; affinity tag; protein purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lymphocyte activator protein 33; body fluid immunity disorder; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 39;
                                         Human Her-2 protein cytoplasmic kinase domain PCR primer.
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Pred. No. 1e+04;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                               Colussi PA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 29; 74pp; English
                                                                                                                                                                                                                                                                                                                                                             Taron CH,
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                                                                                                                                                                                                                                                                                                                      (NEWE ) NEW ENGLAND BIOLABS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.7%;
89.5%;
                                                                                                                                                                                                                                                                                   28-FEB-2002; 2002US-0360354P.
                                                                                                                                                                                                                                                26-FEB-2003; 2003WO-US005851
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 15-JAN-2004 (first entry)
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                           Ferrandon SM,
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-712883/67.
                                                                                               PCR; primer; ss.
                                                                                                                                                                     WO2003074660-A2
                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                           12-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                         substrate
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                                                                                                                                                                                                                                                                                                                                                           Xu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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                                                                                                                                                                                                                                                                                                                    Adaptor molecule; nucleic acid cloning; nucleic acid ligating; internal deletion mutagenesis analysis; cloning vehicle; ss.
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 Indels
                                                                                                                                                                                                                                                                               Nucleic acid cloning associated adaptor molecule #54.
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 Mismatches
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                                                        GIACCCCTGCAGCGCGGCC 1
                                                                                                                                                                     BP.
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                                     GTACCCCAGCAGCCCGGCC
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ACD82353 standard; DNA; 19
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                                                                                                                                                                                                                                          (first entry)
17; Conservative
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nes 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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Best Loc Matches

ઠ 셤 ACF79913/c ID ACF79 XX AC ACF79 XX

RESULT 27

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Gaps

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proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
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13-SEP-1993
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                                                                                                                                  organisms
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                                                                                                                                                                                                                                                                                      RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunosuppressive; immunostimulatory; antinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopietin; apoptosis related protein; cabterin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; miterfleukin; G-protein coupled receptor; thioesterase; intlammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to oligonuclectides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related
                                                                                                                The invention relates to a lymphocyte activator protein 33, the encoding polymuclectide, and a method for preparing the polypeptide by DNA recombination technique. The polypeptide is used in treating diseases such as body fluid immunity disorder and tumours. The current sequence represents a lymphocyte activator protein 33 related probe sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                         protein 33 and encoding polynucleotide, useful for
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                               52.7%; Score 15.8; DB 6; Length 41; ilarity 74.1%; Pred. No. 1e+04; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                        Sequence 41 BP; 11 A; 13 C; 13 G; 4 T; 0 U; 0 Other;
                                                                                           Example 6; Page 19 (disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                              4 GTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                     GGACCCCACACAGCAGCCTTGGAGAA 28
                                                                     treating body fluid disorder and tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 3387; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Human SNP oligonucleotide #6994.
                                                                                                                                                                                                                                                                                                                                                 ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2000; 2000WO-US035498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
                                                                                                                                                                                                                                                                                                                                               AAL33786 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets RA, Leach M;
                                                          activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                  WPI; 2002-436421/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-465210/50.
                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200147944-A2
            Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2002
                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2001
                                                           Lymphocyte
                                                                                                                                                                                                                                                                                                                                                                       AAL33786;
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                      AAL33786/c
                                                                                                                                                                                                                                       Matches
            Mao
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protein coupled receptors manually of positive in the present sequence is one such oligonucleotide. The oligonucleotides and the present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune systemic lupus erythromatosus and Grave's diseases, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the expression of heteromeric receptor proteins, e.g. from an immunoglobulin (Ig) superfamily, in cells containing the heteromeric receptor genes on a single plasmid. Especially mentioned, the cell may be a bacteriophage, where the receptor protein are expressed as fusion proteins with the surface protein gVIII. Primers AAX16911-X16936 were used in the construction of plasmid M13IX30 (AAX16937) for expression of receptor heavy chain proteins. Light chain genes are cloned into the plasmid M13IX11 (AAX16953). The methods can be used to generate diverse populations of heteromeric receptors which mimic the natural immune system and can be used for diagnostic and therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heteromeric; receptor; immunoglobulin; superfamily; plasmid; primer; PCR; bacteriophage; fusion protein; amplification; heavy chain; light chain; immune system; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New surface expression libraries expressing heteromeric receptors -
comprising cells containing vectors containing combinations of DNA
sequences encoding first and second polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.7%; Score 15.8; DB 4; Length 50; 89.5%; Pred. No. 1e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50 BP; 7 A; 20 C; 18 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer #17 for constructing plasmid M13IX30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Col 12; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 CCCCAGCAGCCCGGCCTTG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 CCCCAGCAGCGCGCCCTTG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-00590219.
91US-00767136.
93US-00120648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-00349131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX16927 standard; DNA; 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.7
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-166647/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IXSY-) IXSYS INC.
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42 GCGTTACCCAAGCTTAATCGCCTTGCAGAA 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding polypeptides which from heterometic receptors. The kit simply and efficiently generates a large repertoire of diverse combinations of heteromeric receptors. Only proper combinations of vector portions are randomly brought together for the coexpression of different DNA sequences without loss of population size or diversity. AAZ91524 to AAZ91528 represent bacteriophage M13 vector nucleotide sequences constructed in the exemplification of the present invention. AAZ91529 to AAZ91529 represent oligonucleotides used in the construction of vectors in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a kit (I) for the preparation of vectors for the coexpression of two or more DNA sequences encoding polypeptides comprising two vectors which operatively combine through two pairs of restriction sites to form a single vector. The kit is useful for the preparation of vectors for the coexpression of two or more DNA sequences
                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage M13 vector; prokaryotic cell; heteromeric receptor; antibody; immune system; filamentous bacteriophage; cloning; screening; coexpression; PCR primer; mutagenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kit for the preparation of vectors for the coexpression of two or more DNA sequences encoding proteins that form heteromeric receptors.
                                                                       Gaps
                                                                     ;
                               Match 52.0%; Score 15.6; DB 2; Length 43; Local Similarity 70.0%; Pred. No. 1.2e+04; les 21; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.0%; Score 15.6; DB 3; Length 43; 70.0%; Pred. No. 1.2e+04;
A; 8 C; 15 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43 BP; 12 A; 8 C; 15 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           Lac Z mutagenesis oligonucleotide SEQ ID NO:43
                                                                                                      1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                        GCGTTACCCAAGCTTAATCGCCTTGCAGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Col 13; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90US-00590219.
91US-00767136.
93US-00120648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00470297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00349131
                                                                                                                                                                                                                                AAZ91566 standard; DNA; 43
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteria phage M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-194835/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
BP; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IXSY-) IXSYS INC.
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13-SEP-1993;
01-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1995;
Sequence 43
                                                                                                                                                                                                                                                                                                     25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6027933-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                    AAZ91566;
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huse WD;
                                                                   Matches
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The invention describes adaptor molecules, where each end of the adaptor is compatible with a nucleic acid digested with a restriction enzyme or a nucleic acid comprising an end that is compatible with a nucleic acid digested with a restriction enzyme. The adaptor molecules, compositions, kits and arrays are useful for cloning nucleic acid molecules, compositions, hot require the design and synthesis of oligonucleotides or PCR primers. The adaptors, kits and arrays are also useful for ligating two ends of a single nucleic acid molecule, or ligating two or more nucleic acid molecules. The kits can also be used for performing internal deletion mutagenesis analysis. The adaptor molecules are ligated to a cloning vehicle, making the cloning procedure more rapid and efficient, and less error-prone. This sequence represents a nucleic acid cloning associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New adaptor molecules, useful for cloning nucleic acid molecules does not require the design and synthesis of oligonucleotides or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                           Adaptor molecule, nucleic acid cloning, nucleic acid ligating, internal deletion mutagenesis analysis; cloning vehicle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                           Nucleic acid cloning associated adaptor molecule #243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer for human MSH receptor DNA amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.4; DB 9;
Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 5; 100pp; English.
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                                                                                                                                                                                                                                                                                       13-JUN-2001; 2001US-00880313.
                                                                                                                                                                                                                                                                                                                       13-JUN-2001; 2001US-00880313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 51.3%;
Local Similarity 94.1%;
hes 16; Conservative
             ACD82542 Btandard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 GTACCCCTGCAGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GTACCCCAGCAGCCCGG
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                       (FLEM/) FLEMINGTON E K.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-521745/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adaptor molecule
                                                                                                                                                                                                                         US2003044791-A1.
                                                                                                                                                                                                                                                                                                                                                                                       Flemington EK;
                                                                             19-SEP-2003
                                                                                                                                                                                                                                                         06-MAR-2003.
                                                                                                                                                                                           Synthetic.
                                             ACD82542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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ACD82542/
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Indels

0; Mismatches

21; Conservative

Matches

1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30

Gaps

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transcription PCR. By contacting the amplification products of the PCR t at least one of the genotype specific hybridisation probes described in AAQ83902-Q83928, the genotype of the amplified HCV can be determined. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
nucleotide(s), peptide(s) and proteins, used in diagnosis and in
vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; non-A non-B; reverse transcription; diagnosis;
                                                          Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
nucleotide(s), peptide(s) and proteins, used in diagnosis and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription PCR. By contacting the amplification products of the PC at least one of the genotype specific hybridisation probes described AAQ83902-Q83928, the genotype of the amplified HCV can be determined. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ83896-Q83901 are primers for hepatitis C virus (HCV) reverse
                                                                                                                                                                                   AAQ83896-Q83901 are primers for hepatitis C virus (HCV) reverse
                                                                                                                                                                                                                                                                                                                                                / Match 51.3%; Score 15.4; DB 2; Length 40; Local Similarity 76.0%; Pred. No. 1.5e+04; nes 19; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.3%; Score 15.4; DB 2; Length 40; llarity 76.0%; Pred. No. 1.5e+04; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                         Sequence 40 BP; 7 A; 9 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus reverse transcription PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GGTACCCCAGCAGCCCGGCCTTGAA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 19; Page 119; 186pp; English.
                                                                                                                                              Claim 19; Page 120; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВЪ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ83897 standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukh J, Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-061006/08
                   WPI; 1995-061006/08
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9501442-A2
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19-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ83897;
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                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 35
AAQ83897/c
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a viral vector constructed by the fusion of a viral protein with a ligand which binding specifically to the melanocytestimulating hormone (MSH) receptor. The vector contains one of four linkers represented by sequences AAA3815-A93818 and AAB2383-B23586, and DNA encoding a fibre protein selected from those represented by AAA93819-93826 and AAB23867-B23594. The vector has cytostatic activity, and can be used for gene therapy and in the diagnosis and treatment of tumours, particularly malignant melanomas. The present sequence represents a PCR
Viral vector; melanocyte-stimulating hormone receptor; MSH; cytostatic; tumour; malignant melanoma; fibre protein; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; non-A non-B; reverse transcription; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                             Virus vector useful in diagnosis and treatment of tumors particularly malignant melanoma, constructed by fusing viral protein with ligand binding specifically to melanocyte-stimulating hormone receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.4; DB 3; Length 27;
Pred. No. 1.4e+04;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus reverse transcription PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 BP; 5 A; 10 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer used in the construction of the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 46; 145pp; Japanese.
                                                                                                                                                                                                                                                                       (NICA-) JAPANESE FOUND CANCER RES
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                                                                                                                                                                                       24-FEB-2000; 2000WO-JP001069
                                                                                                                                                                                                                                99JP-00093263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.0%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-549414/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer; ss.
                                                                Homo sapiens
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                                                                                                                                                                                                                                24-FEB-1999;
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19-SEP-1995
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                                                                                                                                                31-AUG-2000
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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                          AAT16689-T16694 are a set of RT-PCR primers used for the identification of the CDRA sequence of the B1 (envelope-1) gene of 51 HCV isolates. The isolated sequences are useful for the proof. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; inducible promoter; HCV infection; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other;
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Pred. No. 1.5e+04;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCACATCAATAGCACGGCCTTGAA 16
                                                                                                                                                                                                                                                                                                                                                Example 1; Page 224; 340pp; English.
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                                                                                                                   95WO-US010398
                                                                                                                                                     94US-00290665
                                                                                                                                                                                                                         Purcell
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hes 19; Conservative
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                                                                                                                                                                                                                         Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCHM/) SCHMIDT E V. (CHUN/) CHUNG R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-897533/82.
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                                                  WO9605315-A2
                                                                                                                                                     15-AUG-1994;
                                                                                                                     15-AUG-1995;
                                                                                  22-FEB-1996.
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                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT16689-T16694 are a set of RT-PCR primers used for the identification of the CDNA sequence of the B1 (envelope-1) gene of 51 HCV isolates. The isolated sequences are useful for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                     HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine; hepatitis; reverse transcriptase polymerase chain reaction; RT-PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine; hepatitis; reverse transcriptase polymerase chain reaction; RT-PCR; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                  Hepatitis C virus El gene RT-PCR primer.
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            27
                            3 GGTACCCCAGCCAGCCCGCCCTTGAA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 224; 340pp; English.
          GGTACCCCAGCCAGCCCGGCCTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purcell RH;
                                                                                                                                 BP.
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76.0%;
                                                                                                                              AAT16692 standard; cDNA; 40
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                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukh J, Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-139709/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                         Synthetic.
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The invention relates to a method for identifying a compound that increases the mutation rate of hepatitis C virus (HCV), comprising checking an increase in HCV quasispecies produced by the cell in the presence of the candidate compound by e.g. sequencing HCV nucleic acid molecules isolated from the test cell. The method involves providing a test cell containing a nucleic acid molecule comprising a first nucleotide sequence consisting of an infectious hepatitis C viral genome or its DNA copy, a second nucleotide consisting of a ribozyme or its DNA copy, and an inducible promoter operably linked to the first and second nucleotide sequences, where the ribozyme is configured to remove a 3 contacting the test cell with a candidate compound and detecting an increase in HCV quasispecies produced by the cell in the presence of the candidate compound compared to tend in the absence of the compound increase in the HCV quasispecies indicates that the compound increases that may be used for treating HCV The method is useful in identifying compounds the mutation rate of HCV. The method is useful in identifying compounds the increase in the mathod sequence represents a configured to amplify an HCV genomic DNA region, used in the method
Identifying a compound that increases the mutation rate of hepatitis C virus (HCV) comprises detecting an increase in HCV quasispecies produced by the cell in the presence of the candidate compound.
                                                                                                               Example 10; SEQ ID NO 8; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention.
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ö Gaps ö Score 15.4; DB 10; Length 40; Pred. No. 1.5e+04; Indels Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other; 9 0; Mismatches 3 GGTACCCCAGCCCGGCCTTGAA 27 40 GGCACATCAATAGCACGGCCTTGAA 16 51.3%; 76.0%; Query Match
Best Local Similarity 76.us,
Section 19; Conservative ð

Human SNP oligonucleotide #5090. AAL31882 standard; DNA; 50 BP (first entry) 24-JAN-2002 AAL31882; RESULT 39 AAL31882

neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss. Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;

28-DEC-1999; 99US-0173419P. 27-DEC-2000; 2000US-00173419. 28-DEC-2000; 2000WO-US035498. (CURA-) CURAGEN CORP. WO200147944-A2 Homo sapiens Shimkets RA,

WPI; 2001-465210/50.

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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apptiosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, Groteins, cytochromes, kinesins, cytokines, interferons, interleukins, Groteins coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune conserved in the proteins listed above. Siscases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, contrained the proteins listed and infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. paratuberculosis; PCR; milk; faeces; blood;M. paratuberculosis infection; Johne's disease; polypeptide purification;primer; ss; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to Mycobacterium avium subsp. paratuberculosis (M. paratuberculosis) nucleic acid molecules. A nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acids and encoded polypeptides useful for detecting Mycobacterium paratuberculosis, and as antibacterial vaccines.
                Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.4; DB 4; Length 50; Pred. No. 1.5e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50 BP; 11 A; 17 C; 16 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 GAGGCACAGCAGCCGGCCCTG 46
                                                                                                 Claim 1; Page 2851; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCGGTACCCCAGCAGCCCGGCCTTG
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76.0%;
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les 19; Conserv
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CCXSXLLLXBXLXBXBXBXBXBXBXBXBXBXBXBXBXCCCC
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combined with a second nucleic acid will generate an amplification product from M. paratuberculosis but not from human, Pseudomonas acruginosa, Strepfomyces viridochromogenes, mouse, cat or Xanthomonas campestris. The nucleic acids and other sequences specific for Mycobacterium paratuberculosis are used to detect M. paratuberculosis in e.g. milk, faeces or blood. The polypeptides encoded by these sequences, and antibodies directed against them, are also used to detect M. paratuberculosis by immunoasay. The nucleic acids and the polypeptides are also used as vaccines to prevent infection (Johne's disease) by M. paratuberculosis. The antibodies are also useful for polypeptide paratuberculosis. The sequence represents a PCR primer used to amplify an M. paratuberculosis nucleic acid of the invention.
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Sequence 25 BP; 6 A; 10 C; 6 G; 3 T; 0 U; 0 Other;

ö Gaps ; Ouery Match 50.7%; Score 15.2; DB 11; Length 25; Best Local Similarity 85.0%; Pred. No. 1.7e+04; Matches 17; Conservative 0; Mismatches 3; Indels 0

6 ACCCCAGCAGCCCGGCCTTG 25 Acrecadeadeadeacered 25

ò g Search completed: November 18, 2005, 11:52:28 Job time : 207.578 secs

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H99826 yx28d12.81 CC02213 35911_28 AJ580013 35911_28 AZ868876 2M0180F17 CG774406 1123018G0 BZ586362 3590 1_16 CC182796 XG533 Bay AI019594 ua91a06.r A1019594 ua91a06.r AL585781 AL585781 AA238784 mx82h02.r H3817 yp58c07.81 BX629147 BX629147 BH902004 SALK_0911 AA739463 v54a11.r BZ582545 3590 1_46 AU105801 AU105801 AZ733951 2M00601F1 AZ733951 2M00601F1

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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AU104878 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone AU104878 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone AU104878
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Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Bakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S., Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.7%; Score 15.8; DB 1; Length 50; 74.1%; Pred. No. 1e+05; rive 0; Mismatches 7; Indels
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/organism="Homo sapiens"
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AZ868876
W05202
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BZ586362
CC1585781
AL585781
AAZ38784
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BH902004
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                  90907994447
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Matches 20; Conservative
  149-156 (1997)
40
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AU104878/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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BH88266 32526 1 22
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AZS03949 1M0343124
BH909575 AU103065
AU103064 AU103065
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AI168501 0w90901.8
                                                                 November 18, 2005, 11:22:09; Search time 1434.98 Seconds (without alignments) 795.779 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                        159776
        GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                   34239544 segs, 19032134700 residues
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                               - nucleic search, using sw model
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AZ487251
AA547556
BH892666
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9b_htc:;

9b_htc:;

9b_est4:;

9b_est6:;

9b_gs81:;
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15.8 15.4 15

Result

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Gaps

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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Seal: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Yr. Yoshitono-Nakagawa,Kr. Maruyama,Kr. Suyama,A. and
Sugamo,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugamo,S. Construction and characterization of a full
1-ength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sees, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO REPED 2 (5), 388-393 (2001)
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/db_xref="texcon:9606"
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/clone_lib="Sugano Homo sapiens cDNA library"
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mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CAS01336"
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AU105799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 78.3<sup>3</sup>
Matches 18, Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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                                                                              11375929
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LOCUS
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MEDLINE
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SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: info@genetrap.de
Rosabetageo gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone_id=W191D04' ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
'l' Inhouse Sequence Identifier: 11106
                                           43 bp mRNA linear GSS 30-JUN-2004 W191D04 GGTC Gene Trap Library GV04C04 Mus musculus cDNA clone CL211120
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                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Embryonic stem cell"
/cell_line="ES cells 12952 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV04C04"
/note="Vector: ROSAbetageo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: GGTC
German Genetrap Consortium (GGTC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10090"
clone="W191D04"
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                                                                                                                                                                                                                          Mus musculus (house mouse)
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Best Local Similarity 73.1
Matches 19; Conservative
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                                                                                                                                                                                                                                                   Mus musculus
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ORGANISM
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AU102519/c
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                         RESULT 2
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-6-1, Shirokane, Holyo, ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
1199-156 (1997).
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: yauzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitono-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 28-JAN-2004
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Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bakaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Baka,H., Ota,T., 1sogai,T., Tanaka,T., Morishita,S., Okubo,K.,

Sakaki,Y., Nakamra,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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AU102978 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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48.7%; Score 14.6; DB 1;
Best Local Similarity 69.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14.6; DB 1
Pred. No. 3e+05;
0; Mismatches
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="HRP16119"
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AU102978
AU102978.1 GI:13552499
                                             Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                       48.7%;
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Best Local Si
Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
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5-6-1, Shirokane, U-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1-length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
                                                                                                                                                                     AU102973 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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1 (Dases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Bata,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S., Okubo,K., Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Salzuki,Y., Nakamura,Y., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
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Pred. No. 3e+05;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AU102977.1 GI:13552498
                                                        42 ccraecaecceecrie 25
                                                                                                                                                                                                           HEP09976, mRNA sequence
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                    8 CCCAGCAGCCCGGCCTTG
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Best Local Similarity 69.0
Matches 20; Conservative
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AU102973/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (gilfa732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 38)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Ralam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lb="Mouse 10kb plasmid UUGCNM lbrazy"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                   Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.3%; Score 14.2; DB 8; Length 39; Best Local Similarity 84.2%; Pred. No. 4.2e+05; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
                                                                                                                                                                                                              Std Error: 0.00
                                                                                                                                                                                                                                     Plate: 0076 row: G column: 19
Seg primer: CGTYCTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 39.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
        University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0076G19"
                                                                                                          Tel: 601 585 5606
Fax: 801 585 7177
Email: ddundgenetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0076 row: G column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
                                                                                              84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                             AU104624 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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2M0076G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Primates; Catarrhini, Hominidae, Homo.
L bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 39)
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Unpublished (2000)
Contact: Robert B. Weiss
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30 CGAGACCAGAGCAGCCGGTGGCGAGGAA 2
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="E. Coli strain Xil0-Gold, Tl-resistant, F-"
/lab host="E. Coli strain Xil0-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dntp://www.jax.org/resources/documents/dntps://ww.jax.org/resources/documents/dntps://ww.jax.org/resources/documents/dntps://ww.jax.org/resources/documents/dntps://ww.jax.org/resources/documents/librares/). The DNA
was blunt end-repaired by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with Tq DNA polymerase and Tq
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gil 4732114)gb|AR129072.1), a copy-number
inducible derivative of plasmid Rl. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                B
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
               University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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IMAGE:961284 5' similar to TR:G517115 G517115 MRNA ;, mRNA
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66.7%; Pred. No. 5e+05;
ive 0; Mismatches 10; Indels
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                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
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                                                                                                                                                                                          Plate: 0316 row: A column: 18
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ende
High quality sequence stop: 38.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        ....38
organism="Mus musculus"
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University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="taxon:10090"
'clone="UUGC1M0316A18"
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Matches 20; Conservative
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AA547556/c
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43 bp DNA linear GSS 14-AUG-2002

3526-122-1A12.2EL_x_1 3526 - RescueMu Grid K Zea mays genomic,

BH892666
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Site_1: MluI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(dT): 5'-CGGTGGACGTCGACCTTTTTTTTTTTTTTTT]; cDNAs were cloned into the MluI(SalI sites of a modified pBluescribe vector using commercial linkers (NEB).

Average insert size: 1.2 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize genomic sequences found using engineered RescueMu transposon topublished (2001)
Contact: Walbot Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3526_1_22_1 row: 28
Class: transposon-tagged.
                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:550076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                        Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Knowles Solter mouse 2 cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/Brzain="C57BL/6J x DBA/2J Fl"
/db xref="taxon:10090"
/clone="IMAGE:961284"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14; DB 1;
Pred. No. 5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                    AZ503949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                       g
                                                                                                                                                      /ione libe 1526 - RescueMu Grid K"
/clone libe 1526 - RescueMu Grid K"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: Bamil; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.isatate edu' and follow the links for 'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter 2000-2001. DNA was extracted from leaf punches, double digested using Bamil and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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/mol_type="genomic DNA"

/mol_type="genomic DNA"

/mol_type="genomic DNA"

/db xref="taxon.4577"

/clone="0180615-06B1-A12"

/clone="buniformMu MuTAIL Library"

/clone="buniformMu MuTAIL Library"

/note="vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo assymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 18-AUG-2003
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC940831 43 bp DNA linear GSS 18-AUG-20 01S0615-06B1-A12 UniformMu MuTAIL Library Zea mays genomic clone 01S0615-06B1-A12, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence flanking probable Mu insertion site in UniformMu line: 0180615-06, Primer set: B Class: transposon insertion site. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 43)
Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                       cultivar="mixed background W23/A188/B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 46.7%; Score 14; DB 8; Length 43; Best Local Similarity 77.3%; Pred. No. 5e+05; Matches 17; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dopublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
TEL: 352-392-1928 x322
Email: drm@wfl.edu
type="genomic DNA"
                                                     db xref="taxon:4577"
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                                                                               tissue_type="leaf"
                                                                                                          /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CCCAGCAGCCCGGCCTTGAAGA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 cccadaadcccdaaarrdaaga 41
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ORGANISM
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VERSION
KEYWORDS
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TITLE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwMD42 (gilfa732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                             0;
                                                                                                                                                                                                                                                                                                                               GSS 05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bass 1 to 45)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                      AZ503949
1M0343L24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0343L24 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse_lokb_plasmid UGGCIM_library"
/note="Vector: PWD42nv; Purlited genomic_DNA_from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
                                                                Gaps
                                                             .;
0
Length 43;
                                                          10; Indels
DB 9;
5e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Std Error: 0.00
                                                          0; Mismatches
                                                                                                                                                            GAGGCACCTCAGCCCCGCCACCTTGGAGCA 38
                                                                                                                    1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84112, USA
Tel: 801 585 5606
Email: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error
   Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0343L24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 45.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ503949.1 GI:10685265
   46.7%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: plasmid ends
Query Match
Best Local Similarity 66.7
Matches 20; Conservative
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ORIGIN

RESULT 15 BH909575/c DEFINITION

ઠ ద ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

ACCESSION VERSION KEYWORDS SOURCE

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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatcku, Tokyo 108-8639, Japan
Email: yauzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AU103065 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC01582, mRNA sequence.
                                                                                                                          Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
                                                                                                                                                                                                Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hada, H., Ota, T., 1 Bogaì, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.8; DB 1;
Pred. No. 6.1e+05;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC00745"
                                                                                                                                                                                                                                                                                                     mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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                          AU103064.1 GI:13552585
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                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .50
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Best Local Similarity
Matches 18; Conser
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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dadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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/clone="SALK O54521.15.30.x"
/clone="SALK O54521.15.30.x"
/clone="lb="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used car be found at http://signal.salk.edu/tdna_protocols.html"
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Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute Genomic Analysis Laboratory (SIGnAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
11 1911 858 453 4100 x1752
Fax: 858 558 659 678
Email: ecker@salk.edu
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                                              Score 14; DB 8; Length 45;
Pred. No. 5e+05;
                                                                                                Indels
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/mol_type="genomic DNA"
/ecotype="Col-0"
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Pred. No. 5.9e+05;
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72.0%;
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Best Local Similarity 77.3%;
Matches 17; Conservative
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Class: TDNA tagged.
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Homo sapiens (human)
                 Homo sapiens (human)
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Matches 18; Conservative
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Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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EMBO Rep. 2 (5), 388-393 (2001)
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                                              /mol_type="mRNA"
/db_xref="texaon:9606"
/clone="HRC01582"
/clone_lib="Sugano Homo sapiens cDNA library"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC09549"
/clone_lib="Sugano Homo sapiens CDNA library"
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                ch 46.0%; Score 13.8; DB 1; Length 50; Similarity 72.0%; Pred. No. 6.1e+05; 18; Conservative 0; Mismatches 7; Indels
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organism="Homo sapiens"
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Hef-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Yr. Yoshitokomo-Nakagawa,Kr. Maruyama,Kr. Suyama,A. and
Sugamo,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2),
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo. Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2),
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Toa,T., Tanaka,T., Morrishita,S., Okubo,K., Sakaki,Y., Nakmura,Y., Suyama,A. and Sugano,S., Okubo,K., Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
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```

AU104917/c DEFINITION

RESULT 21

ACCESSION VERSION KEYWORDS

Matches

ORIGIN

ORGANISM

SOURCE

REFERENCE AUTHORS

```
/mol_type="remove or properties" / mol_type="remove or properties" / mol_type="remove or properties" / mol_type="remove or primary large fibroblasts" / clone_lib="HIV-vector integration sites in human IMR90 primary lung fibroblasts" / lung fibroblasts (IMR90) were / note="Human primary lung fibroblasts (IMR90) were infected with an HIV-based vector. DNA was isolated and cleaved with restriction enzymes; linkers were ligated onto the cleaved DNA and DNAs were amplified using one primer that bound to the linker DNA and one that bound to the HIV cDNA. Junctions between integrated HIV proviruses and cellular DNA were cloned and sequenced."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU105070 50 bp mRNA linear EST 28-JAN-2004 AU105070 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@inms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                1 (bases I to 46)
Mitchell, R.S., Beitzel, B.F., Schroder, A.R.W., Shinn, P., Chen, H.,
Mitchell, R.C., Ecker, J.R. and Bushman, F.
Retroviral DNA Integration: ASLV, HIV and MLV Show Distinct Target
Site Preferences
                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
                                                                                                                                                                                                                              Unpublished (2004)
Contact: Frederic Bushman
Salk Institute Infectious Disease Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1630
Fax: 858 554 0341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 46;
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Pred. No. 7.2e+05;
0; Mismatches 4;
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EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bushman@salk.edu
Class: PCR with specific prin
Location/Qualifiers
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  Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Iengch-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 50)

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Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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                  /clone="ADSE00422"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                         46.0%; Score 13.8; DB 1; Length 50; 72.0%; Pred. No. 6.1e+05; ive 0; Mismatches 7; Indels
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0; Mismatches 7;
'organism="Homo sapiens"
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/db_xref="taxon:9606"
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Location/Qualifiers
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CL529006.1 GI:47422217
GSS.
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Conservative
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COMMENT

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Gaps ö Euteleostomi;

DEFINITION

RESULT 22

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ACCESSION

KEYWORDS

VERSION

FEATURES

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ORIGIN

Matches

RESULT 24 AI168501/c LOCUS

DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

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Homo sapiens had acca; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

El (Dases 1 to 36)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CONA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CONA Library Preparation: Michael J. Brownstein (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10729 row: e column: 22

High quality sequence stop: 36.

Location/Qualifiers
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                                                                                                                      BG717269 36 bp mRNA linear EST 08-MAY-
C22689583F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4821885 5'
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44.7%; Score 13.4; DB 4; Length 36;
Best Local Similarity 73.9%; Pred. No. 8.5e+05;
Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4821885"
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/clone_lib="NIH_MGC_97"
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AGCAGCCCGGCCTGG 10
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H99826/c
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Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 28)

NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

L Unpublished (1997)

Contact: Rober Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality
Insert Length: 890 std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

Location/Qualifiers
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                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT06679"
/clone_lib="Sugano Homo sapiens cDNA library"
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                                                                                                                                                                                                       ch 45.3%; Score 13.6; DB 1; Length 50; l Similarity 67.9%; Pred. No. 7.3e+05; 19; Conservative 0; Mismatches 9; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1654128"
                                                                                                                                                                                                                                                                                         1 GCGGTACCCCAGCAGCCCGGCCTTGAAG 28
                                          1. .50
/organism="Homo sapiens"
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                               Best Local Similarity
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source

FEATURES

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Gaps

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EST 15-DEC-1995

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/clone libe 1351 - RescueMu Grid P"
/clone libe 1351 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlucScript backbone); Site 1: BamHi, Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units: Por more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH108 cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidosis thaliana T-DNA flanking sequence, left border, clone A.590023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Ahauvin, S., Bechloid, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, T. T. DNA integration into the Arabidopsis genome depends on sequences
   sequences found using engineered RescueMu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                       Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon.4577"
/tiseue_type="leaf"
/ledy stage="adult"
/lab_host="DH10B"
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                                                                                            Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tal: 650 723 2221
Fax: 650 725 8221
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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EMBO Rep. 3 (12), 1152-1157 (2002)
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   Maize genomic sequ
Unpublished (2001)
Contact: Walbot V
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Balzergue, S.
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1 (bases 1 to 47)
Walbot,V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Source: IMAGE Consortium, LINIA
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality of the possible reversed clone: similarity on wrong strand possible reversed clone: similarity on wrong strand Insert Length. 732 Std Error: 0.00
Seq primer: mail -40 forward
High quality sequence stop: 1.
Location/Qualifiers
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                           1 (bases 1 to 43)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
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44.7%; Score 13.4; DB 7; Length 43;
Best Local Similarity 73.9%; Pred. No. 8.6e+05;
Matches 17; Conservative 0; Mismatches 6; Indels
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/db_xref="GDB:3872705"
/db_xref="taxon:9606"
/clone="IMAGE:263063"
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High quality sequence stops: 1
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                                                                                                                                                                                                                        The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
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Gaps

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/db_xref="taxon:9606"
/clone="IMAGE:295249"
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Matches 15; Conserv
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ORGANISM
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W05202
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VERSION
KEYWORDS
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JOURNAL
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Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ868876 29 bp DNA linear GSS 21-FEB-2001 2M0180F17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0180F17 R, genomic survey sequence.
  PCR was performed on DNA from transformants of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. Loaces 1 to 29)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
           plants from INRA (versailles). The DNA fragment(s) regulation the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at the typ://dbsgap.versailles.inra.fr/publicalines/. This sequence has program 'Genoplante' (http://www.genoplante.org. infobiogen.fr).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.7%; Score 13.4; DB 9; Length 47; 70.8%; Pred. No. 8.7e+05; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
cultivar="Wassillewskija"
/db xref="taxon:3702"
/clone="562D09"
                                                                                                                                                                                                                                                                                                                                                                                                                           1. .47<sup>-</sup>
/note="T-DNA flanking sequence
left border"
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Blate: OlbO row: F column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0180F17"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GTACCCCAGCAGCCCGGCCTTGAA 27
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AZ868876/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gplAR128072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complamentary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-GG1d (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 37)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
/lab host="B. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.0%; Score 13.2; DB 8; Length 29; 83.3%; Pred. No. 1e+06; ive 0; Mismatches 3; Indels
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/db_xref="GDB:1240170"
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High quality sequence stop: 1.
Location/Qualifiers
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Unpublished (1995)
Contact: Wilson RK
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Gaps

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41 bp DNA linear GSS 17-DEC-2002 3590 1 16 1 D07.2EL v 13590 - RescueMu Grid M Zea mays genomic, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/mol type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.2; DB 8; Length 41; Pred. No. 1e+06; 0; Mismatches 8; Indels
                                              Length 40;
                                          44.0%; Score 13.2; DB 9;
69.2%; Pred. No. 1e+06;
tive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences
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                                                                                                                                          4 GTGGTCCTCCAGCAGCAGATCTGGA 29
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                                                                                18; Conservative
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Best Local Similarity 69.2
Matches 18; Conservative
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                                          Query Match
Best Local Similarity
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TITLE
JOURNAL
COMMENT
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/Woll type="mixed background W23/A188/B73/K55"
/Woll type="mixed background W23/A188/B73/K55"
/Worst="worn:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="wlh108"
/lab_host="wlh108"
/clone_lib="1123 - RescueMu Grid L"
/note="Organ: leaf; Vector: RescueMu (engineered from note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: BgllI; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units: For more information on RescueMu, go to the web site 'www zmdb iastate.edu' and follow the links for 'RescueMu. Grid Laws grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamH1 and BglII, and ligated to form circular plasmids. DH10B ampicillin."
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1123018G05.2EL_y1 1123 - RescueMu Grid L Zea mays genomic, genomic
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1 (bases 1 to 40)
Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 1123018 row: 12
                                                                                                                                                                                                                                                                                                 Gaps
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0
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44.0%; Score 13.2; DB 7; Length 37;
Best Local Similarity 69.2%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 8; Indels
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Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Walbot V
Department of Biological Sciences
Stanford University
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/organism="Zea mays"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG774406.1 GI:38030394
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Zea mays
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AUTHORS
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CG774406
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Gaps

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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALS85781 ALS85781 BP Chicken Embryo Library Gallus gallus cDNA clone
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Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                     This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                              Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS029H11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
                                                                                                                                                                                                                /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: frazer.murray@bbsrc.ac.uk
Seq primer: T3.
    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:1364818"
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Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
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                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6J"
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AL585781.1 GI:13164514
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AI019594

Lagland Inhand Nahwa linear EST 16-JUN-1998
Lugland C. Aland Nahwa Musculus cDNA clone
LIPAGE:1364818 5' similar to SW:HBP HUMAN Q00341 HIGH DENSITY
LIPOPROTEIN BINDING PROTEIN ; MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46)
Marram, Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                   CC182796 45 bp mRNA linear GSS 08-MAY-2003
XG533 BayGenomics Gene Trap Library pGT1Lxf Mus musculus cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XG533
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                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
                                                                                                                                                                                                                                                                                                              Contact: Baydenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Bamil: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT1Lxf"
/note="Vector: pGT1Lxf"
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Pred. No. 1e+06;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                         http://baygenomics.ucsf.edu/
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="129 ola"
                                                                                                                                                                                                                                                                                                                                                                                                                                               information available from
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                                                                                                         GI:30426696
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CC182796.1
                                                               sequence.
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Query Match
Best Local Similarity 69.2<sup>3</sup>
Matches 18; Conservative
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H38217/c
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Marray M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                         AA238784 46 bp mRNA linear BST 03-MAR-1997 mx82h02.rl Soares mouse NML Mus musculus cDNA clone IMAGE:692883 5' similar to SW:NED4_HUMAN P46934 NEDD-4 RELATED PROTEIN ;, mRNA
                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                 Gaps
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                              1; Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                               8; Indels
                                                                                                                                                                          ch 44.0%; Score 13.2; DB 1
| Similarity 69.2%; Pred. No. 1e+06;
18; Conservative 0; Mismatches
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/db_xref="taxon:10090"
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tissue_type="Embryo'
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lab_host="DH10B"
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                                                                                                                                                                                                                                       yps8c07.81 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:191628 3' similar to SP:KGUA_PIG P31006 GUANYLATE KINASE ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 46)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: escewateon.wuetl.edu
Insert Size: 1641
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (infe@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1641 Std Error: 0.00
Seq primer: Promega -21m13
                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1e+06;
0; Mismatches 5; Indels
                                          8; Indels
                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                              mRNA
  Score 13.2; DB 1
Pred. No. 1e+06;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3761417"
/db_xref="taxon:9606"
                                                                                  5 TACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                            46 bp
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Location/Qualifiers
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Unpublished (1995)
Contact: Wilson RK
44.0%;
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ilarity 75.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                              H38217.1 GI:907716
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Best Local Similarity
Matches 15; Conserv
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5 TACCCCAGCAGCCCGGCCTTGAAGAA 30
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Best Local Simi
Matches 18;
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JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                 JOURNAL
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                                                                                                              TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dlone="Name | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All | All
                                                                                                                                                                                                                          BX629147 BX629147 Anopheles gambiae cDNA clone ANGNP2364C01T7, mRNA
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lines
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 48)
Lobo, N.L., Gardner, M., Romans, P. and Collins, F.H.
Anopheles gambiae EST, Center for Tropical Disease Research and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH902004 138.90.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana GUI114.48.90.x, genomic clone SALK_091114.48.90.x, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Frank H. Collins
Center for Tropical Disease Research and Training
University of Notre Dame
Notre Dame, IN 46556, USA
Tel: 574-631-3945
Fax: 574-631-396
Email: frank.h.collins.75@nd.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae (African malaria mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.2; DB 5;
Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Anopheles gambiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:7165"
                          23
                                                                             46 GCAGCCAAGNANCCCGGCCT 27
                                                                                                                                                                                                                                                                                                              BX629147
BX629147.1 GI:33558282
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Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles gambiae
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Best Local Similarity
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VERSION
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TITLE
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/organism="Arabidopsis thaliana"
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/ecotype="col.0"
/db xref="taxon:3702"
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/clone="SALK 091114.48.90.x"
/clone="DR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was diemetty sequenced to determine the genomic sequence diemetly sequenced to determine the genomic sequence the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 49)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Joske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA739463 49 bp mRNA linear EST 14-JAN vV54811.r1 SOares thymus 2NbH7 mus musculus CDNA clone IMAGE:1226204 5' similar to SW:GBG5 BOVIN P30670 GUBNINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(5)/G(0) GAMMA-5 SUBUNIT: ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 1e+06;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
TH: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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The WashU-HHMI Mouse EST Project
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Query Match
44.0%; Score 13.2; DB 1; Length 49;
Best Local Similarity 69.2%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps

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Search completed: November 18, 2005, 21:12:48 Job time : 1436.98 secs

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             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-164-219-9
US-09-154-219-9
US-08-592-411-11
US-08-592-411-11
US-09-268-311-13
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US-08-086-428B-104
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30
1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
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                                                                                                                                                                                                                                                1202784 segs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
                          Copyright
                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 50
                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                         Scoring table:
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106, App 104, App 206, App 210, App 210, App 104, App 208, App 208, App 21573, App 11573, App 11573, App 317, App 317, App 313, App 31, App 31, App 31, App 31, App 31, App 31, App 31, App 31, App		0	
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51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3	SULT 1 Pacence 6, Application US/079891 Pacent No. 5429923 APPLICANT: SEIDMAN, CHRISTINE APPLICANT: SEIDMAN, JOHN APPLICANT: SEIDMAN, JOHN APPLICANT: WATKINS, HUGH APPLICANT: WATKINS, HUGH APPLICANT: WATKINS, HUGH APPLICANT: WATKINS, HUGH APPLICANT: WATKINS, HUGH APPLICANT: WATKINS, HUGH APPLICANT: WATKINS, HUGH APPLICANT: BOSTON SEQUENCES: 10 CURRESPEDIONDERESS: ADDRESSE: LAHIVE & COCKFIE STREET; BOSTON STATE: MASSACHUSECTS CUNTRY: BOSTON STATE STREET, SU SIPP. 102109 CLOWITRY: US.A. EXPLICATION OF SUBJECT OF SOURCESS SOFTWARE: ASCII COMPUTER: LAMICATION DATA: APPLICATION NUMBER: US/07/9 FILING DATE: 11-DEC-1993 CLASSIFICATION NUMBER: US/07/9 FILING DATE: 11-DEC-1993 CLASSIFICATION NUMBER: US/07/9 FILING DATE: 11-DEC-1993 CLASSIFICATION NUMBER: 33,505 REFERENCE/DOCKET NUMBER: 33,505 REFERENCE/DOCKET NUMBER: (617) 227-7400 TELEFORMUTICATION INFORMATION: TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 227-7400 TELEFAK: (617) 22	Similarity 100 0; Conservative GCGGTACCCAGAG	
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IIILE OF INVENTION: 3-(Carboxymethylthio)propionyl-7-ADCA
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STREET: 2000 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:
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Patent No. 5795733
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TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 82.6'
Matches 19; Conservative
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                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Shi, Yanggu
APPLICANT: Shi, Yanggu
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REPERENCE: PF939RP1
CURRENT APPLICATION NUMBER: US/09/268,311
CURRENT FILING DATE: 1990-03-16
EARLIER APPLICATION NUMBER: 60/059,133
EARLIER FILING DATE: 1997-09-17
EARLIER FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTION NUMBER: 09/154,219
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APPLICANT: Shi, Yanggu
APPLICANT: Ruben, Steve M.
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REFERENCE: P7398
CURRENT APPLICATION NUMBER: US/09/154,219
CURRENT FILING DATE: 1998-09-16
EARLIER APPLICATION NUMBER: 60/059,133
EARLIER APPLICATION NUMBER: 60/059,133
SOFTWARE: PATENT NOW: 1397-09-17
NUMBER OF SEQ ID NOS: 13
SSEQ ID NOS: 13
SSEQ ID NOS: 20
SEQ ID NOS: 20
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Pred. No. 2.5e+02;
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Patent No. 5726032
GENERAL INFORMATION:
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US-09-154-219-9
; Sequence 9, Application US/09154219
...ant No. 6635443
                                                                                                                                                                                                          Sequence 9, Application US/09268311
Patent No. 6482923
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87.0%;
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ORGANISM: Homo sapiens
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US-09-154-219-9
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TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
Matches 20; Conserva
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US-08-592-411-11
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LENGTH: 26
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GENERAL INFORMATION:

APPLICANT: BOVERNBERG, ROELOF ARY LANS
APPLICANT: MOCKMAN, BERTUS PIETER
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: VAN DER LAAN, JAN METSKE
APPLICANT: VERWEIJ, JAN
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APPLICANT: VERW
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Perentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,411
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COUNTRY: USA
ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,501
FILING DATE: 13-MAY-1996
CLASSIFICATION: 455
ATTORNEY/AGENT INFORMATION:
NAME: ADDER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/POCKET NUMBER: 24615-20065.00
TELECOMMUNICATION NUMBER: 24615-20065.00
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US-09-154-219-11
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LENGTH: 28
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LENGTH: 28
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                                                                                                           Query Match 55.3%; Score 16.6; DB 1; Length 48; Best Local Similarity 82.6%; Pred. No. 1.2e+03; Matches 19; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08244010
Fatent No. 5698763
GENERAL INFORMATION:
APPLICANT: Weissmann, Charles
APPLICANT: Aguet, Michel
APPLICANT: Aguet, Michel
APPLICANT: Aguet, Michel
APPLICANT: Aguet, Marek
APPLICANT: Aguet, Marek
APPLICANT: Aguet, Marek
APPLICANT: Aguet, Marek
APPLICANT: Aguet, Marek
APPLICANT: Aguet, Marek
APPLICANT: Sailet, Andreas
TITLE OF INVENTION: TRANSGENIC ANIMALS LACKING PRION
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,010
FILING DATE: 12-MAY-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
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                                                                                                                                                                                                                                               18 ACCGCCGCCCCCCGCCTTTGAAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10020
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 11, Application US/09268311
Patent No. 6482923
GENERAL INFORMATION:
APPLICANT: Shi, Yanggu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION INFORMATION:
TELEPHONE: (212) 596-9000
TELER: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS: LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDENESS: single
                         single
; TYPE: nucleic acid
; STRANDEDNESS: sing]
; TOPOLOGY: linear
US-08-591-501-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09154219

Patent No. 6635443

GENERAL INPORMATION:

APPLICANT: Shi, Yanggu

APPLICANT: Ruben, Steve M.

TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein

FILE REPRENCE: PF398

CURRENT APPLICATION NUMBER: US/09/154,219

CURRENT FILING DATE: 1998-09-16

EARLIER APPLICATION NUMBER: 60/059,133

EARLIER PILING DATE: 1997-09-17

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Shi, Yanggu
APPLICANT: Ruben, Steve M.
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein; TITLE REFERENCE: PF938P1
CURRENT APPLICATION NUMBER: US/09/268,311
CURRENT APPLICATION NUMBER: 60/059,133
EARLIER APPLICATION NUMBER: 60/059,133
EARLIER FILING DATE: 1997-09-17
EARLIER FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein FILE REFERENCE: PF398P1
CURRENT APPLICATION NUMBER: US/09/268,311
CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: 60/059,133
EARLIER PILING DATE: 1997-09-17
EARLIER FILING DATE: 1997-09-17
EARLIER FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                      Score 16.2; DB 4;
Pred. No. 1.6e+03;
0; Mismatches 3;
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; Sequence 13, Application US/09268311
; Patent No. 6482923
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85.7%;
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-09-268-311-13
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Best Local Similarity
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TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                           linear
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HYPOTHETICAL: 1
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LENGTH: 25
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| Sequence 20, Application US/07640476
| Patent No. 5376536
| GENERAL INFORMATION:
| APPLICANT: UITEN, RUDOLF G.M. |
| APPLICANT: UITEN, RUDOLF G.M. |
| APPLICANT: SCHUURHUIZEN, PAUL W. |
| APPLICANT: MIABLET, NADIR |
| TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASE ENZYMES AND |
| TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASE ENZYMES |
| TITLE OF INVENTION: THERR USE |
| NUMBER OF SEQUENCES: 2 |
| CORRESPONDENCE ADDRESS: ADDRESSE: MORTISON & FOETSTER |
| STREET: 545 Middlefield Road, Suite 200 |
| CITY: Menlo Park |
| STREET: CA
                                                                                 54.0%; Score 16.2; DB 4; Length 28; 85.7%; Pred. No. 1.6e+03; live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.0%; Score 16.2; DB 4; Length 28; 85.7%; Pred. No. 1.6e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Shi, Yanggu
APPLICANT: Ruben, Steve M.

TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
TILE REFERENCE: PF398
CURRENT APPLICATION NUMBER: 08/09/154,219
CURRENT PILING DATE: 1998-09-16
ERALIER APPLICATION NUMBER: 60/059,133
EARLIER APPLICATION NUMBER: 60/059,133
EARLIER APPLICATION NUMBER: 1997-09-17
NUMBER OF SEQ ID NOS: 13
SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/07/640,476
FILING DATE: 19910110
                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/09154219
Patent No. 6635443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                       3 GGTACCCCAGCAGCCCGGCCT 23
                                                                                                                                                                                                               6 geracceaecerecegerr 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 gdraccccagccrcccgcrr 26
                                                                                   Query Match
Best Local Similarity 85.73
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7
Matches 18; Conservative
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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US-07-640-476-20/c
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                                            US-09-154-219-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-09-396-196G-25759/C
iSequence 25759 Application US/09396196G
Fatent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
TITLE OF INVENTION: Methode of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOSTWARE: FEALSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 109792, Application US/09396196G
Fatent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
FITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.2; DB 1;
Pred. No. 1.6e+03;
0; Mismatches 8;
ATTORNEY/AGENT INFORMATION:
NAME: Kate H. Murashige
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20009.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEPHONE: (415) 327-2551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CGGTACCCCAGCCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 CGCGACTCCATCATCTCGACCTTCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GTACCCCAGCCCCGGCCTTGAA 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.4%;
Matches 21; Conservative
                                                                                                                                             TELEFAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 33 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CGGTACCCCAGCAGCCCGGCCTTG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 CGGTACCASAGSAGSGGCTTS 9
                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45, Application US/08510646B Patent No. 6077699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 base pairs
                                      ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1300 I ST
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 16
US-08-510-646B-45/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-403-852D-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Biosynthesis Of Streptogramins, Nucleotide S
Coding For These Polypeptides And Their Use
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                                                                                                                                                                                                Length 25;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                            52.7%; Score 15.8; DB 4;
89.5%; Pred. No. 2.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymerix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1990-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PastSRQ for Windows Version 4.0
SEQ ID NO 125627
LENGTH: 25
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 109792
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 125627, Application US/09396196G Patent No. 6821724
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US-08-043-852D-43/c
Sequence 43, Application US/08403852D
Patent No. 5891695
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Debussche, Laurent
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Jacques, Nathalie
Lacroix, Patricia
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APPLICANT: Michael Mittmann
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Best Local Similarity 89.5
Matches 17; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan,
STREET: 1300 I Street
                                                                                                                TYPE: DNA
CRGANISM: mus musculus
US-09-396-196G-109792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: mus musculus
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Lacroix,
Thibaut,
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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US-09-396-196G-125627
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Lacroix, Particle
APPLICANT: Thibaut, Denis
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
TITLE OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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1300 I Street, N.W., Suite 700
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 105/08/403,082D
FILING DATE: 105/08/403,082D
FILING DATE: 105/08/403,082D
FILING DATE: 25-82F-1993
PRIOR APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-82F-1993
ATTORNEY/AGBMT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 3806.0054-00000
TELECOMMUNICATION: NIFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.0%; Score 15.6; DB 2; Best Local Similarity 62.5%; Pred. No. 2.9e+03; Matches 15; Conservative 5; Mismatches 4;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TOPOLOGY:
US-09-231-818-43
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Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
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NUMBER OF SEQUENCES:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

CITY: Washington

STRIE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER: READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/231,818
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           PILING DAIE:

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: PR 92/11441

FILING DATE: 25-SEP-1992

ATOMNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 25,146

REJEPRANCE (202) 408-4400

TELEPAN: (202) 408-4400

TELEPAN: (202) 408-4400

TELEPAN: 22 base pairs

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CARACTERISTICS:

LUMGTH: 32 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.0%; Score 15.6; DB 3; 62.5%; Pred. No. 2.9e+03; tive 5; Mismatches 4;
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FILING DATE: 10-MAX-1995
APPLICATION NUMBER: P3/00923
FILING DATE: 25-SEP-1993
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APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Inv
TITLE OF INVENTION: Biosynthesis Of
TITLE OF INVENTION: Coding For These
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US-09-231-818-43/c
Sequence 43, Application US/09231818
Patent No. 6171846
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Patricia
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Blanche, Francis
  03-AUG-1995
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PRIOR APPLICATION DATA:
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Lacroix, 1
Thibaut, 1
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Best Local Similarity
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APPLICANT: Blanc,
APPLICANT: Blanche
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US-08-510-646B-45
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APPLICANT:
APPLICANT:
APPLICANT:
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De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
Blosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUU TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/635,359B
FILING DATE: 10-AM3-1999
APPLICATION NUMBER: US 09/231,818
FILING DATE: 15-AM3-1995
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1955
APPLICATION NUMBER: PCT/PR 93/00923
APPLICATION NUMBER: PR 92/11441
FILING DATE: 25-SEP-1992
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REFERENCE/DOCKET NUMBER: 03806.0054-03000
                                                                 NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-4400
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CGGTACCCCAGCAGCCCGGCCTTG 25
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; Sequence 43, Application US/09635359B
; Patent No. 667015;
; GENERAL INFORMATION:
FR 92/11441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zagorec, Monique
Debussche, Laurent
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Lacroix, Patricia
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Blanche, Francis
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                                                                                                                                                                                                                                                      Ouery Match 52.0%; Score 15.6; DB 4; Length 32; Best Local Similarity 62.5%; Pred. No. 2.9e+03; Matches 15; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43, Application US/08464136
Patent No. 5698426
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
TITLE OF INVENTION: HETEROMERIC RECEPTORS
NUMBER OF EGUNCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY SCHRÖEDER, BRUEGGEMANN & CLARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRUEGGEMANN & CLARK
SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,136
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                                                                                                                                                   ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-635-359B-43
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NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 8882
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-901
TELEPHONE: 619-535-901
TELEPHONE: 619-535-901
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               2 CGGTACCCCAGCAGCCCGGCCTTG 25
                                                                                                                                                                                                                                                                                                                                                                     32 CGGTACCASAGSAGSGGGGGTTS 9
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; Sequence 42, Application US/08440787A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSËE: PRETTY, SCHROEDËR, I
STREET: 444 SO. FLOWER STREET,
CITY: LOS ANGELES
STATE: CALIFORNIA
TELECOMMUNICATION INFORMATION
                    TELEPHONE: (202) 408-400
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                          408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UNITED STATES ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 70.0
Matches 21; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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Soluble Peptides Having Constrained,
Secondary Conformation in Solution and Method of Making
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSER: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 SO: FLOWER STREET, SUITE 200
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43, Application US/08349131
Patent No. 5871974
GENERAL INFORMATION:
APPLICANT: HUSS, WILLIAM D.
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
TITLE OF INVENTION: HETEROMERIC RECEPTORS
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,787A
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/349,131
                                                                                                                                                E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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Pred. No. 3e+03;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 1435

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-IX 1586
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                             ZIP: 92122
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
STOFFWARE: Patentin Release
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70.0%;
               APPLICANT: Huse, William D.
TITLE OF INVENTION: Scluble
TITLE OF INVENTION: Seconda
TITLE OF INVENTION: Same.
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Best Local Similarity 70.04
Matches 21, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
                                                                                                   NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                        CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
TITLE OF INVENTION: RANDOMIZED PEPTIDES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Plower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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0; Mismatches
                                                               1 GCGGTACCCCAGCCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
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                                                                                                                              42 GCGTTACCCAAGCTTAATCGCCTTGCAGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/110,494
FILING DATE:
APPLICATION NUMBER: US/07/767,436
FILING DATE:
NAME: Campbell, Cathryn A
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 9072
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.vv
Best Local 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 444 South
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Los Angeles
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PCT-US91-07141-42/c
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US-08-367-685-42
      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.0%; Score 15.6; DB 2; Length 43; 70.0%; Pred. No. 3e+03; ive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: HUSE, WILLIAM D.
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
TITLE OF INVENTION: HETEROMERIC RECEPTORS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,297A
FILING DATE: Unne 5, 1995
CLASSIFICATION: 0315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 GCGTTACCCAAGCTTAATCGCCTTGCAGAA 13
                                                                                                             FILING DATE:
APPLICATION NUMBER: US/08/120,0426
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 8882
TELEPHONE: 619-535-8949
TELEPHONE: 619-535-8949
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGRAL 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-IX 1611
                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/120,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-470-297A-43/c; Sequence 43, Application US/08470297A; Patent No. 6027933
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REGISTRATION NUMBER: 31,815
REFERENCE DOCKET NUMBER: P-IX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.0%;
70.0%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.0
Best Local Similarity 70.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity
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OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
                                                            Length 43;
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US-09-196-196G-25761/C
Sequence 25761/Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Lockhart
APPLICANT: David Lockhart
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE PASISEQ for Windows Version 4.0
SEQ ID NO 25761
LANDITH . 25
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                                                        Score 15.6; DB 5
Pred. No. 3e+03;
0; Mismatches
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                                                                                                                                                                                             42 gcgrracccaagcrraarccccrrcaaga 13
                                                                                                                                                   1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
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APPLICANT: BUXH, J., MILLER, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUC
TITLE OF INVENTION: OF S1 ISOLATES OF HE
TITLE OF INVENTION: OF REAGENTS DERIVED
TITLE OF INVENTION: OF REAGENTS DERIVED
TITLE OF INVENTION: DIAGNOSTIC METHODS A
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NOMBER: US/08/086,428B FILING DATE: 29-JUN-1993
CLASSIFCATION: 435
ATTORNEY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCGGTACCCCAGCAGCCCGGCCTTG
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
                                                            52.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 76.0°
Matches 19; Conservative
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-25761
                                          Query Match
Best Local Similarity
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                PCT-US91-07149-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43, Application PC/TUS9107149
Sequence 43, Application PC/TUS9107149
GENERAL INFORMATION:
FITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
TITLE OF INVENTION: HETEROMERIC RECEPTORS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSE: PRETTY, SCHROEDER, BRUGGEMANN & CLARK
STREET: 444 SO. PLOWER STREET, SUITE 200
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: UNITED STATES

ZIP: 90071
COUNTRY: Unic.

ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07141
FILING DATE: 19910927
CLASSIFICATION NUMBER: PCT/US91/07141
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A
REGISTRATION NUMBER: P31 9072
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPRAN: (619) 535-901
TELEPRAN: (619) 535-901
TELEPRAN: (619) 535-901
TELEPRAN: (619) 535-901
TELEPRAN: RASE DID NO: 42:
SEQUENCY: A13 base pairs
THELEPRAN: SEQUENCY: SINGLE ACID
THELEPRAN: SEQUENCY: SEQUENCY: SINGLE ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTE: POCKM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07149
FILING DATE: 19910927
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: CAMPBELL, CATHEND A.
REGISTRATION NUMBER: 31,815
REFERRICE/DOCKET NUMBER: 31,815
REFERRICE/DOCKET NUMBER: 9118882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
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TELEPHONE: 619-535-9001
TELEPHONE: 619-535-9949
INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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2026-4070US1
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ITITLE OF INVENTION: AND ACID SEQUENCY TITLE OF INVENTION: AMINO ACID SEQUENCY TITLE OF INVENTION: OF 51 ISOLATES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-UIN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-UIN-1993
CLASSIFICATION: 424
      3 GGTACCCCAGCAGCCCGGCCTTGAA 27
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                                            27 GGCACATCAATAGCACGCCTTGAA 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 202
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.3%;
76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
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Best Local Similarity '
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: USA
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                             51.3%; Score 15.4; DB 1; Length 40; 76.0%; Pred. No. 3.6e+03; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BUCH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUC
TITLE OF INVENTION: AMINO ACID SEQUENCES
TITLE OF INVENTION: OF 51 ISOLATES OF HE
TITLE OF INVENTION: OF RAGGENTS DERIVED
TITLE OF INVENTION: DIAGNOSTIC METHODS AND OFFICE OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARLICATION NUMBER: US/08/086,428B
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                 40 GGCACATCAATAGCACGGCCTTGAA 16
                                                                                                                                                                                                                                                                                                                                                                                             3 GGTACCCCAGCAGCCCGGCCTTGAA 27
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-086-428B-106/c'
; Sequence 106, Application US/08086428B
; Patent No. 5514539
; GENERAL INFORMATION:
                                                                                                                                                 104:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.0'
Matches 19; Conservative
                                                                                                                     TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.0
Matches 19; Conservative
                                                                                                                                                                                                          ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-086-428B-104
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STATE: NEW YORK
COUNTRY: USA
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US-08-086-428B-106
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Sequence 104, Application US/08468570
Fatent No. 5871962
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKH, J., MILLER, R.H.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CF REAGENTS DERIVED FROM THESE SEQUENCES IN NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESS
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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
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Pred. No. 3.6e+03;
0; Mismatches 6;
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Score 15.4; DB 2;
Pred. No. 3.6e+03;
0; Mismatches 6;
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC CONFATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGMAT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOSCET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPRAX: (212) 751-6849
                                                                   APPLICATION NUMBER: US/08/290,665A FILING DATE: 15-AUG-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
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STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TELERAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 76.01
Matches 19; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 base pairs
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-290-665A-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-290-665A-210/c
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
263
                     OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
159
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TITLE OF INVENTION: OF REAGENTS DERIVE
TITLE OF INVENTION: DIAGNOSTIC METHODS
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTYRY: USA
ZIP: 10154
COMPUTER: ELOPPY DISK
COMPUTER: ELOPPY DISK
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COMPUTER: ELOPPY DISK
COMPUTER: USA
ZIP: CARDICATION NUMBER: USA
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REPERBUNCE/DOCKET NUMBER: 2026-4070US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGTACCCCAGCAGCCCGGCCTTGAA 27
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADD
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TELEX: 421792
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEBNESS: single
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Best Local Similarity 76.0
Matches 19; Conservative
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Gaps
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Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUCH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CRE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORRESPONDENCE ADDRESS:
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Length 40;
                                                       6; Indels
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BUKH, J., MILLER, R.H. AND

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APPLICANT:
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1S Sequence 104, Application US/08466601A

1 Patent No. 6572864

1 PATENT NO. 6572864

1 APPLICANT: BUKH, J., MILLER, R.H. AND

APPLICANT: BUKH, J., MILLER, R.H.

1 TITLE OF INVENTION: AMINO ACID SEQUENCES OF HEREATITIS C AND THE USE

1 TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IT TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES INVENTION: DIAGNOSTIC METHODS AND VACCINES

1 TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES

1 TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES

2 NUMBER OF SEQUENCES: 160

3 CORRESPONDENCE ADDRESS: 160

3 CORRESPONDENCE ADDRESS: 160

3 ADDRESSEE: MORGAN & FINNEGAN

5 STREET: 345 PARK AVENUE
                                                                     Gaps
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                       Score 15.4; DB 2; Length 40;
Pred. No. 3.6e+03;
0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,601A
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-UNN-1993
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2026-4070US2
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2.08-46-611A-106/c
; Sequence 106, Application US/08466601A
; Patent No. 6572864
                       51.3%;
76.0%;
Query Match
Best Local Similarity 76.0.
Local 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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Best Local Similarity
Matches 19; Conserve
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NEW YORK
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US-08-466-601A-104
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STATE:
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GENERAL INFORMATION:

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Gaps
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Sequence 208, Application PC/TUS9510398

GENERAL INFORMATION

APPLICANT: BUKEL, R.H.

APPLICANT: PURCELL, R.H.

TITLE OF INVENTION: MUNCLECTIDE AND DEDUCED

TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND

TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND

TITLE OF INVENTION: SEQUENCES OF ISOLATES OF HEPATITIS C VIRUS

TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

TITLE OF SEQUENCES: 263

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN
PURCELL, R.H.
VENTION: NUCLEOTIDE AND DEDUCED
VENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
VENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
VENTION: OF REAGENTS DERIVED PROM THESE SEQUENCES IN
VENTION: DIAGNOSTIC METHODS AND VACCINES
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Pred. No. 3.6e+03;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,601A
APPLICATION NUMBER: US/08/466,601A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION NUMBER: 36,428
ATYGNEY/ACRIT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GGTACCCCAGCAGCCCGGCCTTGAA 27
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                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                            FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 421792
INFORMATION FOR SEQ ID NO: 106:
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76.0%;
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                                                                                                                                                                                         ADDRESSEE: MORGAN & FINS
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                               160
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Best Local Similarity 76.0%
                   TITLE OF INVENTION: MUCL
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: OF F
TITLE OF INVENTION: DIAG
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                            NEW YORK
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                           10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
TELEX: 43
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                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.3%; Score 15.4; DB 5; Length 40; Best Local Similarity 76.0%; Pred. No. 3.6e+03; Matches 19; Conservative 0; Mismatches 6; Indels
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Sequence 91572, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT PAPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE FRAESEQ for Windows Version 4.0
SEQ ID NO 91572

LENGTH: 25
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Natchael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; FILE REFERENCE: 310.1.
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT PAPPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 127806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GGTACCCCAGCAGCCCGGCCTTGAA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 GGCACATCÁATAGCACGGCCTTGAA 3
                                     NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 758-4800
TELEFAX: (212) 751-6849
TELEFIX: 421792
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
PCT-US95-10398-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 CAGCAGCCCGGCCTTGAAGA 29
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                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: mus musculus
US-09-396-196G-91572
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NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MINO ACID SEQUENCES
TITLE OF INVENTION: AMINO ACID SEQUENCES
TITLE OF INVENTION: CORE GENES OF ISOLAT
TITLE OF INVENTION: CORE GENES OF ISOLAT
TITLE OF INVENTION: SEQUENCES IN DIAGNOS
NUMBER OF SEQUENCES: 263
COURRESOEDE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
RIGH APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTONNEY, AGENT THORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
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ZIP: 1154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: 1BM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGTACCCCAGCAGCCCGGCCTTGAA 27
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APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 76.0
nes 19; Conservative
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GENERAL INCORMATION:
MITAKE, KOICHIRO; HASHIMOTO, Shinichi; MOTOVAMA Hiroaki;
APPLICANT: MITAKE, KOICHIRO; Haruo; KUZAYAMA, Tomohisa; TAKAHASHI, Shunji
ITILE OF INVENTION: A process for producing isoprenoid compounds by
ITILE OF INVENTION: antibiotic or weeding activity
FILE REFERENCE:
CURRENT APPLICATION NUMBER: U5/09/673,198
CURRENT FILING DATE: 1998/103101
PRIOR FILING DATE: 1998/013101
PRIOR FILING DATE: 1998/021910
PRIOR FILING DATE: 1999/035739
PRIOR FILING DATE: 1999-02-15
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 23
LENGTHA: 22
LENGTHA: 22
LENGTH: 23
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Sequence 161, Application US/08998099A

Patent No. 6103890

GENERAL INFORMATION:
APPLICANT: ARCHIGGEN, JAMES A.

APPLICANT: ARCHIGGEN, JAMES A.

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES

TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS

TITLE OF INVENTION: DAY T.

TILE OF INVENTION: BAZYMATIC NUCLEIC ACID TREATMENT OF DISEASES

TITLE OF INVENTION: BAZYMATIC NUCLEIC ACID TREATMENT OF DISEASES

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES

TITLE OF INVENTION: ENZYMATIC NUMBER: US/08/998,099A

CURRENT FILING DATE: 1997-10-23

EARLIER FILING DATE: 1997-01-23

EARLIER PELING DATE: 1995-01-13

EARLIER PELING DATE: 1995-01-13

EARLIER FILING DATE: 1995-01-18

EARLIER FILING DATE: 1994-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA US-09-673-198-23
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                                                                                                                                                                                           Query Match 50.7%; Score 15.2; DB 4; Length 25; Best Local Similarity 85.0%; Pred. No. 4.1e+03; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.3%; Score 14.8; DB 4; Length 32; ilarity 73.1%; Pred. No. 6.1e+03; Conservative 0; Mismatches 7; Indels
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 91573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCGGTACCCCAGCAGCCCGGCCTTGA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGGATCCTGCCAGCCAGGCCTTGA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 23, Application US/09673198 ; Patent No. 6806076
                                                                                                                                                                                                                                                                                                            10 CAGCAGCCCGGCCTTGAAGA 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                TYPE: DNA ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                    ÚS-09-396-196G-91573
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US-09-673-198-23
                                                      LENGTH:
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Sequence 1 Sequence 1 Sequence 1

Sequence

Sequence Sequence

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Scoring table:

Searched:

Database

Perfect score:

Sequence:

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Sequence 6, Application US/08469172;
Publication No. US20030054343A1
SENERAL INFORMATION:
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: ROSENZWEIG, ANTHONY
ITILE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
4 US-10-645-702-9
2 US-10-119-900-167992
2 US-10-119-900-167992
3 US-10-719-900-167992
6 US-10-098-263B-28065
6 US-10-098-263B-28065
6 US-10-098-263B-41023
1 US-09-796-844-13
1 US-09-796-844-13
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2 US-10-645-702-13
4 US-10-645-702-13
4 US-10-645-702-13
4 US-10-645-702-13
5 US-09-949-145-26
5 US-10-809-189-109792
5 US-10-110-002-39
6 US-10-809-189-109792
6 US-10-809-189-109792
7 US-09-880-313A-140
1 US-09-949-145-26
7 US-10-110-002-39
6 US-10-110-002-39
6 US-10-110-002-39
6 US-10-110-002-39
6 US-10-110-002-39
6 US-10-110-002-39
7 US-10-719-956-273121
7 US-10-719-956-273131
7 US-10-719-956-273131
7 US-10-719-956-273131
7 US-10-719-956-273131
7 US-10-719-956-273131
7 US-10-719-900-675526
7 US-10-119-900-675526
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7 US-10-119-900-675526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,172
FILLING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD STREET, 60 STATE STREET, Suite
   Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
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CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02109
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                                                                                                 November 18, 2005, 06:36:48; Search time 403.232 Seconds (without alignments) 615.265 Million cell updates/sec
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Sequence 9,
Sequence 9,
Sequence 9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                            US-10-788-779-6
30
1 GCGCTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-788-779-6
US-09-796-844-9
US-10-645-702-9
US-10-686-639-9
                                                                                                                                                                                                                                                                     9794790 seqs, 4134909567 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match 1
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30 30 18.2 18.2

12 E 4 E

Score

Result Š.

Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 243, Appl Sequence 468543, Sequence 675526, Sequence 75305,

675526, 763075, 25761, 7

Sequence Sequence S

Sequence 11, Appl Sequence 13, Appl Sequence 25, Appl Sequence 26, Appl Sequence 140, Appl Sequence 140, Appl Sequence 19792, Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 48747, A Sequence 186720, Sequence 220107, Sequence 273121, Sequence 273121, Sequence 273121, Sequence 627239,

Gaps

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Indels

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GENERAL INVENTATION:

GENERAL INVENTATION:

APPLICANT: Shi, Yanggu
APPLICANT: Ruben, Steve M.

TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REPERENCE: PET988P2
CURRENT APPLICATION NUMBER: US/09/796,844
CURRENT FILING DATE: 2001-03-02
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PRILING DATE: 2000-03-06
PRIOR PRILING DATE: 1999-03-16
PRIOR PRILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
PRIOR PRILING DATE: 1999-03-16
PRIOR PRILING DATE: 1998-09-16
PRIOR PRILING DATE: 1997-09-17
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Sequence 9, Application US/10645702

Sequence 9, Application US/10645702

BUBLICALION NO. US20040115698A1

GENERAL INFORMATION:

APPLICANT: Shi, Yanggu

TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein

TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein

CURRENT PRILING DATE: 2003-08-22

PRIOR FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: US/9/796,844

PRIOR APPLICATION NUMBER: 60/187,015

PRIOR APPLICATION NUMBER: PCT/US00/05759

PRIOR FILING DATE: 2000-03-06

PRIOR FILING DATE: 2000-03-06
                                                                                                                                                                                Score 30; DB 20;
Pred. No. 0.0072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18.2; DB :
Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-796-844-9; Sequence 9; Application US/09796844; Sequence 9; Publication No. US20040096935A1; GENERAL INFORMATION:
                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 30; Conservative 0
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Best Local Similarity 87.0%;
Matches 20; Conservative
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ORGANISM: Homo sapiens
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US-10-788-779-6
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APPLICANT: SELDMAN, CHRISTINE
SELDMAN, JOHN
WATKINS, HUGH
ROSENZWEIG, ANTHONY
TITLE OF INVENTION:
DISEASE-ASSOCIATED MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/788,779
FILING DATE: 27-Eb-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/469,172
FILING DATE: «Unknown»
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
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NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GML-111
TELECOMMUNICATION INFORMATION:
TELEPANE: (617) 227-7400
TELEPAN: (617) 227-5941
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10788779
Publication No. US20040152121A1
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STATE: Massachusetts
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STRANDEDNESS: single
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Best Local Similarity 100.
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Indels

Length 26;

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Sequence 167892. Application US/10719900

Sequence 167892. Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Publication No. US20050026164A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR RELING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
NUMBER OF SEQ ID NOS: 98294
NUMBER OF SEQ ID NOS: 98294
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 60.7%; Score 18.2; DB 24; Length 26; 1 Similarity 87.0%; Pred. No. 7e+02; 20; Conservative 0; Mismatches 3; Indels
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                    PRIOR APPLICATION NUMBER: PCT/USO0/05759
PRIOR FILING DATE: 2000-03.06
PRIOR APPLICATION NUMBER: PCT/US99/21048
PRIOR PILING DATE: 1999-09.15
PRIOR PLING DATE: 1999-09.16
PRIOR PLING DATE: 1999-09.16
PRIOR PELING DATE: 1999-09.16
PRIOR PELING DATE: 1998-09.16
PRIOR PELING DATE: 1998-09.16
PRIOR PELING DATE: 1998-09.16
PRIOR PLING DATE: 1998-09.16
PRIOR PLING DATE: 1999-09.16
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
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Matches 18; Conservative
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CORGANISM: Mus musculus
US-10-719-900-167892
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-645-702-9
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US-10-719-900-189296
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/10686639;
Sequence 9, Application US/10686639;
Publication No. USC004017579041
GENERAL INFORMATION:
APPLICANT: Shi, Yanggu
APPLICANT: Shi, Yanggu
APPLICANT: Ruben, Steve M.
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REFERENCE: PF398
CURRENT APPLICATION NUMBER: US/10/686,639
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: US/09/154,219
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 1997-09-17
NUMBER: OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
SEQ ID NO 9
LENGTH: 26
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APPLICANT: Shi, Yanggu
APPLICANT: Ruben, Steve M.
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein; FILE REFERENCE: PF398P2
  PRIOR PILING DALE.

PRIOR APPLICATION NUMBER: U9/20-1

PRIOR PLING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: PCT/US98/19121

PRIOR PILING DATE: 1998-09-16

PRIOR PILING DATE: 1998-09-16

PRIOR PILING DATE: 1998-09-16

PRIOR PILING DATE: 1998-09-16

PRIOR PILING DATE: 1998-09-16

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1

LENGTH: 26
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CURRENT FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: US/09/796,844
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/187,015
APPLICATION NUMBER: PCT/US99/21048
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Matches 20; Conservative
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US-10-645-702-9
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ORGANISM: Homo sapiens
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US-10-645-702-9
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SOFTWARE: SEQ ID NO 11
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APPLICANT: Mittman, Michael; TILE OF INVENTION: Human Microarray; FILE REFERENCE: 3118.118.108.10/098,263B; CURRENT FILING DATE: 2003-01-08; PRIOR APPLICATION NUMBER: 60/276,759; PRIOR APPLICATION NUMBER: 60/276,759; NUMBER OF SEQ ID NOS: 131066; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 41023
                                                                                                                                                                                                                                                                                                                        Sequence 28065

Sequence 28065, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mitchman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT FILING DATE: 2001-03-02-03

FRIOR APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 28065

LENGTH: 25
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                                                                                                                                Length 25;
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                                                                                                                              56.0%; Score 16.8; DB 22;
90.0%; Pred. No. 2.8e+03;
iive 0; Mismatches 2;
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                                                                                                                            Query Match
Best Local Similarity 90.04
Matches 18; Conservative
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Best Local Similarity 85.7
Matches 18; Conservative
                      LENGTH: 25
TYPE: DNA
CRGANISM: Mus musculus
US-10-719-900-189296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo Bapien
US-10-098-263B-28065
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ORGANISM: Homo sapien
US-10-098-263B-41023
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US-10-098-263B-41023
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Sequence 11, Application US/10686639

Publication No. US20040175790A1

GENERAL INFORMATION:
APPLICANT: Shi, Yanggu

TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REFERENCE: PF398

CURRENT APPLICATION NUMBER: US/10/686,639

CURRENT APPLICATION NUMBER: US/20/154,219

PRIOR PILING DATE: 1998-09-16

PRIOR PILING DATE: 1998-09-16

PRIOR APPLICATION NUMBER: 60/059,133

PRIOR FILING DATE: 1997-09-17

NUMBER OF SEQ ID NOS: 13
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APPLICANT: Shi, Yanggu
APPLICANT: Ruben, Steve M.
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
TILE REFERENCE: PF398
CURRENT APPLICATION NUMBER: US/10/686,639
CURRENT FILING DATE: 2003-10-17
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Pred. No. 4.9e+03;
0; Mismatches 3;
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Pred. No. 4.9e+03;
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 09/268,311
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: PCY/US98/19121
PRIOR PILING DATE: 1998-09-16
PRIOR PILING DATE: 1998-09-16
PRIOR PLING DATE: 1998-09-16
PRIOR PLING DATE: 1998-09-16
PRIOR PLING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/059,133
PRIOR FILING DATE: 1997-09-17
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85.7%;
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Best Local Similarity 85.7
Matches 18; Conservative
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ORGANISM: Homo sapiens
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US-10-645-702-13
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Best Local Similarity
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LENGTH: 28
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Publication No. US20040115698A1
GENERAL INFORMATION.
APPLICANT: Shi, Yanggu
APPLICANT: Ruben, Steve M.
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REPERENCE: PF938P2
CURRENT APPLICATION NUMBER: US/10/645,702
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; Sequence 13, Application US/10645702
; Publication No. US20040115698A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanggu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
                                               54.0%; Score 16.2; DB 11; 85.7%; Pred. No. 4.9e+03;
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PURRENT FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: US/09/796,844
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-16
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PRIOR PILING DATE: 1999-09-16
PRIOR PILING DATE: 1998-09-16
PRIOR FILING DATE: 1998-09-16
PRIOR FILING DATE: 1998-09-16
PRIOR PILING DATE: 1998-09-17
SEQ ID NO 11
LENGTH: 28
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CURRENT FILING DATE: 2003-08-22
PRIOR PILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: PCT/US00/05759
PRIOR APPLICATION NUMBER: PCT/US99/21048
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                                        Query Match
Best Local Similarity 85.7
Matches 18; Conservative
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Matches 18; Conservative
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US-09-796-844-13
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; OTHER INFORMATION: Primer sequence, ExonlB, for F. solani cutinase gene
US-09-923-760-2
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Sequence 2, Application US/09923760

PUDLication No. US20030119054A1

GENERAL INFORMATION:

APPLICANT: Mrksich, Milan

APPLICANT: Hodon-land, Christian

TITLE OF INVENTION: POLYPEPTIDE IMMOBILIZATION

FILE REPERENCE: 7814/45

CURRENT APPLICATION NUMBER: US/09/923,760

CURRENT FILING DATE: 2001-08-07

NUMBER: OF SEQ ID NOS: 5

SOFTWARE: PATENTIN version 3.1
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Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITILE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                               PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: PCT/US99/21048
PRIOR APPLICATION NUMBER: PCT/US99/21048
PRIOR PELING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-16
PRIOR FILING DATE: 1998-09-16
PRIOR PELING DATE: 1998-09-16
PRIOR PRICATION NUMBER: 09/154,219
PRIOR APPLICATION NUMBER: 09/154,219
PRIOR APPLICATION NUMBER: 60/059,133
PRIOR FILING DATE: 1998-09-16
PRIOR FILING DATE: 1997-09-17
SOFTWARE: PATENTING NUMBER: 60/059,133
PRIOR FILING DATE: 1997-09-17
SOFTWARE: PATENTING NUMBER: 60/059,133
PRIOR FILING DATE: 1997-09-17
SOFTWARE: PATENTING NUMBER: 60/059,133
PRIOR FILING DATE: 1997-09-17
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                                    APPLICATION NUMBER: 60/187,015
FILING DATE: 2000-03-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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LENGTH: 38
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                                                                                                                                                                                                                                        Query Match 54.0%; Score 16.2; DB 20; Length 28; Best Local Similarity 85.7%; Pred. No. 4.9e+03; Matches 18; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Shi, Yanggu
APPLICANT: Shi, Yanggu
APPLICANT: Shi, Stanggu
APPLICANT: Ruben, Steve M.
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REFERENCE: PF939B2
CURRENT APPLICATION NUMBER: US/10/645,702
CURRENT FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: US/09/796,844
PRIOR PILING DATE: 2001-03-02
PRIOR PLILING DATE: 2000-03-06
PRIOR PLILING DATE: 2000-03-06
PRIOR PLILING DATE: 1909-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-16
PRIOR PLILING DATE: 1999-09-16
PRIOR PLILING DATE: 1998-09-16
PRIOR PLILING DATE: 1998-09-17
PRIOR PLILING DATE: 1998-09-17
PRIOR PLILING DATE: 1998-09-17
PRIOR PLILING DATE: 1998-09-17
PRIOR PLILING DATE: 1998-09-16
PRIOR PLILING DATE: 1998-09-17
PRIOR PLILING DATE: 1998-09-17
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PRIOR PLILING DATE: 1997-09-17
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Publication No. US20050181372A9

GENERAL INFORMATION:

APPLICANT: Shi, Yangqu

TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein

FILE REFERENCE: PF398P2

CURRENT APPLICATION NUMBER: US/10/645,702

CURRENT FILING DATE: 2003-08-22

PRIOR APPLICATION NUMBER: US/09/796,844
                                                                                                                                                                                                                                                                                                                                                                                          6 GGTACCCCAGCCTCCCGGCTT 26
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NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 28
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                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-686-639-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-645-702-11
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Matches 18; Conserv
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US-10-645-702-11
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US-10-645-702-13
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                                                 Indels
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| Sequence 109792, Application US/10809189
| Publication No. US20050048531A1 |
| GENERAL INPORMATION: |
| GENERAL INPORMATION: |
| APPLICANT: Michael Mittmann |
| APPLICANT: Michael Mittmann |
| APPLICANT: David Mack |
| APPLICANT: Affymetrix, Inc. |
| TITLE OF INVENTION: Methods of Genetic Analysis |
| FILE REFERENCE: 3101.1 |
| CURRENT APPLICATION NUMBER: US/10/809,189 |
| CURRENT APPLICATION NUMBER: US/09/396,196 |
| PRIOR APPLICATION NUMBER: US/09/396,196 |
| PRIOR PILLING DATE: 1999-09-15 |
| PRIOR FILLING DATE: 1999-09-17 |
| NUMBER OF SEQ DI NOS: 127806 |
| SORTWADEN FILLING DATE: 1998-09-17 |
| NUMBER OF SEQ DI NOS: 127806 |
| SORTWADEN FILLING DATE: 1998-09-17 |
| NUMBER OF SEQ DI NOS: 127806 |
| SORTWADEN FILLING DATE: 1998-09-17 |
| NUMBER OF SEQ DI NOS: 127806 |
| SORTWADEN FILLING DATE: 1998-09-17 |
| SORTWADEN FILLING DATE: 1098-09-17 |
| SORTWADEN FILLING DATE: 1098-0
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Pred. No. 7.5e+03;
0; Mismatches 2;
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             Best Local Similarity 89.5%; Pred. No. 7.5e+03; Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Flemington, Erik K
TITLE OF INVENTION: Adaptors and Methods of Use
FILE REFERENCE: 9397/1000
CURRENT APPLICATION NUMBER: US/09/880,313A
CURRENT FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 276
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 140
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                                                                                                                                                                                                                                                                                             US-09-880-313A-140/c
Sequence 140, Application US/09880313A
Publication No. US20030044791A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Oligonucleotide US-09-880-313A-140
                                                                                                             4 GIACCCCAGCCCGGCC 22
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                                                                                                                                                                  19 GTACCCCTGCAGCGCGGCC 1
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Best Local Similarity 89.5%;
Matches 17; Conservative
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SEQ ID NO 109792
LENGTH: 25
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US-10-375-913-39/c
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Patent No. US20020055622A1
GENERAL INFORMATION:
APPLICANT: New York Blood Center
TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and Glycc TITLE REFERENCE: Docket 454-31
CURRENT APPLICATION NUMBER: US/09/949,145
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/230660
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Version 3.1
SEQ ID NOS: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.3%; Score 16; DB 22; Length 25; Best Local Similarity 79.2%; Pred. No. 6e+03; Matches 19; Conservative 0; Mismatches 5; Indels
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; Sequence 54, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
; APPLICATT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 201-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: Patentin Ver. 2.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1990-09-15
PRIOR FILING DATE: 1990-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NO 25759
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus
US-10-809-189-25759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-145-26
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LENGTH: 19
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Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative (
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Best Local Similarity 81.8°
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-48747
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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| Publication No. US20050196804A1
| GENERAL INRORMATION:
| APPLICANT: Wing-Qun
| APPLICANT: Ferrandon, Sebastien
| APPLICANT: Ferrandon, Sebastien
| APPLICANT: Taron, Christopher
| TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
| TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
| TITLE OF INVENTION: MODIFIED TOWNER: US/11/110,001
| TITLE OF INVENTION WINBER: US/10/375,913
| PRIOR APPLICATION NUMBER: US 60/360,354
| PRIOR APPLICATION NUMBER: US 60/360,354
| PRIOR FILING DATE: 2002-02-28
| NUMBER OF SEQ ID NOS: 49
| SEQ ID NO 39
| LENGTH: 39
; Sequence 39, Application US/10375913
; Publication No. US20030216550A1
; Publication No. US20030216550A1
; GENERAL INFORMATION:
    APPLICANT: Xu, Ming-Oun
; APPLICANT: Ferrandon, Sebastien
; APPLICANT: Taron, Chistopher
; APPLICANT: Colussi, Paul
; TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
; FILE REFERENCE: NEW-200-US
; CURRENT APPLICATION NUMBER: US/10/375,913
; CURRENT FILING DATE: 2003-02-26
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.7%; Score 15.8; DB 26; Length 39; 89.5%; Pred. No. 6.9e+03; Live 0; Mismatches 2; Indels
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US-11-110-002-39/c
'Sequence 39, Application US/11110002
'Publication No. US20050196841A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 GGTACCCCAGCAGGCGGC 10
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: primer US-10-375-913-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: unknown
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US-11-110-001-39/c
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APPLICANT: Ferrandon, Sebastien
APPLICANT: Taron, Christopher
APPLICANT: Taron, Christopher
TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
FILE REPRENCE: NEB-200-US
CURRENT FILING DATE: 2005-04-20
FRIOR PPLICATION NUMBER: US/11/110,002
CURRENT FILING DATE: 2005-04-20
FRIOR PPLICATION NUMBER: US/10/375,913
FRIOR FILING DATE: 2002-02-6
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.1
SEQ ID NO 39
TYPE: ...
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; Sequence 48747, Application US/10719900
; Publication No. US2050026164A1
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
; TITLE OF INVERTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT PILING DATE: 2003-11-20
; PRIOR RILING DATE: 2002-11-20
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48747
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Sequence 48748, Application US/10719900

PUBLICATION NO. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

TITLE OF INVENTION WEARS: US/10/719,900

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT PILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR PILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914
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Pred. No. 6.9e+03;
0; Mismatches 2;
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; Sequence 220107, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
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Publication No. US20040146910A1
GENERAL INFORMATION:
                                           8 CCCAGCCCGGCCTTGAAGA 29
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81.8%;
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; ORGANISM: Rattus norvegicus
US-10-719-956-220107
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Best Local Similarity 81.8
Matches 18; Conservative
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US-10-719-956-220107/c
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US-10-719-956-254406/c
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APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT PILIG DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,836

PRIOR PLING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Pred. No. 8.8e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                    Length 25;
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SRQ ID NO 48748
LENGTH: 25
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APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affectix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILIG DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
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PRIOR APPLICATION NUMBER: 60/100,678
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Publication No. US20050048531A1
GENERAL INFORMATION:
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; Publication No. US20040146910A1
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81.8%;
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; ORGANISM: Rattus norvegicus
US-10-719-956-186720
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Best Local Similarity 81.8
Matches 18; Conservative
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Best Local Similarity 81.8
Matches 18; Conservative
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; ORGANISM: mus musculus
US-10-809-189-125627
                                                                                                 ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-48748
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US-10-809-189-125627
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APPLICANT: Xue Mei Zhou
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR PILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-11 20
NUMBER: OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 220107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION Methods of Genetic Analysis of Rat TITLE OF INVENTION: Methods of Genetic Analysis of Rat FILE REFERENCE: 357.1 CURRENT APPLICATION NUMBER: US/10/719,956 CURRENT FILING DATE: 2003-11-20 PRIOR APPLICATION NUMBER: 00/427,836 PRIOR FILING DATE: 2002 11 20 NUMBER OF SEQ ID NOS: 699466 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 254406 LENGTH: 25
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFRENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
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US-10-716-803-43/c
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; Dublication No. US20040146910A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Xue mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; TILE REFERENCE: 3527.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; TENGEN: 202240
                                                                                                                                                                                                                        52.0%; Score 15.6; DB 24; Length 25; 81.8%; Pred. No. 8.8e+03; tive 0; Mismatches 4; Indels
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              NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 271121
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR PELING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 627239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.0%; Score 15.6; DB 24.81.8%; Pred. No. 8.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 627239, Application US/10719956
Publication No. US20040146910A1
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
                                                                                                                                                                                                                                                                                                       9 CCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 CCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                                                                              23 ccascascascacircas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-627239
                                                                                                                                           ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-273121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rattus norvegicus
US-10-719-956-627240
                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 52.0
Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 81.8
Matches 18, Conservative
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US-10-719-956-627239/c
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US-10-719-956-627240/c
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Debussche, Laurent
Debussche, Laurent
De Crecy-Lagard, Valerie
INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEB: Finnegan, Henderson, Farabow, Garrett & Dunner
STREEF: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
PRIORE DATE: 20-Nov-2003
PRIOR APPLICATION DATA:
APPLICATION DATA:
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REGISTRATION NUMBER: 46,063
REFERENCE/DOCKET NUMBER: 03806.0054-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.0%; Score 15.6; DB 21;
62.5%; Pred. No. 8.6e+03;
tive 5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/635,359
FILING DATE: 09-AUG-2000
APPLICATION NUMBER: US 09/231,818
FILING DATE: 15-JAN-1999
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
FILING DATE: 25-SEP-1992
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9 CCAGCAGCCCGGCCTTGAAGAA 30
                                                                                      22 ccascasccassicricaasca 1
                                                                                                                                                                                                                                                                                                        Sequence 43, Application US/10716803
Publication No. US20040229236A1
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacques, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lacroix, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blanche, Francis
Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thibaut, Denis
Zagorec, Monique
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LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 43:
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Best Local Similarity
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SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.0%; Score 15.6; DB 22; Best Local Similarity 70.0%; Pred. No. 8.3e+03; Matches 21; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-00-80-313A-243/C
Sequence 243, Application US/09880313A
Sequence 243, Application US/09880313A
Publication No. US20030044791A1
GENERAL INFORMATION:
TITLE OF INVENTION: Brik K
FILE REPREBENCE: 9397/1000
CURRENT PILING DATE: 2001-06-13
CURRENT PILING DATE: 2001-06-13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 243
LINGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.3%; Score 15.4; DB 10; Best Local Similarity 94.1%; Pred. No. 1.1e+04; Matches 16; Conservative 0; Mismatches 1;
             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/767,869
FILING DATE: 28-Jan-2004
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Gay, David A.
RECISTRATION NUMBER: 39,200
REFERENCE/DOCKET NUMBER: 66797-397
TELECOMMUNICATION INFORMATION:
TELEPAX: 619-535-9901
TELEPAX: 619-535-9901
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 ecerracceaaecrraarcecerrecaeaa 13
                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: Single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: November 18, 2005, 15:41:06 Job time : 403.232 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Oligonucleotide US-09-880-313A-243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GTACCCCAGCAGCCCGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-767-869-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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                                    Sequence 42, Application US/09727311
Sequence 42, Application US/09727311
Sequence 42, Application US/09727311
SERVERAL INFORMATION: STREAGE EXPRESSION LIBRARIES OF TITLE OF INVENTION: STREAGE: 61
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Perty, Schroeder, Brueggemann & Clark STREET: 444 South Flower Street, Suite 2000 CITY: Los Angeles STATE: California COUNTRY: United States
IP: 90071
COMPUTER: READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/09/727,311
FILING DATE: CLARGE OF TAXES APPLICATION NUMBER: US/09/727,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/10767869
Publication No. US20050003384A1
GENERAL INFORMATION:
APPLICANT: HUSE, WILLIAM D.
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
HETEROMERIC RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSE: McDermott Will & Emery
STREET: 4770 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 30
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P31 9072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/767,436
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MANUE: Campbell, Cathryn A
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CALIFORNIA COUNTRY: UNITED STATES
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Best Local Similarity
Matches 21; Conserv
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US-10-767-869-43/c
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TOPOLOGY:
US-09-727-311-42
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Gaps

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Gaps

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OM nucleic

Run on:

Sequence:

Searched:

Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     Unclassified.
1 (bases 1 to 30)
Seidman, C., Seidman, J., Watkins, H. and Rosenzweig, A.
Method for detecting hypertrophic cardiomyophathy associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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ilarity 100.0%; Pred. No. 0.034;
Conservative 0; Mismatches n
                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQ848568 50 bp DNA Sequence 28 from Patent WO2004065628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGAATTCGCGGAGCCAGACGCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAATTCGCGGAGCCAGACGCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                         mutations
Patent: US 5429923-A 7 04-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="unassigned DNA"
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Sequence 7 from patent US 5429923.
112900
                                                                                                             AR095549
CQ818101
CQ818101
CQ847433
BD002760
AR274129
AR444946
BD271888
AX080183
AX592510
                                         AR003508
AR070729
AR118062
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AR009935
176260
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        AR084293
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                                                                    I17115
I62404
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Homo sapiens
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Query Match
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Matches 30; Conserv
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AR030683 Sequence
AR030683 Sequence
AR124104 Sequence
B23386 DNA encodin
BD226997 Plasmin i
A37856 Sequence
AR099291 Sequence
AR124175 Sequence
AR141782 Sequence
AK1516500 Sequence
AX518285 Sequence
AX518285 Sequence
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E31233 Device for
AR566423 Sequence
A51539 Sequence 24
                                                         November 18, 2005, 11:12:34; Search time 832.357 Seconds (without alignments) 1746.433 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
        GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                             1 GGGAATTCGCGGAGCCAGACGGCACTGAAG 30
                                                                                                                                                         4708233 seqs, 24227607955 residues
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                         nucleic search, using sw model
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AR076191
AR124104
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BD226997
A37856
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E31233
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AX515690
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CQ818454
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Gapop 10.0 , Gapext 1.0
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PAT 26-JUL-1995

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AR04338 Sequence AR095549 Sequence CQ818101 Sequence CQ817433 Sequence BD002760 Gene comp AR274129 Sequence AR444946 Sequence AX080183 Sequence AX080183 Sequence AX592510 Sequence AX592510 Sequence AX592510 Sequence AX080183 Sequence AX592510 Sequence AX080183 Sequence AX592510 Sequence

AR307679 Sequence AR003508 Sequence AR070729 Sequence AR118062 Sequence

AR084293 Sequence CQ795411 Sequence I95571 Sequence 26

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PAT 19-AUG-2004

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C12N15/09, C12N1/21, C12N9/12// (C12N15/09, C12R1:91), (C12N1/21,
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(C12N9/12,C12R1:19),C12N15/00,(C12N15/00,C12R1:91)
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/organism='Unidentified'
Location/Qualifiers
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1 (bases 1 to 23)

Akira,S. and Kawai,T.

DNA coding for serine/threonine kinase
Patent: US 6171841-A 5 09-JAN-2001;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
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Shizuo, S. and Taro, K.
DNA encoding serine/threonine kinase
Patent: JP 1999098984-A 3 13-APR-1999;
SCIENCE & TECH AGENCY
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DNA encoding serine/threonine kinase.
                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
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Sequence 5 from patent US 6171841.
AR124104

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JP 1999098984-A/3
13-APR-1999
26-SEP-1997 JP 1997261589
      1 GGGAATTCGCGGAGCCAGACG 21
                                GGGAATTCGCGGAGCAGGAGG 21
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PN JP 199908984-A/3
PD 13-APR-1997
PF 26-SEP-1997 JP 1997
PR SHIZUO SHINRA, TARO
PC (12N15/10), CI2N1/21,
PC (12N15/10), CI2N1/21,
PC (12N9/10, CI2N1/21,
PC (12N9/10, CI2N1/19),
CC Topology: Linear;
FH Key
FH Key
FT SOURCE

/OX
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Cowart, M.Daniel., Halbert, D.N., Kerwin, J.F. Jr. and McNally, T. Adenosine kinase polypeptides
Patent: US 5861294-A 20 19-JAN-1999;
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                                                                                                                                                                                    62.7%; Score 18.8; DB 6; Length 50; 76.7%; Pred. No. 2.5e+03; Live 0; Mismatches 7; Indels
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Pu,G.
Quantitative multiplex detection of nucleic acids
Patent: WO 2004065628-A 28 05-AUG-2004;
Fu, Guoliang (GB)
Location/Qualifiers
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Akira, S. and Kawai, T.

DNA coding for serine/threonine kinase
Patent: US 5958748-A 5 28-SEP-1999;

Location/Qualifiers
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                                                                                                                                                                                                                                                                          14 GAGAATTCGACGATCCAGGTGTCACTGAAG 43
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Sequence 20 from patent US 5861294.
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/organism="unknown"
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Sequence 5 from patent US 5958748.
AR076191
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Best Local Similarity 85.7
Matches 18; Conservative
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AR076191 LOCUS

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AR030683 LOCUS RESULT 3

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PAT 18-FEB-2000

LOCUS

BD226997

8 g ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

us-10-788-779-7.rge

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1 (bases 1 to 38)
Blanc, V., Blanche, F., Crouzet, J., Jacques, N., Lacroix, P.,
Thibaut, D., Zagorec, M., Debussche, L. and De Crecy-Legard, V.
Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
Patent: US 5891695-A 42 06-APR-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 38)
Blanc, V., Blanche, F., Crouzet, J., Jacques, N., Lacroix, P.,
Thibaut, D., Zagorec, M., Debussche, L. and De Crecy-Lagard, V.
Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
Patent: US 6077699-A 44 20-JUN-2000;
Location/Qualifiers
                                                                                                                                                                                                                                        Query Match 54.0%; Score 16.2; DB 6; Length 38; Best Local Similarity 66.7%; Pred. No. 3.3e+04; Matches 18; Conservative 3; Mismatches 6; Indels
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publication CA 2145523 940414
publication ZA 9307102 940422
publication FI 951403 950324
publication FR 2696189 940401
publication JP 8501696T 960227.
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    .38
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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Sequence 42 from patent US 5891695.
AR069894
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Sequence 44 from patent US 6077699.
AR099291

    .38
    /organism="unknown"
    /mol_type="unassigned DNA"

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                                                                                                                                                                                                                                                                                                                                              1 GGGAATTCGCGGAGCCAGACGCCACTG 27
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    .38
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Matches 18; Conservative
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                                                                                                                                                       BD226997 31 bp DNA linear PAT 17-JUL-2003
Plasmin inhibitor from Australia brown snake Pseudonaja textilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ပ္ပ
                                                                                                                                                                                                                                                                                                                   other sequences; artificial sequences.
1 (bases 1 to 31)
Masci,P.P., Lavin,M.F. and Gaffney,P.J.
Plasmin inhibitor from Australia brown snake Pseudonaja textilis
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Blanc, V., Blanche, F., Crouzet, J., Jacques, N., Lacroix, P.,
Thibaut, D. and Zagorec, M.
POLYPEPTIDES INVOLVED IN STREPTOGRAMIN BIOSYNTHESIS, NUCLEOTIDE
SEQUENCES CODING FOR SAID POLYPEPTIDES AND USE THEREOF
PATCHE: WO 9408014-A 26 14.APR-1994;
RHONE POULENC RORER SA (FR)
Other publication AU 4823993 940426
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PANTALEONE PAUL MASCI, MARTIN FRANCIS LAVIN, PATRICK JOSEPH
                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: JP 2002514404-A 17 21-MAY-2002;
THE UNIVERSITY OF QUEENSLAND, NATIONAL INSTITUTE OF BIOLOGICAL STANDANDS AND CONTROL UNITED KINGDOM
OS Artificial Sequence
PN JP 2002514404-A/17
PD 21-MAY-1999 JP 2000548371
PR 11-MAY-1999 AU PP 3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COTKI4/81,C12N15/00,A61K37/02,A61K37/465
Description of Artificial Sequence:gene-specific reverse primer for Txln1
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85.7%; Pred. No. 3.3e+04;
ive 0; Mismatches 3; Indels
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    .31
    ^organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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Sequence 26 from Patent WO9408014.
A37856
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                                                 1 GGGAATTCGCGGAGCAGGAGG 21
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                    GGGAATTCGCGGAGCCAGACG
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JP 2002514404-A/17.
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synthetic construct
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Best Local Similarity 85.7
Matches 18; Conservative
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PAT 14-FEB-2001

PAT 05-OCT-2002

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Homo sapiens
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                                                                                                                                                                                                                                                          Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 38)
1 - (bases 1 to 38)
Blanc, V., Blanche, F., Crouzet, J., Jacques, N., LaCroix, P.,
Thibaut, D., Zagorec, M., DeBussche, L. and De Crecy-Lagard, V.
Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
Patent: US 6171846-A 42 09-JAN-2001;
Location/Qualifiers
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Blanc, V., Blanche, F., Crouzet, J., Jacques, N., Lacroix, P.,
Thibaut, D., Zagorec, M., Debussche, L. and De Crecy-Lagard, V.
Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
Patent: US 6670157-A 42 30-DEC-2003;
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               Length 38;
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                                           Indels
                                          9
            Score 16.2; DB 6;
Pred. No. 3.3e+04;
3; Mismatches 6;
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                                                                                                                                                                           AR124175 38 bp I
Sequence 42 from patent US 6171846.
AR124175
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                       GGGAATTCGCGGAGCCAGACGGCACTG 27
                                                                                                   11 GSGAGTTCGCSGCSTGGGACGGCACCG 37
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AR442782.1 GI:42670186
         54.0%;
       Query Match
Best Local Similarity 66.7<sup>3</sup>
Matches 18; Conservative
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Matches 18, Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
Detection of genetic polymorphisms
Patent: WO 02052044-A 4483 04-JUL-2002;
Riken (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.3%; Score 15.4; DB 6;
llarity 70.4%; Pred. No. 7.4e+04;
Conservative 1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.3%; Score 15.4; DB 6; Best Local Similarity 70.4%; Pred. No. 7.4e+04; Matches 19; Conservative 1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4483 from Patent WO02052044. AX518285
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Sequence 15 from Patent WO2004029088.
CQ818454
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AX515690 41 bp DNJ
Sequence 1888 from Patent WO02052044.
AX515690

    .41
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                             AX515690.1 GI:23563011
                                                                                                           Homo sapiens (human)
Homo sapiens
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REFERENCE AUTHORS TITLE JOURNAL

FEATURES

ORIGIN

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unidentified
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unidentified
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unidentified
unclassified.

I (bases 1 to 33)

Mitsuharu, O., Takayuki, K. and Ikuo, M.

Bytice for separating CD4-positive cells and separation method
L Patent: JP 199332594-A 11 07-DEC-1999;
ASAHI CHEM IND CO LTD
OS Unidentified
PP 1999332594-A/11
PD 07-DEC-1999
PP 26-MAY-1998 JP 1998163023
PP 26-MAY-1998 JP 1998163023
PP 1998 JP 1998163023
PP 190704, CO7K16/28, CO7K16/46, C12M1/34, G01N33/53 CC
PC C12Q1/04, CO7K16/28, CO7K16/46, C12M1/34, G01N33/53 CC
PT source 1.33
PT 50 Lorganism='Unidentifier'
/organism='Unidentified'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 33)
Muller, S. and Kohler, H.
Nucleotide sequences encoding variable regions of heavy and light
Chains of monoclonal antibody 1F7, an anti-idiotypic antibody
reactive with anti-HIV antibodies
Patent: US 6768004-A 3 27-UUL-2004;
Location/Qualifiers
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Pred. No. 9.1e+04;
0; Mismatches 3;
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85.0%; Pred. No. 9.1e+04;
iive 0; Mismatches 3;
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Sequence 24 from Patent EP0728842.
A51539 GI:2304360

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Best Local Similarity 85.0%;
Matches 17; Conservative 0
JP 1999332594-A/11.
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          Roth, C.W., Brey, B.T., Holm, I., Grailles, M. and Rzhetsky, A. Multidrug resistance proteins in drosophila and anopheles Patent: WO 2004029088-A 15 08-APR-2004; INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
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C12N15/02, A61K39/395, A61K39/395, C07K16/28, C12N15/09, C12P21/08,
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85.0%; Pred. No. 9.1e+04;
tive 0; Mismatches 3; Indels
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Antibody and nucleic acid encoding the same.
E30624
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/organism='Unidentified'
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Mitsuharu,O., Takayuki,K. and Ikuo,M.
Antibody and nucleic acid encoding the Patent: JP 1999332563-A 11 07-DEC-1999;
ASAHI CHEM IND CO LTD

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JP 1999332563-A/11
07-DEC-1999
26-MAY-1998 JP 1998163034
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JP 1999332563-A/11.
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Matches 17; Conservative
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Unclassified.

1 (Dases 1 to 31)

Audonnet, J.-C. Francis., Bublot, M. Joseph. Marie., Darteil, R. Jean.,

Duinat, C. Veronique., Laplace, E. Louise. Francedillaoise. and

Rivierch, M. Albert. Emile.

Live recombinant avian vaccine using an avian herpesvirus as vector

Patent: US 5980906-A 27,09-NOV-1999;
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1 (bases 1 to 31)
Audonnet, J.-C. Francedillais., Bublot, M.Joseph.Marie.,
Darteil, R.Jean., Duinat, C.Veronique.,
Laplace, B. Louise. Francedillaoise. and Riviere, M.Albert. Emile.
Avian herpesvirus-based live recombinant avian vaccine, in
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="oligonucl otide servant d'amorce de
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Pred. No. 1.1e+05;
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Patent: US 5733554-A 26 31-MAR-1998;
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Sequence 26 from patent US 5733554.
195571
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                                               Audomnet,J. F., Bublot, M.J., Darteil, R.J., Duinat, C.V., Laplace, E.L. and Riviere, M.A.
and Riviere, M.A.
Live recombinant avian vaccine based on an avianherpes virus, against Gumboro disease
Patent: EP 0728842-A 24 28-AUG-1996;
RHONE MERIEUX (FR)
Other publication FR 2728794 960705
Other publication AU 406371 960701
Other publication AU 4063195 960711.
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Audonnet,J.F., Bublot,M.J., Darteil,R.J., Duinat,C.V., Laplace,E.L. and Riviere,M.A.
Recombinant live avian vaccin, using an avian herpes virus as
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Patent: BP 0719864-A 27 03-JUL-1996;
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    .31
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Sequence 27 from patent US 5980906.
AR084293
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Sequence 27 from Patent EP0719864.
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Bitler, C.Mastroni., Bowersox, S.Scott., Crea, R., Demo, S.Dunham., Horne, W.A. and Zhou, M.
Bax.omega. protein and methods
Patent: US 6140484+A 1 31-OCT-2000;
Location/Qualifiers
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Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
Screening assays for identifying agents that regulate the
expression of genes involved in cell death
Patent: US 590750-A 8 01-JUN-1999;
Location/Qualifiers
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Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels
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/mol_type="unassigned DNA"
                                                       27 bp
Sequence 8 from patent US 5908750.
AR070729
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Sequence 1 from patent US 6140484.
AR118062.1 GI:14098968
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Kandel,E.R., Santoro,B., Bartsch,D., Siegelbaum,S., Tibbs,G. and
                                                                                                                          Gaps
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Patent: US 6551821-A 26 22-APR-2003;
Location/Qualifiers
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49.3%; Score 14.8; DB 6; Length 26;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels
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Sequence 26 from patent US 6551821.
AR307679
AR307679.1 GI:31698384
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/organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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/mol_type="genomic DNA"
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Location/Qualifiers
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Reed, J.C.
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AR307679
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Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
Promotors that regulate the expression of genes involved in cell
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Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
Method of down-regulating a gene linked to a P-53 responsive
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49.3%; Score 14.8; DB 6; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels
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/organism="unknown"
/mol_type="unassigned DNA"
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                       Patent: US 5484710-A 8 16-JAN-1996;
Location/Qualifiers
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Location/Qualifiers
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Sequence 8 from patent US 5659024.
162404
162404.1 GI:2480352
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Sequence 4 from patent US 5702897.
186716.1 GI:3206434
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1 (bases 1 to 27)

Reed, J.C. and Sato, T.
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Katz,L., Donadio,S. and McAlpine,J.B.
Recombinant DNA method for producing erythromycin analogs
Patent: US 5824513.A 25 20-OCT-1998;
Location/Qualifiers
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Reed, J.C. and Sato, T.
Interaction of proteins involved in a cell death pathway
Patent: US 5702897-A 12 30-DEC-1997;
Location/Qualifiers
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Sequence 25 from patent US 6004787.
AR095549
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                                                                                                               186724 27 bp 1
Sequence 12 from patent US 5702897.
186724
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Sequence 25 from patent US 5824513.
AR049388.1 GI:6005427
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GGAATTCGCGGTGATGGACGGGTCCG
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Fadel, A. Affinity proteins for controlled application of cosmetic substances Patent: WO 2004069211-A 161 19-AUG-2004; L-MADS B.V. (NL) Coation/Qualifiers
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unclassified.
unclassified.
sha,N., walinton,J. and Patel,N.
Gene composition and method
Patent: JP 2000245487-A 426 12-SEP-2000;
AFINETKICS INC
OS Unknown
PN JP 2000245487-A/426
PD 12-SEP-2000
PP 27-JAN-2000 JP 2000019392
PR 27-JAN-1999 US 09/238.402
PR 27-JAN-1999 US 09/238.402
PR 27-JAN-1999 US 09/238.402
PR 27-JAN-1999 US 09/238.702
PR 27-JAN-1999 US 09/238.702
PR 27-JAN-1999 US 09/238.702
PR 27-JAN-1999 US 09/238.702
PR 27-JAN-1999 US 09/238.402
Best Local Similarity 69.0%; Pred. No. i.7e+05; Matches 20; Conservative 0; Mismatches 9;
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/organism='Unknown'
Location/Qualifiers
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JP 2000245487-A/426.
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Patent: WO 2004044004-A 128 27-MAY-2004;
Avidex Limited (GB)
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Unclassified.

Unclassified.

1 (bases 1 to 50)
Shimkets,R.A. and Leach,M.
Shimkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: US 6670464-A 940 30-DEC-2003;
Location/Qualifiers
1 (bases 1 to 30)

Katz,L., Donadio,S. and McAlpine,J.B.
Method of directing biosynthesis of specific polyketides
Patent: US 6040487-A 25 21-DEC-1999;
Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
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Sequence 940 from patent US 6670464.
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20; Conservative
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AR444529
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           Query Match
Best Local Similarity 83.3%; Pred. No. 2e+05;
Matches 15; Conservative 1; Mismatches 2; Indels
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Barbour,E., Meyer,T.E.C. and Saad,M.E. Maize Gos-2 promoters
Patent: US 6504083-A 15 07-JAN-2003;
Location/Qualifiers
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Barbour,E., Meyer,T.E.C. and Saad,M.E.
Maize promoters
Patent: US 6670467-A 15 30-DEC-2003;
Location/Qualifiers
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Sequence 15 from patent US 6504083,
AR274129
AR274129.1 GI:29706106
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AR444946.1 GI:42672823
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BD271888.1 GI:33081656

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Synthetic construct

Synthetic construct

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Synthy 20024376-A 1 24-DEC-2002;

TATSULI SELL, KAZUHITO FULIYAMA

OS ALTIficial Sequences

PN JP 200254376-A 1 24-DEC-2002;

TATSULI SELL, KAZUHITO FULIYAMA

OS ALTIficial Sequence

PN JP 2002543760-A 1 24-DEC-2002;

TATSULI SELL, KAZUHITO FULIYAMA

OS ALTIFICIAL SEQUENCE

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PN JP 2002543760-A 1

PN JP 2002543760-A 1

PN JP 2002543760-A 1

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PN JP 2002543760-A 1

C121N5/00,

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CC Description of Artificial Sequence:primer hGT-5ECO FH Key
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GAATTCGCGGAGCCAGACG 21
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(without alignments)
859.686 Million cell updates/sec
                                                                                                                  November 18, 2005, 05:29:23 ; Search time 206.578 Seconds
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                           US-10-788-779-7
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1 GGGAATTCGCGGAGCCAGACGGCACTGAAG 30
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4167226 Total number of hits satisfying chosen parameters: 4390206 segs, 2959870667 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 50 Scoring table: Searched:

Listing first 45 summaries 100% Post-processing: Minimum Match 0%
Maximum Match 100 Database :

geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* N_Geneseq_16Dec04:* geneseqn2000s:* geneseqn2001as:* geneseqn1980s:* geneseqn1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description		Aca63117 Human bet	Adr05303 Human bet	Adq31570 Multiplex	Aaz58040 Porcine r	Aaz54807 Neisseria	Aat48848 Rat brain	Aax01108 PCR prime	Aax34658 Sense pri	Aaz29034 Txln 1 ge		Aas98482 Human pro	Aal55433 Specific	Abq76067 Anticance	Abv75124 Mutant HG	Adi80425 Anti-tumo	Aaa11359 Human Myx	Abz47699 Human ATP	Abz45104 Human ATP	Aci97483 Human mic
ID	AAQ91127	ACA63117	ADR05303	ADQ31570	AAZ58040	AAZ54807	AAT48848	AAX01108	AAX34658	AAZ29034	ABZ99545	AAS98482	AAL55433	ABQ76067	ABV75124	AD180425	AAA11359	ABZ47699	ABZ45104	ACI97483
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ACK28325 Human mic Aa254975 Neisseria Aaa30422 Single-do Aag90440 RT-PCR pr Aa244213 Murine CD Aa39128 Murine CD Aa39128 Murine mo Aa44120 Murine mo Aa44120 Murine Ma Aa296102 Polynucle Aa61849 Murine TR Aba03393 Sindbis v Aa45898 Marek dis Aat3933 Marek dis Aat3933 Marek dis Aat35930 Marek dis Aat35930 Marek dis Aat35930 Marek dis Aat35930 Marek dis Aat35930 Marek dis Aat35930 Marek dis Aat3696 Marek dis Aat3696 Marek dis Aat36930 Marek dis Aat36930 Marek dis Aat36930 Marek dis Aat36930 Marek dis Aat36930 Marek dis Aat4163 PCR prime Aat36930 Marek dis Aat4163 PCR prime Aat418489 Bax omega	⊢
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ALIGNMENTS

Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy; diagnosis; primer; mutation; detection; ss. Beta-cardiac myosin heavy chain PCR primer C' (BGHM) BRIGHAM & WOMENS HOSPITAL. (GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA. AAQ91127 standard; cDNA; 30 BP. 92US-00989160. 92US-00989160. 19-FEB-1996 (first entry) (HARD) HARVARD COLLEGE. 11-DEC-1992; 11-DEC-1992; 04-JUL-1995. US5429923-A. Synthetic. AAQ91127; RESULT 1 AAQ91127

Watkins H, Rosenzweig A; Seidman J, Seidman C, WPI; 1995-245715/32. Non-invasive method for diagnosis of hypertrophic cardio-myopathy useful for testing asymptomatic individual(8).

Example 1; Col 10; 22pp; English

AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hyperrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain

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us-10-788-779-7.rng

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with hypertrophic cardiomyopathy (sporadic or familial) and FHC) comprises detecting a mutation associated with hypertrophic cardiomyopathy in an amplified product of a beta cardiac myosin heavy chain DNA. The mutations associated with SHC/FHC are detected in the myosin gene isolated from blood, by detecting mis-matched areas in RNA-DNA hyprid double strands (RNA from the normal gene, DNA from the suspect sample). FHC associated point mutation can be classified and used to determine life expectancy in affected individuals e.g. using a Kaplan-Meier curve for the classified type of FHC causing point mutation. Also included are an RNA probe comprising ribonuclectides arranged in a sequence which is complementary to at least a portion of beta-cardiac myosin heavy-chain DNA and a set of DNA oligonuclectide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two
asymptomatic individuals suspected of having the disease. The method has a broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC; familial hypertrophic cardiomyopathy; SHC; Gaucher's disease; sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia; Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease; phenylketonuria; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting a presence or absence of a mutation associated with hypertrophic cardiomypathy, useful for diagnosing cystic fibrosis or hemophilia, by detecting a mutation in an amplified product of a beta cardiac myosin heavy-chain DNA.
                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to detecting the presence or absence of
                                                                                                                                                 Length 30;
                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human beta cardiac myosin heavy chain PCR primer C'.
                                                                                                          Sequence 30 BP; 8 A; 7 C; 12 G; 3 T; 0 U; 0 Other;
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                                                                                                                                               DB 2;
0.0028;
                                                                      anaemia, Tay-Sachs disease and phenylketonuria
                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                      GGGAATTCGCGGAGCCAGACGCACTGAAG 30
                                                                                                                                                                                                                                                        1 GGGAATTCGCGGAGCCAGACGCCACTGAAG 30
                                                                                                                                               Score 30;
Pred. No.
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                                                                                                                                             100.0%;
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                                                                                                                                                                                 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSENZWEIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-512374/48.
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SEIDMAN J.
WATKINS H.
                                                                                                                                             Query Match
Best Local Similarity
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DNA. The method is useful for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. This method is sepecially useful for diagnosing SHC and FHC, as well as for determining the estimated the life expectancy of a person with familial hypertrophic cardiomyopathy. In particular, the method is useful for determining an individual's genetic information, and diagnosing e.g. Gaucher's disease, haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease, phenylketonuria or cystic fibrosis. The present sequence is a nested PCR primer used to amplify a region of the beta cardiac myosin heavy chain cDNA containing an FHC-associated mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting mutations associated with hypertrophic cardiomyopathy to diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac myosin heavy-chain DNA and detecting the mutation in the amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (familial or sporadic, FHC, SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy, comprising amplifying beta-cardiac myosin heavy-chain DNA forming an amplified product, and detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy in the amplified product, thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also included are a set of DNA oligomiclectide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two oligonuclectides
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, beta cardiac myosin, heavy chain, PCR; primer, ss, FHC, SHC,
familial hypertrophic cardiomyopathy,
sporadic hypertrophic cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human beta cardiac myosin heavy chain mutation detection primer C'
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0
                                                                                                                                                                                                                                                             100.0%; Score 30; DB 9; Length 30; 100.0%; Pred. No. 0.0028; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                             Sequence 30 BP; 8 A; 7 C; 12 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watkins H, Rosenzweig A;
                                                                                                                                                                                                                                                                                                                                            1 GGGAATTCGCGGAGCCAGACGCCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                  GGGAATTCGCGGAGCCAGACGCACTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2004; 2004US-00788779.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-592586/57.
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SEIDMAN J.
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c diagnosis of hypertrophic cardiomycathy (comprising a first container holding an RNA probe completely hybridisable to the beta-cardiac myosin heavy chain DNA, where the RNA probe is capable of detecting a character and the second container and hypertrophic cardiomyopathy associated mutation, a second container by hypertrophic cardiomyopathy associated mutation, a second container conforms for amplifying beta-cardiac myosin heavy-chain DNA and instructions for using the components of the kit to detect the presence or absence of a hypertrophic cardiomyopathy contain DNA). The method is used for detecting the presence or absence of a mutation associated with cardiomyopathy for facilitating the diagnosis of for hypertrophic cardiomyopathy. Presently, the diagnosis of individuals hypertrophic cardiomyopathy relies on the presence of typical cardiomyopathy. Presently, the diagnosis of individuals hypertrophy. The present invention is non-invasive and based, at least in chart, on the discovery that hypertrophic cardiomyopathy is caused by point mutations in the beta cardiac myosin heavy-chain gene. Prior art creveals that there are no extensive studies involving a large number of families which established that this particular disease or disorder was caused by point mutations in the beta cardiac myosin heavy-chain gene.

The present sequence is a PCR primer used to amplify a region of the beta and is and in the beta cardiac myosin heavy-chain gene. which amplify beta-cardiac myosin heavy-chain DNA (the set of objorucialeotide primers being useful for facilitating the disanosis of hypertrophic cardiomyopathy by being capable of detecting a hypertrophic cardiomyopathy by being capable of detecting a hypertrophic cardiomyopathy-associated mutation) and a kit for facilitating the chain having a disease-related point mutation. cardiac myosin heavy

Sequence 30 BP; 8 A; 7 C; 12 G; 3 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 30; DB 13; Length 30; 100.0%; Pred. No. 0.0028; 0; Indels 100.0%; Prec. ... 1 GGGAATTCGCGGAGCCAGACGGCACTGAAG 30 GGGAATTCGCGGAGCCAGACGGCACTGAAG 30 30; Conservative Local Similarity Query Match Best Loca Matches ð 원

ADQ31570 standard; DNA; 50 RESULT 4 ADQ31570

BP.

(first entry) 21-OCT-2004 ADQ31570;

Multiplex detection of human SNPs, primer F7C.

Human; Multiplex nucleic acid detection; ss; PCR; primer; SNP; single nucleotide polymorphism.

Homo sapiens.

US2004146866-A1.

29-JUL-2004.

24-JAN-2003; 2003US-00349780.

24-JAN-2003; 2003US-00349780.

(FUGG/) FU G.

Fu G;

WPI; 2004-552653/53.

Analyzing multiple targets in polynucleotide, by providing multiple primers with target nucleic acids, digesting nucleic acid products with cognate restriction enzymes, amplifying digested products, and detecting amplified products.

Example 1; SEQ ID NO 28; 65pp; English

The invention relates analysing multiple targets in polynuclectide, involves providing a set or sets of multiple primers with target nucleic acids in separate reactions of primer setension or amplification, where the acids in separate reactions of products in that each nucleic acid fragments comprise at least one restriction sites with cognate to products of the separate reactions on the restriction sites with cognate reactions together, where randomly joining nucleic acid fragments from the separated reactions are created, amplifying the joined products, and detecting the amplified products. Also included are an oligonucleotide primer for detecting transparently products. Also included are an oligonucleotide of primer for detecting arget nucleic acid sequence (comprising as included are an oligonucleotide or primer for detecting arget nucleic acid sequence (comprising as a fetterion marker in the process of detecting trattic manipulation on restriction site of reaction product is captured; manipulation on restriction site of reaction product is indicative of the presence of target nucleic acid sequence) and a kit for use in analysis and detection of multiple targets in a polynucleotide (comprising as set or sets of multiple primers, universal primers, creatriction enzymes, and dorsal primers, universal primers, creatriction enzymes, but and for genotyping mutations, preferably single cucle from any source. The method enables analysis of multiple cargets genomic methylation patterns and any specific cargets from any source. The method enables analysis of multiple targets defined acids from any source. The method enables analysis of multiple cargets quantitatively. An experiment was performed, using the method of the invention, where 8 SNPs were detected in human genomic DNA.

Sequence 50 BP; 16 A; 10 C; 14 G; 10 T; 0 U; 0 Other;

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Gaps ö Score 18.8; DB 13; Length 50; Pred. No. 2.2e+02; 0; Mismatches 7; Indels 0 0; Mismatches Match 62.7%; Local Similarity 76.7%; 23; Conservative Query Match Matches

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à g

AAZ58040 standard; DNA; 31 RESULT 5 AAZ58040

AAZ58040;

(revised)
(first entry) 06-AUG-2003 25-APR-2000 PRRS; raccoonpox virus; vaccine; homology vector 934-64.2; PCR primer;

Porcine reproductive and respiratory syndrome virus ORF3 3' primer.

Porcine reproductive and respiratory syndrome virus.

WO200003030-A2.

20-JAN-2000.

99WO-US015565. 09-JUL-1999; 98US-00113750 10-JUL-1998; (SCHE) SCHERING-PLOUGH LTD.

Junker DE; Cochran MD,

WPI; 2000-171150/15.

æ New recombinant raccoonpox virus containing foreign DNA inserted into non-essential region within the HindIII U genomic region, useful as a

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Example 16; Page 145; 1453pp; English.
  vaccines and diagnostics
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                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cowart MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                              AAT48848;
                                                                                                                                                                                                                                                                                                                                 RESULT 7
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                                         The present sequence is that of downstream primer 9/97.10 used in the PCR amplification of open reading frame 3 (DRF3) of swine reproductive and respiratory syndrome virus (PRRS). It is based on the 3' end of the PRRS ORF3, and introduces an EcoRI site at the 3' end of the gene. The PCR product was used in the construction of homology vector 934-64.2, which incorporates a beta-glucuronidase marker gene and the PRRS ORF3 gene incorporates a beta-glucuronidase marker gene and the PRRS ORF3 gene incorporates a beta-glucuronidase marker gene and the PRRS ORF3 gene purpose of inserting foreign DNA into recombinant RPV. Recombinant RPVs of the invention have foreign DNA intestred into non-essential regions of the RPV genome. They can be included in vaccines against animal pathogens, useful for immunising animals (especially avian species or mammals, including humans) against animal pathogens (claimed), e.g. felline pathogens (claimed) or human inmunodeficiency virus, human influenza etc. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; PCR primer; ss.
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Scarselli M;
                                                                                                                                                                                                                                                                          Gaps
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0
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Pred. No. 1e+03;
0; Mismatches 8; Indels
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Scalato E, S
vaccine against pathogens in mammalian and avian species
                                                                                                                                                                                                                             Sequence 31 BP; 6 A; 9 C; 10 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria species ORF cloning PCR primer #192.
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Ratti G,
                                                                                                                                                                                                                                                                                                1 GGGAATTCGCGGAGCCAGACGGCACTGAAG 30
                                                                                                                                                                                                                                                                                                                    2 GGGAATTCCTATCGCCGTACGGCACTGAGG 31
                      Disclosure, Page 55; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galeotti C, Grandi G,
, Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0083758P.
98US-0094869P.
98US-0098994P.
98US-0103762P.
                                                                                                                                                                                                                                                                                                                                                                             AAZS4807 standard; DNA; 35 BP
                                                                                                                                                                                                                                                   57.3%;
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                                                                                                                                                                                                                                     Query Match
Best Local Similarity 73.3%,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-062150/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Neisseria sp.
                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9957280-A2
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Tettelin H,
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02-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                  AAZ54807;
                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polymucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polymucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nested PCR primers (AAT48848-51) were designed to obtain a full-length coding sequence for rat brain adenosine kinase (AK). These primers bind to the 5' and 3' untranslated regions of the gene. Rat brain cDNA was initially amplified with outer primers (AAT48849, AAT48849), AAT48851). The PCR fragment was cloned into pGEM-T and inserts from multiple clones were sequenced. A full-length consensus sequence (AAT48843) coding for rat brain AK (AAM08369) was obtd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat brain, and human placenta short and long forms of adenosine kinase - used. e.g. for assaying for AK (ant)agonists or for prodn. of monoclonal antibodies against AK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.8; DB 3; Length 35;
Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adenosine kinase; agonist; antagonist; monoclonal antibody; polymerase chain reaction; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35 BP; 16 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat brain adenosine kinase outer forward primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GAATTCGCGGAGCCAGACGCCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATTCGCACAGCAAAACGGTTTTGAAG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 52; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used in gene therapy protocols
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75.0%;
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us-10-788-779-7.rng

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AAX34658 standard; DNA; 23
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                                                                                                                                                                                                                                                                                                                                                    Adenosine kinase, cytotoxic nucleoside resistance, anticancer, antiviral, liver tumour; gout, acquired immune deficiency syndrome, tissue injury, adenosine concentration, cytoprotection, rat, PCR primer, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding adenosine kinases and related oligo-nucleotides - expression vectors and transformed cells, used to modulate adenosine levels and to screen for specific modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is a PCR primer for DNA encoding the rat brain adenosine kinase (AK) of the invention. Cells transformed with the DNA are used to produce recombinant AK. The AK is used: (i) to screen for specific agonists and antagonists; (ii) to raise antibodies; and (iii) the rapeutically (reduced levels of AK are associated with resistance to nucleoside analogues with cytotoxic, anticancer and antiviral properties, with liver tumours, gout and acquired immune deficiency syndrome). Fragments of the DNA sequence are used as primers and probes to screen ban libentifying AK-encoding nucleic acid, also as antisense therapeutics (particularly to increase local adenosine concentrations at the site of tissue injury, increasing the level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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              Score 16.2; DB 2; Length 23; Pred. No. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 54.0%; Score 16.2; DB 2; Length 23; Best Local Similarity 85.7%; Pred. No. 2.7e+03; Matches 18; Conservative 0; Mismatches 3; Indels
                                                Indels
                                                                                                                                                                                                                                                                                                                  PCR primer for rat adenosine kinase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23 BP; 6 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cowart MD;
           / Match 54.0%; Score 16.2; I Local Similarity 85.7%; Pred. No. 2.7e les 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcnally T,
                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 43; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GAATTCGCGGAGCCAGACGGC 23
                                                                                                                     1 GAATTCGTGGAGCCAAACCGC 21
                                                                                    3 GAATTCGCGGAGCCAGACGGC
                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00479614.
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                                                                                                                                                                                                           AAX01108 standard; DNA; 23
                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytoprotection)
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                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                               AAX01108;
             Query Match
                                              Matches
                                                                                                                                                                          RESULT 8
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GAATTCGTGGAGCCAAACCGC 21

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RESULT 9

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The invention provides human and murine recombinant Zipper Interacting Protein Kinase (ZIP-kinase) proteins. These proteins are serine/threonine kinases which bind the leucine Zipper domain of transcription factor ATF4. Host cells containing vectors comprising the ZIP-kinase nucleic acids are used for the recombinant expression of the proteins. ZIP-kinase protein and DNA are useful as gene therapeutic agents against cancer, and as anti-cancer agents
                                                                                                                  Zipper Interacting Protein Kinase; ZIP-kinase; serine/threonine kinase;
leucine zipper domain; transcription factor ATF4; gene therapy; cancer;
human; murine; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Recombinant Zipper Interacting Protein Kinase (ZIP-kinase) protein and DNA, useful as anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jene; Txln; plasmin inhibitor; reverse primer R1; ss; content; untranslated region; UTR; Australian brown snake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                Sense primer for leucine zipper domain of mouse ATF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 5 A; 4 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Txln 1 gene-specific reverse primer, R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NISC-) JAPAN SCI & TECHNOLOGY CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                        (first entry)
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-246420/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawai T;
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                                      01-JUL-1999
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increase GC
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                                                                                                                                                                                                             Synthetic
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AAX34658;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Akira S,
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Homo sapiens
                                                                                                                                                           12-MAR-2002
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                                                                                                                                            AAS98482;
                                                                                                                      AAS98482/c
                                                                                                             RESULT 12
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                                                                                                                                                                                                                                                                                                                                                          Human; guanosine monophosphate reductase; GMPR2; tumour; PCR; primer; ss.
                                                                                                                                          The present DNA sequence is the Txln 1 gene specific reverse primer, R1. This is specifically designed, increasing the GC content, to determine the 5'and 3'untranslated regions (UTR) of the Txln cDNA, from the Australian brown snake, Pseudonaja textilis textilis. It includes an
                                                                                                                                                                                                                         Gaps
                                                                                                     anti-tumor
                                                                     Filippovich IV;
                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human-phosphoguanosine reductase, its coding sequence and
                                                                                                                                                                                                        Score 16.2; DB 3; Length 31; Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                            Human guanosine monophosphate reductase GMPR2 PCR primer 2.
                                                                                                    Pseudonaja textilis textilis plasmin inhibitors useful as
                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                        Sequence 31 BP; 8 A; 9 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMU-) INST IMMUNOLOGY NO 2 MILITARY MEDICAL CO.
                                                                      Sorokina NI,
                              BIOLOGICAL STANDARDS & CO.
                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                            Example 2; Page 61; 112pp; English
                                                                    Gaffney PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 19; 30pp; Chinese
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                                                                                                                                                                                                                                       1 GGGAATTCGCGGAGCCAGACG
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       98AU-00003450
                                                                                                                                                                                                         54.0%;
85.7%;
                                                                                                                                                                                                                                                                                             ABZ99545 standard; DNA; 33
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                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                         Conservative
                      UNIV QUEENSLAND
                              (NABI-) NAT INST BIOL
(MASC/) MASCI P P.
(LAVI/) LAVIN M F.
(GAFF/) GAFFNEY P J.
                                                                      Lavin MF,
                                                                                     WPI; 2000-039073/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang J, Zhang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-230990/23
                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
        11-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2001;
                                                                                                                                                                                                                                                                                                                            27-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                          CN1380407-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               application.
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                                                                    Masci PP,
                                                                                                                                                                                                                                                                                                             ABZ99545
                      UYOU )
                                                                                                            agents.
                                                                                                                                                                                                                                                                              RESULT 11
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The invention relates to a novel human guanosine monophosphate reductase GMRR2, and the polymucleotide encoding it. The zymological activity and the relationship of GMPR2 and tumour cell multiplication and cell differentiation are verified. The invention also discloses the strategy of resisting GMPR2 for diagnosing and curing diseases, specially for

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squence, which is a polynucleotide comprising sequences which, when introduced into a cell either predisposed to undergo cell death or in the process of undergoing cell death, prevent, delay, or rescue the cell from death, relative to a corresponding cell into which exogenous nucleic acids have been introduced. The sequences of the invention are useful for diagnosing a protective sequence-mediated condition, disorder or disease in an individual. The treatable disorders are preferably of the central nervous system of humans including ischaemia-related conditions such as stroke, cerebral herniation, septic embolism, cerebral codema, infections such as meningitis, protezoal infections such as malaria, metazoal infections such as meningitis, protezoal infections such as malaria, metazoal concephalopathy, conditions involving the eye such as macular desentation, diabetic retinopathy, trauma such as epidural hematoma, tumours such as primary intracranial tumours, degenerative diseases such as Alzheimer's disease and nutritional, environmental and metabolic conditions. Sequences AAS98409-AAS98544 represent human protective
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ischaemia, open reading frame, ORF, cerebral herniation, septic embolism, cerebral oedema, meningitis, protozoal infection, malaria, CNI-00733; ss, metazoal infection, vascular disease, eye, macular degeneration; trauma, diabetic retinopathy, epidural haematoma; tumour; degenerative disease; nutritional condition, environmental condition, metabolic condition; CNI-00736; CNI-00738; CNI-00742; CNI-00748; cancer; gene therapy.
diagnosing and curing the diseases of tumour. The present sequence represents a PCR primer used to amplify the human GMPR2 of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated polypeptide encoded by a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides and polynucleotides comprising protective sequences useful for preventing, delaying or rescuing a cell from death in disease, condition or disorders such as Alzheimer's disease, stroke, tumors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; protective sequence; cell death; central nervous system; stroke;
                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas MB;
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                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                             Score 16.2; DB 8; Length Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s,
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                                                                                                                    Sequence 33 BP; 8 A; 9 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lo DC,
                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      GGAATTCGCGGAGCCAGACGCCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                          1 deadricerceacecacecreacidade 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 6AR; 228pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                 54.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS98482 standard; cDNA; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Portbury SD, Puranam K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-066433/09.
                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU73320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200181361-A1
                                                                                                                        Ouery Match
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us-10-788-779-7.rng

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Telomerase promoter-controlled recombinant viruses proliferating specifically in tumor cells to highly express antioncogene to kill tumor cells by synergism, applicable in treating tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel recombined virus for specific proliferation and efficient expression of an anticancer gene in tumour cells. By inserting a telomerase promoter in the upstream area of an early virus gene, the recombinant virus is made to proliferate selectively in tumour cells with telomerase activity rather than in normal reals without telomerase activity. This recombinant virus may be used to treat several kinds of tumours. This sequence represents a PCR primer used to illustrate the method described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGFL; RON; MSP; transmembrane; glycoprotein; receptor tyrosine kinase; hepatotropic; liver; hepatocyte growth factor-like protein; human; macrophage stimulating protein; mutagenic; ss.
                                                                                                                                                                                                                                    Proliferation; anticancer gene; tumour cell; telomerase; promoter; early virus gene; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.0%; Score 16.2; DB 6; Length 39; 72.4%; Pred. No. 2.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant HGFL constructing mutagenic oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                      Anticancer gene-associated PCR primer #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 10; 25pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2001; 2001CN-00126113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2001; 2001CN-00126113.
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                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 72.4 tes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-464081/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu M, Cen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (QIAN/) QIAN Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200283074-A2
                                                                                                         30-SEP-2002
                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                            ABQ76067;
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ABV75124/c
ID ABV7511
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telomerase promoter-controlled recombinant viruses proliferating specifically in tumor cells to highly express antioncogene to kill tumor cells by synergism, applicable in treating tumor.
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombination virus; proliferating; tumour cell; anti-oncogene; proliferation; telomerase promoter; therapy; tumour; PCR; primer; 88.
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0
sequence DNA and open reading frames of the polynucleotides
                                                                                                                          ch 54.0%; Score 16.2; DB 6; Length 36; 1 Similarity 72.4%; Pred. No. 2.8e+03; 21; Conservative 0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
                                                             Sequence 36 BP; 4 A; 13 C; 7 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                               2 GGAATTCGCGGAGCCAGACGGCACTGAAG 30
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                                                                                                                                                                                                                                                                                                                            33 GGAACTCTGGGAGGAAGGCGCAAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL55433 standard; DNA; 39 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUL-2001; 2001CN-00126113
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                                                                                                                       Query Match
Best Local Similarity
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Unidentified

23-JAN-2003

Qian O,

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22-MAY-2003

AAL55433;

RESULT 13

AAL55433

Matches

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SXS

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Gaps

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8; Indels

24-OCT-2002

ABQ76067 standard; DNA; 39.BP.

RESULT 14 ABQ76067

Query Match

Local

Matches

8 쉱

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WPI; 2004-122938/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 17
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                                                                                                                                                                                                          The invention relates to a pharmaceutical composition that comprises heterodimeric transmembrane glycoprotein (RON) receptor tyrosine kinase inhibitor with at least one additional component selected from carriers, adjuvants, emulaifiers, solubilizers and stabilizers. The compositions phase action of RON receptor tyrosine kinase in the liver physiology; the composition can be used in the treatment of hepatobiliary damage e.g. acute and chronic liver failure; for preventing hepatobiliary damage due to exposure to hepatotoxic agent (preferably anesthetic, neuropsychotropics, anticonvulsants, analgesics, antimicrobials, neuropsychotropics, anticonvulsants, analgesics, antimicrobials, commones, cardiovascular drugs, immunosuppressives, radation and antineoplastic agents). It is also useful in the treatment and prevention of injury and diseases or liver, biliary tract, bile ducts, gall bladder developing liver damage due to drug overdose, accidental exposure to infected blood samples, aggressive chemocherapy or liver infected blood samples, aggressive chemocherapy or liver infected blood samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                   Pharmaceutical composition useful in prevention and treatment of hepatic disorders comprises heterodimeric transmembrane glycoprotein receptor tyrosine kinase inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                    Sequences ABV75114-125 represent mutagenic oligonucleotides used for creating mutant forms of the human hepatocyte growth factor-like protein (HGFL), also known as macrophage stimulating protein (MSP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant virus; tumour cell; antibody; cytostatic; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.0%; Score 16.2; DB 8; Length 39; 85.7%; Pred. No. 2.9e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-tumour recombinant virus related primer, SEQ ID No 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39 BP; 2 A; 10 C; 18 G; 9 T; 0 U; 0 Other;
                                                          (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SINO-) SINO GENE BIOTECHNOLOGY LTD.
                                                                                                                                                                                      Example 1; Page 36; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CGCGGAGCCAGACGGCACTGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 CGCGGAACCAGACGCCGCTGA 6
                                                                                       Degan SJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI80425 standard; DNA; 39 BP
             15-APR-2002; 2002WO-US011724.
                                    13-APR-2001; 2001US-0283788P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-2003; 2003WO-CN000565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2002; 2002CN-00136028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 85.7
les 18; Conservative
                                                                                      Leonis MA,
                                                                                                             WPI; 2003-067549/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004007703-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                      Waltz SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI80425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qian Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 16
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specific replication in tumour cells, comprising a nucleotide sequence encoding an antibody or its fragment for treating a tumour. The invention functoring application of the virus for killing or inhibiting tumour cells after external infection of such cells with an effective dose of the virus; treating human tumours by external or internal infection of the tumour cells to limit their replication and upgrowth with selectivity after expressing a dose of the antibody or its fragment, with increase of the number of copies of the encoded nucleotide sequence if necessary, for direct killing of such tumour cells, and inhibiting proliferation of tumour, its growth and transfer; use of the virus to inhibit proliferation of tumour cells; use of virus producing remedies for treating a tumour; and drug compositions containing the recombinant virus and plaramecutically-acceptable carriers. The recombinant virus has any platatic activity. The viruses are applicable for killing or inhibiting tumour cells when used in drug compositions to treat tumours. This polynucleotide sequence represents a primer used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Recombinant viruses for expressing anti-tumor antibody or its fragment with high efficiency in tumor cells to kill or inhibit proliferation and transfer of tumors, useful in drug compositions to treat tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human gene coding sequence, its coded polypeptide and preparation
                                                                                                                                                                                                                                              invention relates to a novel recombinant virus that is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primers AAA11358-A11359 were used to PCR amplify the cDNA (AAA11353) encoding the human Myx protein (AAY93137) for subcloning into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 2.9e+03;
0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Myx; Mad; c-myc; tumour; cancer; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGAATTCGCGGAGCCAGACGCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGAATTCGCGGCCGCAGATCTCACAGACG 29
                                                                                                                                                              Disclosure; SEQ ID NO 3; 79pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 7; 13pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР
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Best Local Similarity 72.4%;
Matches 21; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99CN-00113968.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-483210/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the invention.
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               purification of the protein from Chinese Hamster Ovary (CHO) host cells. Myx is a member of the Mad family of proteins which interact with c-myc. The sequence was isolated from a lambda gtll cDNA library. The cDNA and protein can be used for further researching action of Mad family proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, uncleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; drug metabolising enzyme; gene; drug metabolism; chromosome 11; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ATP-binding cassette ABCC8 gene polymorphic site, #4483.
expression vector pcDNA3. This is used for the production and
                                                                                                                                                               Score 15.8; DB 3; Length 29; Pred. No. 4.1e+03;
                                                                                                                                                                                                   7; Indels
                                                                                                                           Sequence 29 BP; 5 A; 9 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  BP
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02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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                                                                                                                                                             Query Match 52.7%;
Best Local Similarity 74.1%;
Matches 20; Conservative
                                                                                           in the treatment of tumours
                                                                                                                                                                                                                                                                                                                                                   699/c
ABZ47699 standard; DNA; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-583571/62.
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variation
                                                                                                                                                                                                                                                                                                                                                                                                     ABZ47699;
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polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to CT drugs. SNRs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur can mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the cyprocation of adverse reactions, thereby increasing safety. The would not only take the guesswork out of selecting the drug with the cyproval processes. For example, individuals could be selected for capable of responding to a particular drug of ascovery and approval processes. For example, individuals could be selected for capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of the invention may therefore lead to a an increase in the range of the invention may therefore lead to a time taken for a drug to be approved, the length of time patients are on medication and the number of different confications a patient needs to take before finding an effective therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; drug metabolising enzyme; gene; drug metabolism; chromosome 11;
polymorphic site; drug evaluation; drug screening; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ATP-binding cassette ABCC8 gene polymorphic site, #1888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 6; Length 41;
Pred. No. 4.3e+03;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41 BP; 5 A; 15 C; 10 G; 11 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AATTCGCGGAGCCAGACGCCACTGAAG 30
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/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.7%;
74.1%;
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27-AUG-2001; 2001JP-00256862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-DEC-2001; 2001WO-JP011592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUL-2002
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Compositions and compositions for identifying individuals who have at least one polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ4317-ABZ50887 using a variety of detection assays, including hybridiation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of arrays and PCR-based methods. The invention also encompasses methods of carrays and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide coplymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to chugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases, conditions, occur DNA sequence variations and human diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur char cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations cut as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolishing enzymes allows the customistion of drug therapies based upon the genetic profile of individual parients.

This would not only take the quesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Wethods of the invention are also useful in the drug discovery and appropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of the invention may therefore lead to a an increase in the ranger of drug trials of the propertions, failed drug trials, the time taken for a drug deserved for the line patients are on medication or drug classe.
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Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                    Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          medications a patient needs to take before finding an effective therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 41 BP; 5 A; 15 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AATTCGCGGAGCCAGACGCCACTGAAG 30
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                                                                                                                                     Claim 23; Page 95; 2785pp; English.
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                                                                                    nucleic acid.
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its compounded is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid for the analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific or probes is useful in in situ hybridisation, in Southern, Northern or dot-comparisons of any gene, in mapping the 5' termini of mRNA molecules by primer extensions of any sequenced. The sequence or specific or unclaic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                            New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.0%; Score 15.6; DB 9; Length 25; 81.8%; Pred. No. 5e+03;
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0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 97474; 9pp; English.
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                16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2002; 2002US-00098263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 81.8
nes 18; Conservative
                                                         (AFFY-) AFFYMETRIX INC.
                                                                                                                                       WPI; 2003-567953/53
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ACK28325/c
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98US-0098994P
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                                             09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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   02-SEP-1998
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                 02-SEP-1998
                                09-0CT-1998
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                                                                                                           (CHIR )
                                                                                                                           (GENO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its correct match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises or hybridising at least one or more nucleic acid states and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, corr family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises is useful in in situ hybridisation, in Southern, Northern or dot-probes is useful in in situ hybridisation, in Southern, Northern or dot-probes is useful and pervised in mapping the 5' terminiof mannaly sequence or specific for additional subclones containing segments of DNA that have been containing segments of DNA that have been mucleic acid probes incorporated in the microarray. Note: The sequence and precipitally sequenced. The sequence presented is one of the mucleic acid probes incorporated in the microarray. Note: The sequence or sequence the uncleic acid probes incorporated in the microarray. Note: The sequence or sequence and probes incorporated in the microarray. Note: The sequence the sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or se
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                                                                                                         New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria species ORF cloning PCR primer #360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Pred. ....
                                                                                                                                          sequence or specific mutations of any gene.
                                                                                                                                                                    Claim 1; SEQ ID NO 128306; 9pp; English.
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98US-0094869P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conservative
              (AFFY-) AFFYMETRIX INC
                                                                          WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria sp.
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                                             Mittmann MP;
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31-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse, phage display, anti-inflammatory, antibody therapy, inflammatory bowel disease; rheumatoid arthritis; septic shock; multiple sclerosis, chronic inflammation; allograft rejection; panning; tumour necrosis factor alpha; TNF; CDR3; complementarity determining region; hybridoma; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                        Ξ
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                                                                                                                                                                                                                                                                                                        Mora M;
Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics.
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                                                                                                                                                                                                                                                                                                     Masignani V,
Scalato E, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 41 BP; 14 A; 10 C; 8 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                     Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGAATTCGCGGAGCCAGACGCCACTGAAG 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 16; Page 150; 1453pp; English.
                                                                                                                                                                                                                                                                                                 Fraser C, Galeotti C, Grandi G,
Petersen J, Pizza M, Rappuoli R,
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used in gene therapy protocols
98US-0099062P.
98US-0103749P.
98US-0103794P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 70.0 tes 21; Conservative
                                                                                                                                                                                                                                      INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-062150/05.
                                                                                                                                                                                                      CHIRON CORP.
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Disclosure; SEQ ID NO 15; 58pp; English.
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                                                                                                                                 Query Match
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Matches
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Matches
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ID AAZ4
XX
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                                                                                                                                                                                      ò
                                                                                                                                          which was used for large scale production of VH single-domain molecules.
A phage library was generated from a gene isolated from a mouse hybridoma. Phage clones contained a random sequence coding for 9 amino acids in the third hypervariable loop (CDR3). CDR3 typically makes most antigen contacts in antibody combining sites. Phage clones capable of binding a specific antigen, e.g. Tumour necrosis factor alpha (ThRalpha), were selected by library panning. The present sequence was used to reamplify plasmid DNA from positive-binding clones in order to insert cloning sites for subcloning into the T7 promoter-based pFT-21a expression vector. Protein was expressed at high levels in BL21 cells upon IPTG induction and accumulated in intracellular inclusion bodies which could then be isolated and purified. Single-domain VH proteins can be used to treat or diagnose disorders associated with the antigens that they bind to. For example, disorders in which TNF plays a role include inflammatory bowel disease, rheumatoid arthritis, septic shock, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide sequence encoding multiple drug resistance proteins from Drosophila melanogaster or Anopheles gambiae, useful in developing effective insecticides.
                                                              Small functional units of antibody heavy chain variable regions useful for diagnosis and treatment of disease.
                                                                                                                                 present sequence is an oligonucleotide designated pET-21aVH3'XhoI
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple drug resistance protein; MRP; Drosophila melanogaster;
Anopheles gambiae; insecticide; ss; primer.
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                                                                                                                                                                                                                                                                                                                                                                                                  51.3%; Score 15.4; DB 3; Length 34; 76.0%; Pred. No. 6.3e+03; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                sclerosis, chronic inflammation and allograft rejection
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 34 BP; 6 A; 10 C; 11 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGAATTCGCGGAGCCAGACGGCAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGAATTCCTCGAGCTATGCGGCAC 25
                                                                                                       Example 3; Page 21; 48pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN97120 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer of the invention #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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(CNRS ) CENT NAT RECH SCI.
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Matches 19; Conservative
                                     WPI; 2000-387610/33
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           Plaksin D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                          Gaps
The present invention relates to a purified polynucleotide or its fragment and comprises a sequence encoding multiple drug resistance protectins (MRPs) from Drosophila melanogaster or Anopheles gambiae. I polynucleotide is useful in developing effective insecticides. The present sequence represents a primer of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT-PCR primer for the production of anti-idiotype antibodies.
                                                                                                                                                                                                                                           Length 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel anti-idiotype antibody against an human anticancer mo
antibody - and DNA sequences encoding the antibody, useful
pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                                                          3; Indels
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                                                                                                                                                                                    Sequence 24 BP; 7 A; 4 C; 8 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                           50.7%; Score 15.2; DB 12; 85.0%; Pred. No. 7.4e+03;
                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 11; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                 1 GGGAATTCGCGGAGCCAGAC 20
                                                                                                                                                                                                                                                                                                                                                                                                       GGGAATTCGCGTGGACAGAC 20
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nes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ44213 standard; DNA; 33
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                                                                                                                                                                                                                                                                    Local Similarity 85.0
nes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fields of research
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The present invention describes the variable heavy and light chain regions (I) of murine monoclonal antibody (mAB) 1F7. AAY91014 to AAY91016 chain. Pepresent specifically claimed amino acid sequences of the variable light chain, and AAY91017 to AAY91019 represent specifically claimed amino acid sequence of the variable heavy chain. The antibodies are used for treatment of HIV (human immunodeficiency virus) infection and AIDS (acquired immunodeficiency syndroms). They are also used for detecting HIV in serum and for stimulating HIV antigen related and committed B cells to produce broadly reactive and neutralising antibodies by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variable heavy and light chain regions of murine monoclonal antibody 1F7,
                                                                                                                                                                                                                                               The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. Sequences AAZ58665-688 represent PCR primers used in the course of the invention for constructing the anti-CD4 antibody 4H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection; AIDS; anti-HIV; human immunodeficiency virus; detection; acquired immunodeficiency syndrome; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine monoclonal antibody 1F7 light chain PCR primer SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.2; DB 3; Length 33; Pred. No. 7.7e+03;
                                                                                                                                                                 An antibody and the nucleic acid coding the antibody.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating HIV infection and AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                          Example 5; Page 9; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 5; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                 50.7%;
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  98JP-00163034,
                                        98JP-00163034.
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                                                                                 (ASAH ) ASAHI KASEI KOGYO KK
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Best Local Similarity
  26-MAY-1998;
                                           26-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel device (I) for separating cluster differentiation (CD) positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leuwenic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. AZ44207-24230 represent PCR primers used to illustrate the method of the
                                                                                                                    Cluster differentiation, cell separation, antibody, CD4, CD34; leukemia, hematopoietic, undifferentiated; lymphocyte; bone marrow transplantation, HIV infection; autoimmune disease; murine; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells.
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                                                                               Murine CD4/CD34 recognizing antibody PCR primer 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ASAH ) ASAHI MEDICAL CO LTD
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                                      (first entry)
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Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                                                                                                               WO9961629-A1
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                                      31-MAR-2000
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AAZ44213;
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RESULT 27 AA258673

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heavy chain; light chain; HIV infection; PCR; primer; ss.
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                                      WO200255668-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09963077-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUN-1998;
                                                                                                                                                                                                 against HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1999,
                                                        18-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ96102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lane MJ,
                   Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 31
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                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to anti-human immunoglobulin B (IgE) monoclonal antibody selected the monoclonal antibodies 4D3, 1A7, 3E8, 4D10, and 11D10, which combine specifically to human IgE. The monoclonal antibody can be used for the detection of human IgE. The present sequence was used in an example from the present invention
clonotypic stimulation. The present sequence represents a PCR primer used in the amplification of the murine monoclonal antibody 1F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR;
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                               88.
                                                                                                                                                                                                                            Murine; immunoglobulin E; monoclonal antibody; IgE; PCR primer;
                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                            Score 15.2; DB 3; Length 33; Pred. No. 7.7e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.7%; Score 15.2; DB 5; Length 33; 85.0%; Pred. No. 7.7e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
                           Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                          Murine immunoglobulin, IgkappaVL-B, PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine Mab 1F7 light chain PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                               Anti-human IgE monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 6; 13pp; Japanese.
                                                                                   1 GGGAATTCGCGGAGCCAGAC 20
                                                                                                1 GGGAATTCATGGAGACAGAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGAATTCGCGGAGCCAGAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH41120 standard; DNA; 33 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                              50.7%;
                                                                                                                                                                                                                                                                                                     99JP-00249805
                                                                                                                                                                                                                                                                                                                        99JP-00249805
                                                                                                                                                                                                                                                                                                                                         (ASAK ) ASAHI BREWERIES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL48649 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 85.0
les 17; Conservative
                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-311336/33.
                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                JP2001074737-A.
                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                     03-SEP-1999;
                                                                                                                                                                                                                                                                                                                       03-SEP-1999;
                                                                                                                                                                                        17-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2002
                                                                                                                                                                                                                                                                                   23-MAR-2001
                                                                                                                                                                      AAH41120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL48649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 30
AAL48649
                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                 RESULT 29
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New polynucleotide encoding a complementarity- or framework-determining region of an anti-idiotypic antibody that binds to human or primate antihuman immunodeficiency virus (HIV) antibodies, for use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to coding sequences of the murine 1F7 antidictypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or primate antihuman immunodeficiency virus (HIV) antibodies and can be used in the treatment of HIV infection. The present sequence is a PCR primer used to isolate a 1F7 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ligand binding; restriction enzyme; nucleic acid determination; pharmaceutical; BamHI; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.7%; Score 15.2; DB 6; Length 33; 85.0%; Pred. No. 7.7e+03; arive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide sequence including binding site for BamHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Faldasz BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGAATTCGCGGAGCCAGAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGAATTCATGGAGACAGAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
11-JAN-2002; 2002WO-US000927.
                                                             11-JAN-2001; 2001US-00759112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0087905P
99US-00324672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TMTE-) IM TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ96102 standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                             (IMMP-) IMMPHERON INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Benight AS,
                                                                                                                                                                                              Muller S, Kohler H;
                                                                                                                                                                                                                                                               WPI; 2002-590668/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
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The invention provides a method for determining the sequence of polymucleotide flanking regions that modulate ligand binding characteristics of an adjacent binding site. The method comprises: (i) providing a number of different duplex polymucleotides, each having the same polymucleotide ligand binding site and a randomly synthesised sequence flanking the binding site; (ii) exposing the duplex to a ligand selective for the binding site; (ii) isolating duplexes which bind or do not bind the ligand, and (iv) determining the nucleotide composition of the flanking duplex sequence by sequencing the duplex sequence adjacent to the binding site. The invention is used to modulate the ligand-binding and more efficient than prior art techniques that moderate ligand binding using small molecule pharmaceuticals. Sequences AAS9576-296170 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TREM-like transcript-1; septic shock; cancer; infectious disease; stroke; heart disease; myocardial infarction; arteriosclerosis; clotting disorder; bleeding disorder; platelet insufficiency; TLT-1 associated disorder; gene therapy; antibacterial; immunosuppressive; cytostatic; antimicrobial; cerebroprotective; vasotropic; cardiant; antiarteriosclerotic; haemostatic; murine; RT-PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New TREM-like transcript-1 nucleic acid molecules, useful for preventing and treating a disorder, e.g. septic shock, cancer, infectious disease, stroke, heart disease, arteriosclerosis, or bleeding disorders.
                                                                                                                                                                                                                                                                                                                                              polynucleotide sequences including the binding site for the restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
 Modulating polynucleotide ligand binding site affinity using
                                                                                                                                                                                                                                                                                                                                                                                                                                           50.7%; Score 15.2; DB 3; Length 40; 71.4%; Pred. No. 7.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor expressed on myeloid cell; TLT-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine TREM-like DNA specific RT-PCR primer, TREM 2 #2.
                                                                                                                                                                                                                                                                                                                                                                  enzyme BamHI and used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40 BP; 8 A; 3 C; 21 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8,
                   determination of the flanking duplex sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GAATTCGCGGAGCCAGACGCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 GAAGGCGAGGAGGTAGACGGTGCTGAGG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quigley L;
                                                       Example 1; Page 44; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reverse transcription; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-2004; 2004US-00802441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2003; 2003US-0455370P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington AV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADS18341 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MCVI/) MCVICAR D. (WASH/) WASHINGTON A V. (QUIG/) QUIGLEY L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-661507/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TREM; triggering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004180409-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcvicar D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS18341;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                The present invention relates to a triggering receptor expressed on maloid cell (TREM)-like transcript-1 (TTT-1) polypeptides and the encoding polymucleorides, where the TTT-1 polypeptide can modulate platelet function. The invention is useful for preventing, diagnosing and tracating a disorder, e.g. septic shock, cancer, infectious disease, stroke, heart disease, myocardial infarction, arteriosclerosis, clotting disorders, platelet insufficiency or a TLT-1 present sequence is the murine TREM DNA specific reverse transcription (RT)-PCR primer. This sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         altered alphavins (AV nonstructural protein 2 (nsp2) gene which when incorporated into an AV replicon particle (ARP) has a reduced level of vector-specific RNA synthesis, increases the time required to reach 50% inhibition of host cell-directed macromolecular synthesis when expressed in mammalian cells and persistently replicates when introduced into mammalian cells, as compared to wild-type ARP. The sequence can be used to deliver a selected heterologous sequence to a vertebrate or insect cell, where it can produce AV replicon particles and make a desired protein, for example erythropoletin, basic fibroblast growth factor, factor VIII, vascular endothelial growth factor and tissue plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid having altered alphavirus nonstructural protein 2 gene which when operably incorporated into alphavirus replicon particle has noncytopathic phenotype and persistently replicates in mammalian cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alphavirus-based vector; nonstructural protein 2; nsP2; replicon; eukaryotic layered initiation system; noncytopathic; gene therapy; persistent replication; recombinant protein expression; gene delivery;
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to an isolated nucleic acid having an
                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                            S0.0%; Score 15; DB 13; Length 28; llarity 78.3%; Pred. No. 9.2e+03; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sindbis virus nonstructural protein gene PCR primer nsP3F.
                                                                                                                                                                                                                                                                       Sequence 28 BP; 6 A; 7 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Belli BA;
Example; SEQ ID NO 10; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             8 CGCGGAGCCAGACGGCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGCGGATCCTGACTGGACTTAAG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 24; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perri S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2001; 2001WO-US013255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-APR-2000; 2000US-0199579P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA03393 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polo JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-049274/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200181553-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sindbis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dubensky TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001
                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA03393;
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                  Aatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA03393
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BP,

standard; DNA; 31

(first entry)

(revised)

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Herpes virus of turkey, open reading frame; ORF; homology; vector; avian herpes virus; recombinant viral vaccine; intergenic region; IBDV; extromegalovirus immediate early promoter; UL55 gene; repeat region; ILTV; antigen; infectious haral disease virus; Marek's disease virus; MDV; infectious larymgotracheitis virus; avian anaemia virus; vaccination; infectious bronchitis virus; IBV; poultry; Gumboro disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant avian vaccine - comprises herpes virus as vector and
1g sequence encoding antigenic polypeptide inserted between ULSS
                                                                                                                           Marek's disease virus 1.8 kb RNA gene upsteam sequence primer MB048.
                                                                                                                                                                                                                                                                        Newcastle disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-364150/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and repeat region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INMR ) RHONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Audonnet J,
Riviere MAE;
                                                                                           21-APR-1997
                                                                                                                                                                                                                                                                                                                                             EP719864-A2.
                                                                                                                                                                                                                                                                                                                                                                               03-JUL-1996.
                                                                        25-MAR-2003
                                                                                                                                                                                                                                                                                                          Synthetic.
   AAT39333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Live
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primers MB047 and MB048 (see AAT35895 and AAT35896) were used in a PCR to amplify a 163 bp fragment from DNA extracted from lymphocytes harvested from chickens infected by Marek disease virus (MDV) strain RB1B. The PCR product was subsequently used in the construction of a plasmid in which a VP2/MCMV-IE/RNA 1.8 kb/MDV 9B double cassette was inserted into the ULA1 site of herpesvirus of turkeys. The final construct was useful as a viral
activator (tPA). The recombinant AV vectors are useful for directing the expression of one or more heterologous gene products in the absence of vector induced cytopathology. The present sequence is a PCR primer used in the construction of a vector containing the Sindbis virus nsP2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Live avian vaccine based on Marek disease virus - has sequence encoding antigenic polypeptide inserted into the UL13 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVT; turkey herpes virus; THV; UL41; Marek disease virus; MDV RNA1.8; promoter; live avian vaccine; Gumboro disease; PCR primer; polymerase chain reaction; infectious bursal disease virus; IBDV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 15; DB 2; Length 31; 78.3%; Pred. No. 9.3e+03; ive 0; Mismatches 5; Indels
                                                                                                                         50.0%; Score 15; DB 6; Length 29; 78.3%; Pred. No. 9.2e+03; ive 0; Mismatches 5; Indels
                                                                                         Sequence 29 BP; 7 A; 10 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine to protect poultry against MDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Darteil R,
                                                                                                                                                                                                                                                                                                                                                                                                                               Marek disease virus PCR primer MB048.
                                                                                                                                                                                               3 GAATTCGCGGAGCCAGACGGCAC 25
                                                                                                                                                                                                                           6 GAATTCGCGCCGTCATACCGCAC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 11; Page 22; 75pp; French.
                                                                                                                                                                                                                                                                                                                         AAT35896 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-FR001763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94FR-00016016
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                           Local Similarity 78.3
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bublot MJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INMR ) RHONE MERIEUX SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-334009/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Audonnet J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riviere MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                            Query Match
                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                       RESULT 34
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gene

Leplace ELF;

Darteil RJ, Duinat CV,

Bublot MJM,

MERIEUX

95EP-00402970. 94FR-00016017

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Transmitted and a view by the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the sectio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  control of the MDV promoter, all inserted into the herpes virus of turkeys intergenic region 1 in plasmid pEL079 (see AAT39310-4) to produc plasmid pEL095. The recombinant vectors can be used to express proteins for vaccinating poultry against Gumboro disease (caused by IBDV), Newcastle disease, Marek's disease, infectious bronchitis, infectious laryngotracheitis and avian anaemia. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                               invention relates to the generation of live recombinant avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%; Score 15; DB 2; I
78.3%; Pred. No. 9.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
Example 13; Col 15; 50pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 18; Conserv
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3 GAATTCGCGGAGCCAGACGGCAC 25

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RESULT 35 AAT39333

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28-DEC-1995; 2003EP-00025194.
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95EP-00402970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                    Audonnet J, Bublot M,
                                                                                                                                                                                                                                                                WPI; 2004-271923/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                            THV; PCR; primer.
                                                                                                                                                                                                          (MERI-) MERIAL.
                                                                                                                                                                 30-DEC-1994;
28-DEC-1995;
                                                                                  EP1403375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                             31-MAR-2004
                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR13841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primers MB047 and MB048 (see AAT35929 and AAT35930) were used in a PCR to amplify a 163 bp fragment from DNA extracted from lymphocytes harvested from chickens infected by Marek disease virus (MDV) strain RB1B. The PCR product was subsequently used in the construction of a plasmid in which a VP2/MCMV-IE/RNA 1.8 kb/MDV gB double cassette was inserted into the UL43 site of herpesvirus of turkeys. The final construct was useful as a viral vaccine to protect poultry against MDV. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                      HVT; turkey herpes virus; THV; UL43; Marek disease virus; MDV RNA1.8; promoter; live avian vaccine; Gumboro disease; PCR primer; polymerase chain reaction; infectious bursal disease virus; IBDV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Live recombinant avian vaccine based on herpes virus - with sequence encoding antigenic polypeptide inserted into the UL43 gene, esp. for protection against Gumboro disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           avian vaccine; avian pathogen; BamHI fragment; vaccine; Gumboro;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Laplace ELF;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Duinat CV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer MBO48 used to produce plasmid pBS002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Darteil R,
                                                                                                                                                                              Marek disease virus PCR primer MB048.
              GAATTCGCGAAGAGAAGGAAC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GAATTCGCGGAGCCAGACGCCAC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 11; Page 22; 67pp; French.
                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
78.3%;
                                                                                                                                                                                                                                                                                                                                                94FR-00016015.
                                                                                                                                                                                                                                                                                                                                                                            94FR-00016015.
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                                                                                AAT35930 standard; DNA; 31
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bublot MJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      (INMR ) RHONE MERIEUX SA
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-335824/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                30-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Audonnet JC,
Riviere MEA;
                                                                                                                                     25-MAR-2003
03-MAR-1997
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                                                                                                                                                                                                                                                                                                                     05-JUL-1996.
                                                                                                                                                                                                                                                                Synthetic
                                                                                                           AAT35930;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 37
                                                                      AAT35930
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The specification describes the use of a recombinant turkey herpes virus (THV) for production of live, recombinant avian vaccines, intended for vaccination in ovo, of day-old chicks, or of adults to protect against an avian pathogen. The recombinant THV includes at least one nucleic acid that encodes and expresses an antigen of the avian pathogen, inserted into intergene region 1, 2 or 3 of the BamHI fragment of the THV genome. The nucleic acid especially encodes the VP2, VP3 or a combination of VP2, and 4, from infectious bursal disease (Gumboro disease) virus; 9B, 9C, or 9D or 9H plus 9L of Marek disease or infectious laryngotracheitis viruses; or NT of NT of Necastle disease virus; S or M of infectious burnelitis viruses; or NT of NT of NT or VP2 (24 kD) of avian anaemia virus. The nucleic acid is inserted under control of the cytomegalovirus immediate-early compression). The recombinant viruses of the invention are used to expression). The recombinant viruses of the invention are used to vaccinate chickens against one or more of the viruses that cause Gumboro (Infectious laryngotracheitis or avian anaemia. PCR primers ADM41162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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    infectious bursal; Marek disease; Newcastle disease;
infectious bronchitis; infectious laryngotracheitis; avian anaemia; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen-coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Riviere M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of a recombinant turkey herpes virus (HVT) with an antigen-codir sequence inserted into an intergene region, to prepare vaccines for preventing e.g. Marek or Gumboro disease in poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human hereditary Haemochromatosis (HFE) gene Flanking probe HC63-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ы
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laplace
Newcastle disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duinat C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Darteil R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GAATICGCGGAGCCAGACGCCAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GAATTCGCGAAGAGAAGGAAC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 13; Page 11; 63pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВЪ.
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The invention relates to a probe set for detecting genetic polymorphisms in target nucleic acids suspected of containing the polymorphisms, comprising a first flanking probe comprising a sequence complementary to a first portion of the nucleic acid sequence, a capture probe comprising a sequence complementary to a second portion of the nucleic acid sequence (the second portion of the nucleic acid sequence complementary to a third portion of the probe comprising the location of the polymorphism, and being adjacent to the first portion) and a second flanking probe comprising sequence complementary to a third portion of target nucleic acid sequence. The probes further comprise stem regions at the 3' and 5' ends which can form non-covalent bonds with the stem regions of a target nucleic acid suspected of concaining the polymorphism.

C adjacent probes and contain a photoactivatable cross-linking agent. Also included is detecting a genetic polymorphism in a nucleic acid sequence of a target nucleic acid suspected of concaining the polymorphism.

C adjacent probe and several probes, where several probes comprises the having the target and several probes, where several probes comprises the polymorphism in a hybridising medium, a nucleic acid sequence comparing the degree of hybridisation of a capture probe to the target sequence lacking the probe set accomprising and a reporter probe which is complementary to the hybridisation of a capture probe to the target sequence of the second portion lacking the comparing the polymorphism and a reporter probe which is complementary to the normal nucleic acid sequence of the second portion lacking the probe is useful for detecting a genetic polymorphism in a nucleic acid sequence of a target nucleic acid suspected of containing the probe is useful for detecting a genetic polymorphism in a nucleic acid sequence of a target nucleic acid suspected of containing the polymorphism as a single nucleotide polymorphism; a polymorphism in a nucleic acid sequence constraints imposed upon ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe set useful for detecting genetic polymorphism in target nucleic acid suspected of containing polymorphism, comprises first flanking probe, capture probe and second flanking probe.
                                                                                                     bound_moiety= "Nucleotides 24-22 of SEQ ID 15"
                                                                                                                                                                                                                                                                                                                                  /*tag= d
/bound_moiety= "Nucleotides 3-1 of SEQ ID 15"
                                                                                                                                                                                                          note = "Non-nucleosidic cross-linking moiety"
                                                                                                                                                                                                                                                                                         'note= "Non-nucleosidic cross-linking moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Non-nucleosidic cross-linking moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; SEQ ID NO 17; 31pp; English
                                        Location/Qualifiers
                                                                                                                                                                                                                                                  /*tag= c
/mod_base= OTHER
                                                                                                                                                                                    base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                       base= OTHER
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                                                                                                                                                                   *tag= b
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                                                                                   *tag=
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                                                                                                                          note
                                                                                                                                                                                        mod/
                                                                                                                                                                                                                                                                                                                                                                                                                                         mod,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (VATT/) VAN ATTA R B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS2004152118-A1
                                                                                                                                                                                                                                                                                                                                                                                              modified_base
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  Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53 responsive element, p53-REU; bax gene; apoptosis; cell death; stroke; cancer; tumour suppressor; polymerase chain reaction; PCR; primer; ss.
cross-linking site near the single nucleotide polymorphism (SNP) site
           in the target sequence, provides more sites for introducing detectable labels, and permits cross-linking in the stem to include reactions between pairs of unactural nucleotide analogues, thus expanding the available option from which to select an appropriate choice of reactants. The probe set enables detection of a genetic polymorphism with increased sensitivity and improved data reliability and allows for high-stringency washes of the hybridised probe-target complexes, which significantly lower background contamination levels and result in improvements in the signal-to-noise ratio. The present sequence is a flanking probe for a probe set of the invention.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p53 responsive element(s) for down-regulation of bcl-2 gene and upregulation of bax gene - and identification of agent(s) useful to modulate cell death, e.g. cancer or stroke.
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                                                                                                                                                                                                                                                         50.0%; Score 15; DB 13; Length 45;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                    Sequence 45 BP; 11 A; 12 C; 11 G; 8 T; 0 U; 3 Other;
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                                                                                                                                                                                                                                                             Score 15,
Pred. No. 9.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harigai M, Hanada M;
                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                    2 GGAATTCGCGGAGCCAGACGGCA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human bax gene forward primer.
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73.1%;
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                                                                                                                                                                                                                                                                            78.3%;
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                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-263824/34.
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Matches 18; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT62767;
                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 39
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88666666666666888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of novel proteins involved in apoptosis - by interaction with proteins involved in apoptosis.
                                                                                                                                                                                                                                                               Mcl-1; Bax; apoptosis; cell death; regulation; Bcl-2; novel; detection;
   Gaps
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49.3%; Score 14.8; DB 2; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 7; Indels
 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27 BP; 4 A; 5 C; 13 G; 5 T; 0 U; 0 Other;
 0; Mismatches
                                              1 GGAATTCGCGGTGATGGACGGGTCCG 26
                              2 GGAATTCGCGGAGCCAGACGGCACTG 27
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                                                                                                                                                                                                                                Human Bax gene forward PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                     AAT03167 standard; DNA; 27 BP.
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 19; Conservative
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Matches
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Gaps

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Search completed: November 18, 2005, 11:52:31 Job time: 209.578 secs

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AZ597065 1M0410N10
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AU108044 AU108044
AA887629 nq96b05.8
AZ60433 1M0419N11
H84563 Yv85c09.81
AZ942204 2M0212M04
AA63428 m131c03.8
C01535 HWGS000853
AU102737 AU102737
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                                                                         November 18, 2005, 11:22:09; Search time 1434.98 Seconds (without alignments) 795.779 Million cell updates/sec
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AA074398 2
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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30
1 GGGAATTCGCGGAGCCAGACGGCACTGAAG 30
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Listing first 45 summaries
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT SAT 88499 LOCUS DEFINIT ACCESSION VERSION KEYNORD SOURCE ORGAN AUTHOI	JOURNI COMMENT COMMENT FEATURES

/lab host="B. Coli strain XLIO-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

/db xref="taxon:10090" /clone="UUGC2M0035E09"

/sex="Male"

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 40)
E 1 (bases 1 to 40)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Contact: Robert B. Weiss
University of Utah Genome Center
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Tel: 801 S85 5606
Fax: 801 585 7177
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40 bp DNA linear GSS 13-DEC-2000
1M0410N10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0410N10 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Insert Length: 10000 Std Error: 0.00
Plate: 0410 row: N column: 10
Seg primer: CACACAGGAAACAGCTATGACC
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mol type="genomic DNA"
strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0410N10"
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GSS.
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Best Local Similarity
Matches 21; Conserv
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AUTHORS
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TITLE

COMMENT

FEATURES

RESULT 2 AZ597065

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SOURCE

ORIGIN

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWMD42 (gil4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Bustiut of Medical Science, University of Tokyo
Busil: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugamo,S. Construction and characterization of a full
Inength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
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AU104279 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP20593, mRNA sequence.
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1 (Dases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ofet,T., 18ogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
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/db_type="mRNA"
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/cl_ore="HRB20893"
/clone_lib="Sugano Homo sapiens cDNA library"
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EMBO Rep. 2 (5), 388-393 (2001)
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EST.
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Science, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
                  AULUBU41 50 bp mRNA linear EST 28-JAN-2004
AULUB041 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
ZRV61366, mRNA sequence.
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                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 50)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 50)

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Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
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Pred. No. 1.3e+05;
0; Mismatches 2; Indels
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Department of Virology
Institute of Medical Science, University of Tokyo
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon.9606"
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AU108042.1 GI:13557564
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Homo sapiens
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yawukigims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Bail: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full
Inength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 50)
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/db_xref="ttanon:9606"
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/clone_lib="Sugano Homo sapiens cDNA library"
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/db_xref="taxon:9606"
/clone="xyv62110"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                    49.3%; Score 14.8; DB 1; Length 50; 88.9%; Pred. No. 1.3e+05; ive 0; Mismatches 2; Indels
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Pred. No. 1.3e+05;
0; Mismatches 2;
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Best Local Similarity 88.27
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Matches 16; Conserv
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RESULT 7

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AZ601433 48 bp DNA linear GSS 13-DEC-2000 1M0419N11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0419N11 R, genomic survey sequence.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                        Trace considered overall poor quality Insert Length: 797 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0419 row: N column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 48.
www-bio.llnl.gov/bbrp/image/image.html
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Fax: 801 585 7177
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, Tokyo
Institute, Tokyo
Institute, Young Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Institute, Ins
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
Clone distribution: N.T.-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AABB7629 40 bp mRNA linear EST 07-APR-1998 nq96bD5.s1 NCI CCAP CO10 Homo sapiens CDNA Clone IMAGE:1160145 3' similar to TR:Q62381 Q62381 TOLLOID-LIKE;, mRNA sequence. AA887629
                                          AU108044 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Otca,T., Isogai,T., Tanaka,T., Worishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="ZRV6C516"
/clone_lib="Sugano Homo sapiens cDNA library"
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                                                                                                                            ZRV6C516, mRNA sequence
                                                                                                                                                              AU108044
AU108044.1 GI:13557566
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Matches 16; Conservative
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GSS 27-APR-2001

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/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
Clone Lib="Mouse lokb plasmid UNGC2M library"
/note="Vector: PWD42Inv; PwD42Inv; PwD42Inv; PwD42Inv; PwD42Inv; PwD42Inv; PwD42Inv; PwD42Inv; PwD42Invilied genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A2949204 200 26 bp DNA linear GSS 27-APR-200 2M0212M04R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0212M04 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
46.0%; Score 13.8; DB 7; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                 /tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: M column: 04
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Seq primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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Location/Qualifiers
                                                 /clone="IMAGE:249520"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 GCGGAGCCAGACGCCAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCAGAGGCAGACGCCAC 17
                                                                          /sex="Male"
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Fax: 801 585 7177
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AZ949204/c
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                                  /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD4Zny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnarea/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by sepated by
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Contact: Wilson RK
Washington University School of Medicine
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL
This clone is available royalty-free through LLNL
Trace considered overall poor quality
Seq primer: Promega -21m13
High quality sequence stop: 1.
High quality sequence stop: 1.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 bp mRNA linear EST 13-NOV. yv85c09.s1 Soares melanocyte 2NbHW Homo sapiens cDNA clone IMAGE:249520 3' similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 (HUMAN);, mRNA sequence.
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clone="UUGC1M0419N11"
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The WashU-Merck EST Project
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Homo sapiens
Query Match
Best Local Similarity 80.04
Matches 16; Conservative
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                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWaP2 (gqi 4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Andrew Berchuck, M.D., Elise Kohn, M.D.,
Tissue Procurement: Andrew Berchuck, M.D., Elise Kohn, M.D.,
Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Linx at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. Ef from Amersham.
Location/Qualifiers
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/lab host="DHIDS"
/clone_lib="NCI_CGAP_Ov5"
/note="Organ: ovary; Vector: pAMP10; mRNA made from normal
ovarian epithelium, cDNA made by oligo-dT priming.
non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Reference: Krizman et al.
(1996) Cancer Research 56:5380-5383."
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nu31c03.s1 NCI_CGAP_Ov5 Homo sapiens cDNA clone IMAGE:1212292, mRNA
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  aboratory Mouse DNA Resource
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/db_xref="taxon:9606"
/clone="IMAGE:1212292"
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Unpublished (1997)
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FEATURES

ORIGIN

COMMENT

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CR230947 100 SO bp DNA linear GSS 06-JUL-2004 Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN54c05, genomic survey sequence.
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 48)

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1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
1-1.3, Yamada-oka, Suita, Osaka Pref. 565, Japan
1-21: 06-877-5111(ex.315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
We are not submitting the same cDNA sequence redundantly to DDBJ
Since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka- u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
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Best Local Similarity 67.9%; Pred. No. 4.1e+05;
Matches 19; Conservative 0; Mismatches 9; Indels
45.3%; Score 13.6; DB 1; Length 50; 80.0%; Pred. No. 4.1e+05; Live 0; Mismatches 4; Indels
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Unpublished (1995)
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GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
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/db_xref="taxon:10090"
/clone="MHPN54c05"
/clone_lib="MHPN"
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AJ668097.1 GI:49352548
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                                                                                                                                                                                                                                                                                                                                                                             Contact: Anderson SI
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Matches 18; Conservative
                                                                                                 Sus scrofa (pig)
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                                                                                                                                 Sus scrofa
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
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1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
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/db_xref="texaon:9606"
/db_xref="texaon:9606"
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/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                       Query Match
44.7%; Score 13.4; DB 6; Length 48;
Best Local Similarity 73.9%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 6; Indels
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44.7%; Score 13.4; DB 1; Length 50;
Best Local Similarity 73.9%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                    /mol_type="mRNA"
/db_xref="taxon.9606"
/dev_stage="adult"
/clone llb="Human adult (K.Okubo)"
/note="One or more human adult tissue"
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    .48
    /organism="Homo sapiens"

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                             Location/Qualifiers
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found there.
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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
ECORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institite,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (Dases 1 to 30)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and BST resources for studying reproduction and unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ594733 34 bp mRNA linear EST 06-DEC-2002 E012441-024-019-SP6 MPIZ-ADIS-024-developing root Beta vulgaris cDNA clone 024-019 5-PRIME, mRNA sequence.
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Beta vulgaris
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 34)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 0.0492215062851
Email: weisshaa@mpiz-koeln.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
db_xref="taxon:9823"
/dlone="c0000044_D15"
/tissue_type="placenta"
/clone_lib="cSEQRAN09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
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GAATITCCGAAACCAGAAGICGCCGA 1
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                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.2
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                /clone lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BZ764154 linear GSS 13-MAR-2003 SALK_124025.49.65.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_124025.49.65.x, genomic
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SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7;
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7;
Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
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                                                                                                            /organism="Beta vulgaris"
|mol_type="mRNA"
|cultivar="KWS2320 (double haploid, monogerm breeding
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
TOULO N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Insert Length: 34 Std Brror: 0.00
Plate: 24 row: 0 column: 19
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
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                                                                                                                                                                                                    /db_xref="GABI:192126"
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/clone="024-024-019"
tissue_type="developing root"
/lab_host="EMDH108"
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69.2%; Pred. No. 6e+05;
iive 0; Mismatches
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/ecotype="Col-0"
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/clone="SALK 124027.37.85.x"
/clone="lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html".
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
As Gequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, errosids II, Brassicales, Brassicaceae, Arabidopsis.
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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AUTHORS
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                                        BG032379 40 bp mRNA linear EST 24-JAN-2001 602301364F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4403174 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="INAGE:4403174"
/tissue type="mammary adenocarcinoma, cell line"
/tissue type="mammary adenocarcinoma, cell line"
/lab_host="Ph108 [phage-resistant)"
/clone lib="NIH MGC 87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1:383 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                   Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 40)
II (March http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Trissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 41)
Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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84.0%; Score 13.2; DB 4; Length 40;
Best Local Similarity 69.2%; Pred. No. 6e+05;
Matches 18; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 40.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db xref="taxon:9606"
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Unpublished (2003)
Contact: Donald R. McCarty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:34734716
                                                                                                                       BG032379.1 GI:12423624
                                                                                                                                                               Homo sapiens (human)
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                                                                                  nRNA sequence.
                                                                                                                                                                                    Homo sapiens
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CG426236.1
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DEFINITION
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JOURNAL
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AUTHORS
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AUTHORS
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COMMENT
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RESULT 20
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KEYWORDS
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                 BG032379
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2 (bases 1 to 42)
Blouin,J.L.C.
Direct Submission
Submitted (07-DEC-1999) Blouin J.L.C., Medical Genetics, University
Hospital and School of Medicine of Geneva, 1 rue Michel-Servet,
1211 GENEVA, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSA275866 42 bp DNA linear GSS 10-DEC-1999 Homo sapiens DNA for trapped exon, clone jlA63F10, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cultivar="UniformMu"

(db xref="taxon:4577"

(clone="taxon:4577"

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Isolation of portion of gene that map on chromosome 21q22 by exon
                                                                                                                                                                                                                                 Sequence flanking probable Mu insertion site in UniformMu line: 0180576-07, Pariner set: C Class: transposon insertion site. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Plant Molecular and Cellular Biology Program
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83.3%; Pred. No. 6e+05;
iive 0; Mismatches 3;
                                                 University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
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                                                                                                                                                                                                                                                                                                                                                                                                                                1.41
/organism="Zea mays"
/mol_type="Genomic DNA"
/strain="W22 (ACR, bz1-m9)"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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AJ275866.1 GI:6562523
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/clone="jlA6
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Best Local Similarity 83.33,
Thes 15; Conservative
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                                                                                                                                                                                          Email: drm@ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Matches

ð 셤 RESULT 23 AA074398/c DEFINITION ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL MEDLINE PUBMED

COMMENT

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/clone lib="NCI CGAP Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
/note="Organ: close december of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the co
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                                                                                                                                                                    BIS56158 45 bp mRNA linear EST 05-SEP-2001 603237933F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5290664 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11735 row: b column: 09
High quality sequence stop: 45.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 50)
Suzukt, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
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National Institutes of Health, Mammalian Gene Collection
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/dev_stage="10 months"
/lab_host="DH108"
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Pred. No. 6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5290664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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      GGACTACGAGAAGCAGCATGGCACTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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EST.
                                                                                                                                                                                                                                                                                                      BIS56158.1 GI:15443472
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Homo sapiens
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                                                                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.
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                                                                                                                                                                                                                                                                                                                           zml6f07.81 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:525829 3' similar to TR:G1136430 G1136430 KIAA0185 PROTEIN ;,
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1 (Dases 1 to 43)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubuque,T., Favallo,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Iacy,M., Ie,M., Ie,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Mardis,E., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R., and Marra,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Insert Length: 1400 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 1. Location/Qualifiers
   Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:3917258"
/db_xref="taxon:9606"
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                                                                                                             19 CGGAGACAGAGNTCACTGA 37
                                                             10 CGGAGCCAGACGGCACTGA 28
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Homo sapiens
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15; Conservative
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Best Local Matches 1

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Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Smail: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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1. (bases 1 to 50)

Suzuki, Y., Taira, H., Teunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="texon:9606"
/clone="lhG09859"
/clone=lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                 Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama
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/gea="Male"
//dab host="B. Coli strain XL10-Gold, Tl-resistant, P-"
//dab host="B. Coli strain XL10-Gold, Tl-resistant, P-"
//clonellb="Wouse lokb plasmid UVGCMI library."
//note="Wetcor: PWMSJNv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labozatory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWMP42 (gil #4732114 gpl AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0548D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0548D16 R, genomic survey sequence.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0548D16"
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AZ666536.1 GI:11803682
83.3%;
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44.0%; Score 13.2; DB 8; Length 50;

Query Match

44.0%; Score 13.2; DB 1; Length 50;

Query Match

EST 21-OCT-2002

RESULT 28 AA776443/c DEFINITION

Matches

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ORGANISM

ACCESSION

VERSION KEYWORDS

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

[Optiniformes; Cyprinidae; Danio.

[I Dasse 1 to 46]

Humphray, S.J., Huckle, E. and Durham, J.L.

Direct Submission

Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished

This sequence was generated from the SP6 end of BAC 54G22. 54G22 is part of the Daniokey BAC Library created by R. Plasterk and N.V.

Keygene. Further details:
                                                                                                                                                                                                                                                                                                         Expressed Sequence Tags from Reproductive Organs of Ipomoea trifida
                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sateride; lamide; Solanales; Convolvulaceae; Ipomoeeae; Ipomoea. (bases 1 to 38)
Tsuchiya,T., Ando,A., Ogawa,C., Futagami,K., Watase,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         אסה שה בא באמו באס שה האם GSS 29-JAN
Danio rerio genomic clone DKEY-54G22, genomic survey sequence.
BX230810
                  AU223982 Ipomoea trifida anther Ipomoea trifida cDNA clone
IAM-0341, mRNA sequence.
    linear
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/clone_lib="Ipomoea trifida anther"
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Location/Qualifiers
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    mRNA
                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Tohru Tsuchiya
Faculty of Bioresources
Mie University
Tsu, Mie 514-8507, Japan
Tel: 81-59-211-9515
Fax: 81-59-211-9515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Ipomoea trifida"
/mol_type="mRNA"
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/dev_stage="tri-nucleate
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tsuchiya@bio.mie-u.ac.jp.
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I (bases 1 to 30.
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality; sequence stop: 1.
Location/Qualifiers
                        Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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69.2%; Pred. No. 6.1e+05;
ive 0; Mismatches 8;
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/organism="Homo sapiens"
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                                                               1 GGGAATTCGCGGAGCCAGACGCACT 26
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/clone="IMAGE:453763"
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                      18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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Gaps

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/tissue_type="Testis"

RESULT 29 AU223982/c

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Matches

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RESULT 31

AU103141

ACCESSION VERSION KEYWORDS

Matches

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REFERENCE AUTHORS MEDLINE PUBMED

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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Brail: Shirokanedai, Minatcku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and s'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
                                                                                                                                                                                                                                                                                                                            Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

BEBO Rep. 2 (5), 388-393 (2001).
   Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Orauki, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
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Pred. No. 7.4e+05;
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                                                                                                                                       mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/db_xref="taxon:9606"
/clone="HEP13475"
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1-length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Sakaki,Y., Taira,H., Tranaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Divèrse transcriptional initiation revealed by fine, large-scale EmBO Rep. 2 (5), 388-393 (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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/mol_type="mRNA"
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                                                                                                 ch 43.3%; Score 13; DB 9; Length 46; 1 Similarity 76.2%; Pred. No. 7.3e+05; 16; Conservative 0; Mismatches 5; Indels
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/note="vector pIndigoBAC-536"
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Homo sapiens
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shizokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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/clone="0384734-00A1-C06"
/clone="1016"UniformMu MuTAIL Library"
/note="vector: TOPO-FCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo assymmetric interlaced PCR (TAIL) protocol using primers specific for
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Sequence flanking probable Mu insertion site in UniformMu line:
03S4734-00, Primer set: A
Class: transposon insertion site.
Location/Qualifiers
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Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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/db_xref="texon:9606"
/clone="KRT09006"
/clone_lib="Sugano Homo sapiens cDNA library"
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Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
Do 110690 Galnesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
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/cultivar="UniformMu"
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/organism="Homo sapiens"
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                                                                                                                        11375929
Contact: Yutaka Suzuki
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Matches 19; Conservative
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitcon-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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L' (bases 1 to 50)
Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T. 1sogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
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/clone_lib="Sugano Homo sapiens cDNA library"
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                               Length 50;
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                          43.3%; Score 13; DB 1; 76.2%; Pred. No. 7.4e+05; ive 0; Mismatches 5

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    organism="Homo sapiens"

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/db_xref="taxon:9606"
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              Query Match
Best Local Similarity 76.2%
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ORIGIN

AI042471/c DEFINITION

à a ORGANISM

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AUTHORS

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JOURNAL

COMMENT

ACCESSION KEYWORDS SOURCE

VERSION

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Losses 1 to 38)

NIH-MGC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11659 row: i column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="hippocampus"
/lab host="DB10B"
/clone_lib="NIH_MGC_95"
/clone_lib="NIH_MGC_95"
/note="Corgan: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (Gregag); Oligo-dT primed using primer
/ctrgraptrTTTTTTTTTTVN-3', size-selected for average insert size 2: & he and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/MGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
  BIS47045 38 bp mRNA linear EST 05-SEP-2001
603190269FL NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5261657 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI836557 41 bp mRNA linear EST 04-OCT-2001
603089520F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5228572 5',
                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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( Dases 1 to 41)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12.8; DB 4; Length 3
Pred. No. 8.9e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 38.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:5261657"
                                                                             BI547045
BI547045.1 GI:15434357
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87.5%;
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                                                                                                                                                             Homo sapiens (human)
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                                                                                                                                                                                                                                                                (bases 1 to 38)
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                                                          mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                 AI042471 33 bp mRNA linear EST 24-SEP-1998 oy14d01.x1 Soares senescent fibroblasts NbHSF Homo sapiens CDNA clone IMAGE:1665793 3' similar to TR:Q99490 Q99490 KIAA0167
PROTEIN. [1] ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 33)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Linuch
Upublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
TMGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Trace considered overall poor quality
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/lab_host="0H10B (ampicillin resistant)"
/clone_lib="Soares senescent_fibroblasts_NbHSF"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker V TYPE: phagemid; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
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                                                                                                                             Query Match 43.3%; Score 13; DB 9; Length 50; Best Local Similarity 76.2%; Pred. No. 7.4e+05; Matches 16; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert Length: 1518 Std Error: 0.00
Seq primer: -40ml3 fwd. BT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:1665793"
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                                                                                                                                                                                                                                                                                   8 ACTITGTGGAGCCAAACGGTA 28
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Best Local Similarity
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FEATURES

RESULT 38 BI547045

Matches

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ORIGIN

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Gaps

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Length 38;

us-10-788-779-7.rst

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/lab_host="DH10B"
/clone lib="NHH MGC 120"
/clone lib="NHH MGC 120"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-8P0RT6; Site_1: Not!; Site_2: EccRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yomale. Library is oligo-dT primed and directionally cloned (EccNV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 59P11. 59P11 is part of the Danlokey BAC Library created by R. Plasterk and N.V. Keygene, Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gow
g column: 05
High quality sequence stop: 41.
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42.7%; Score 12.8; DB 4; Length 41;
Best Local Similarity 87.5%; Pred. No. 8.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels
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Location/Qualifiers
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/db_xref="taxon:7955"
/clone="DKBY-59F11"
/tissue type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5228572"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
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BX121769.1 GI:27952695
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Danio rerio
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BX121769
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           9 GAGAAAACGAAGAGGCAGCCGGCA 32
1 GGGAATTCGCGGAGCCAGACGGCA
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Search completed: November 18, 2005, 21:12:51 Job time : 1437.98 secs

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Query Match 100.0%; Score 30; DB 1; Length 30; Best Local Similarity 100.0%; Pred. No. 0.00071; Matches 30; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                        November 18, 2005, 00:26:13; Search time 58.289 Seconds (without alignments) 842.154 Million cell updates/sec
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Sequence 42,
Sequence 42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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Sequence 3
Sequence 3
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                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/SA_COMB.seq:*
/cgn2_6/ptodata/1/ina/SB_COMB.seq:*
/cgn2_6/ptodata/1/ina/Aa_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-113-750A-46
US-08-479-5
US-09-159-385-5
US-08-403-852D-42
US-08-403-852D-42
US-09-231-818-42
US-09-35-35-35-84
US-09-759-112A-3
US-09-759-112A-3
US-09-759-112A-3
US-08-759-112A-3
US-08-378-685A-26
US-08-38-8803-26
US-08-390-535A-8
US-08-310-535A-8
US-08-310-535A-8
US-08-310-535A-8
US-08-310-535A-8
US-08-688-145-4
US-08-688-145-4
US-08-688-145-4
US-08-688-145-4
US-08-688-145-4
US-08-688-145-4
US-08-688-145-4
US-08-688-145-4
                                                                                                                                            1 GGGAATTCGCGGAGCCAGACGCCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-04600-4
PCT-US95-04600-12
US-07-642-734C-25
US-08-439-009A-25
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                   1202784 segs, 818138359 residues
                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   - nucleic search, using sw model
                                                                                                                                                                  IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                Issued Patents NA:*
                                                                                                                    US-10-788-779-7
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length
                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                   OM nucleic
                                                                                                                                             Sequence:
                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
No.
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17, Appl
3058, Ap
8, Appli
24, Appli
24, Appli
24, Appl
72, Appl
74, Appl
                                                                                                              Sequence 17,
Sequence 3058
Sequence 8, A
Sequence 24,
Sequence 8, A
Sequence 52,
                  Sequence Sequence Sequence 1
                                                                                    Sequence Sequence
                                                                                                                                                                                                                Sequence
                                                                      Sequence
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                          Sequence
US-09-396-196G-68463
US-09-443-199C-940
US-09-410-935B-15
US-09-784-403A-15
US-08-551-200A-3
US-08-551-200A-3
US-08-625-209A-17
US-08-625-209A-17
US-08-821-782-8
US-09-422-978-3058
US-09-821-782-8
US-09-292-435A-8
US-09-292-435A-8
US-09-292-435A-8
US-09-292-435A-8
US-09-198-723A-74
US-09-198-723A-74
US-09-198-723A-74
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: WATKINS, HUGH
APPLICANT: ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GHL-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-740
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
LENGTH: 30 base pairs
TELEGRANDEDNESS: single
TTANDPINGSS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEB: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                   ; Sequence 7, Application US/07989160
; Patent No. 5429923
       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 60 S1
CITY: BOSTON
     444444444
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Gaps

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MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System 7.1
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,614
FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GAATTCGCGGAGCCAGACGGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAATTCGTGGAGCCAAACCGC 21
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US-09-186-277-5
; Sequence 5, Application US/09186277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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Fatent No. 5861294

GENERAL INFORMATION:
APPLICANT: Cowart, Marlon Daniel, Halbert, Donald N.,
APPLICANT: Kerwin, Jr., James F., McNally, Teresa
TITLE OF INVENTION: Adenosine Kinase Polypeptides
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: D-377 AP6D, 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
                                                                                            Sequence 46, Application US/09113750A

Sequence 46, Application US/09113750A

Patent No. 6294176

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Recombinant Raccompox virus
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:
ADDRESSE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
COUNTRY: USA
CONTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                    CORPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/113,750A FILING DATE: CLASSIFICATION: 424 ATTONEYTY AGENT INFORMATION: NAME: 28,678 REGISTRATION NUMBER: 28,678 REGISTRATION NUMBER: 55744 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFRAK: (212) 262-0400 TELEFRAK: (212) 262-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGAATTCGCGGAGCCAGACGCCACTGAAG 30
  1 GGGAATTCGCGGAGCCAGACGCCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGAATTCCTATCGCCGTACGGCACTGAGG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212)664-0525
TELEX: 42253
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-113-750A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: SYN
                                                                                        US-09-113-750A-46
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US-08-479-614-20
                                                                     RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-159-385-5

Sequence 5, Application US/09159385

Sequence 5, Application US/09159385

Sequence 5, Application US/09159385

SERIER INFORMATION:

APPLICANT: KAWAI.

APPLICANT: KAWAI. TARO

TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE

FILE REFERENCE: PH-569

CURRENT APPLICATION NUMBER: US/09/159,385

CURRENT APPLICATION NUMBER: US/09/159,385

CURRENT APPLICATION NUMBER: 1997-09-26

MUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 5

LENGHAR: 23

TENGHAR: 23
                                                                                                                                                                                                                                                                                                                                                                                                     Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 54.0%; Score 16.2; DB 2; Best Local Similarity 85.7%; Pred. No. 7.1e+02; Matches 18; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.0%; Score 16.2; DB 2; 85.7%; Pred. No. 7.1e+02; tive 0; Mismatches 3;
APPLICATION
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REGISTRATION NUMBER: 5749.US.DI
TELECOMMUNICATION INFORMATION:
TELEFAX: (708) 937-4884
ITELEFAX: (708) 938-2623
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
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Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                             Description of Artificial Sequence:Synthetic oligonucleotide
            APPLICANT: AKIRA, TROUGH APPLICANT: AKIRA, TRACON APPLICANT: KAWAI, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REPERENCE: 091356/0128
CURRENT APPLICATION NUMBER: US/09/186,277
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: JP97/261589
EARLIER PILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 54.0%; Score 16.2; DB 3; Length 23; 1 Similarity 85.7%; Pred. No. 7.1e+02; 18; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UGA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATA: 10-MAX-1995
PILING DATA: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTOONEY AGAINT NEORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Inv
TITLE OF INVENTION: Biosynthesis Of
TITLE OF INVENTION: Coding For These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 42, Application US/08403852D Patent No. 5891695 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGAATTCGCGGAGCCAGACG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGAATTCGCGGAGCAGGAGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patricia
                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blanc, Veronique
Blanche, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meyers, Kenneth J
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Lacroix,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crouzet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thibaut,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-403-852D-42
                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-186-277-5
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Debussche, Laurent
De Crecy-Lagard, Valerie
De Crecy-Lagard, Valerie
VENTION: Polypeptides Involved in The
VENTION: Biosynchesis Of Streptogramins, Nucleotide Sequences
VVENTION: Coding For These Polypeptides And Their Use
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 54.0%; Score 16.2; DB 2; Best Local Similarity 66.7%; Pred. No. 7.6e+02; Matches 18; Conservative 3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE, DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                   1 GGGAATTCGCGGAGCCAGACGCACTG 27
                                                                                                                                                                                                                                                                                                                     11 GSGAGTTCGCSGCSTGGGACGGCACCG 37
                                                                                                                                                                                                                                                                                                                                                                                              US-08-510-646B-44;
; Sequence 44, Application US/08510646B
; Patent No. 6077699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nathalie
Patricia
Denis
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blanc, Veronique
Blanche, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zagorec, Monique
             TELEPHONE: (202) 408-400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ 1D NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 408-400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PolyTITLE OF INVENTION: BLOSTITLE OF INVENTION: CodiNUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jacques,
Lacroix,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crouzet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thibaut,
                                                                                                                                              ; TOPOLOGY: linear
US-08-403-852D-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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GGGAATTCGCGGAGCCAGACGGCACTG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Polypeptides is Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-31315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/231,818
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                                                                                                     Query Match 54.0%; Score 16.2; DB 3; Length 38; Best Local Similarity 66.7%; Pred. No. 7.6e+02; Matches 18; Conservative 3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE FOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US/08/403,852
PILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                        1 GGGAATTCGCGGAGCCAGACGGCACTG 27
                                                                                                                                                                                                                     11 GSGAGTTCGCSGCSTGGGACGCCG 37
                                                                                                                                                                                                                                                                                                                                          Sequence 42, Application US/09231818
Patent No. 6171846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Debussche, Laurent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patricia
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Blanche, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thibaut, Denis
Zagorec, Moniqu
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan,
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacques,
Lacroix,
                                      ; TOPOLOGY: linear
US-08-510-646B-44
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Best Local Similarity
Matches 18; Conserv
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US-09-231-818-42
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APPLICANT:
APPLICANT:
APPLICANT:
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De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner STREEF: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/635,359B
FILING DATE: 09-Aug-2000
PRIOR APPLICATION NUMBER: US 09/231,818
FILING DATE: 15-JAW-1999
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-03000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.0%; Score 16.2; DB 4; 66.7%; Pred. No. 7.6e+02; tive 3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-635-359B-42
11 GSGAGTTCGCSGCSTGGGACGCCACCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGAATTCGCGGAGCCAGACGCCACTG 27
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                                                                                                                          Sequence 42, Application US/09635359B Patent No. 6670157 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                         Debussche, Laurent
                                                                                                                                                                                                                                                             Jacques, Nathalie
Lacroix, Patricia
                                                                                                                                                                                           APPLICANT: Blanc, Veronique
Blanche, Francis
                                                                                                                                                                                                                                                                                                                                   Zagorec, Monique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 38 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.74
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                            Thibaut,
                                                                                                         US-09-635-359B-42
                                                                                    RESULT 9
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                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avian Herpesvirus-based live recombinant avian vaccine, in particular against Gumboro disease
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                                                                                                               Score 15.2; DB 4; Length 33;
Pred. No. 2e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 31;
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Pred. No. 2.5e+03;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22202
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,803
FILING DATE: 05-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SARRO, Thomas
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 920-7200
TELEPHONE: (703) 992-8428
INFORMATION FOR SEQ ID NO: 26:
; NAME/KEY: primer bind
; LOCATION: (1)..(33)
; OTHER LINGNATION: 1F7 light chain 5' primer
US-09-112A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: AUDONNET, Jean-Christophe F
APPLICANT: BUBLOT, Michel J
APPLICANT: DARTEIL, Raphael J
APPLICANT: DARTEIL, Raphael J
APPLICANT: DARTEIL, Raphael J
APPLICANT: LAPLACE, Bliane L
APPLICANT: LAPLACE, Bliane L
APPLICANT: RIVIERE, Michel A
TITLE OF INVENTION: Avian Herpesvirus-base
TITLE OF INVENTION: vaccine, in particula:
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: LARSON AND TAYLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GAATTCGCGGAGCCAGACGCCAC 25
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/08368803; Patent No. 5733554; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: LARSON AND TAYLOR
727 SOUTH 23RD STREET
                                                                                                                      50.7%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 78.3%;
Matches 18; Conservative (
                                                                                                                 Query Match
Best Local Similarity 85.04
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 31 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
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US-08-578-096A-27
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Sequence 3, Application US/09759112A

Sequence 3, Application US/09759112A

Sequence 3, Application US/09759112A

Sequence 3, Application US/09759112A

GENERAL INFORMATION:

APPLICANT: Muchler, Spille

APPLICANT: Moller, Heinz

TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

STOURENT APPLICATION NUMBER: US/09/759,112A

CURRENT FILING DATE: 2001-01-11

NUMBER OF SEQ ID NOS: 38

SEQ ID NO 3

LENGTH: 33
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               Sequence 3, Application US/08984277

Patent No. 605721

Patent No. 605721

APPLICANT: Muller, Sybille

APPLICANT: Moller, Heinz

TITLE OF INVENTION: WARTABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE
TITLE OF INVENTION: WONCLONAL ANTIBODY 1F7

NUMBER OF BEQUENCES: 10

CORRESPONDENCE ADDRESSE:
ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza, Suite 300

CITY: Alexandria

STATE: Virginia

COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 2e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,277
FILING DATE: 3-DEC-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50200-012
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGAATTCATGGAGACAGAC 20
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NAME: Bucca, Daniel
REGISTRATION NUMBER: 42,368
REFERENCE/DOCKET NUMBER: 5020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-756-8600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.7%;
                                                                                                                                                                                                                                                                                                                                                       ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-984-277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
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ORGANISM: mouse
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linear
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: mouse;
US-08-997-685A-26
                                                                                                                                                                                                          SEQ ID NO 26
LENGTH: 26
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                                                  TITLE OF INVENTION: Avian herpesvirus-based live recombinant TITLE OF INVENTION: avian vaccine NUMBER OF SEQUENCES: 28 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Avian herpesvirus-based live recombinant TITLE OF INVENTION: avian vaccine
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 15; DB 2; Length 31; 78.3%; Pred. No. 2.5e+03; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 31;
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Pred. No. 2.5e+03;
0; Mismatches 5; Indels
                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/578,096A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/240,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GAATTCGCGGAGCCAGACGCCAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GAATTCGCGAAGAGGAAGGAAC 28
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                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: other nucleic acid
US-08-578-096A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-997-685A-26
; Sequence 26, Application US/08997685A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,096
FILING DATE:
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; Patent No. 6045803
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                                                                                                                                                                                                                                                                 FILING DATE:
INFRMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 bases pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
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Best Local Similarity 78.3
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
; Patent No. 5980906
; GENERAL INFORMATION:
; APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-240-426-27
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GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Miyashita, Toshiyuki
APPLICANT: Harigai, Masayoshi
APPLICANT: Harigai, Masayoshi
APPLICANT: Hanada, Motoi
TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING
TITLE OF INVENTION: CELL DEATH
TITLE OF INVENTION: CELL DEATH
TOWNER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University
APPLICANT: Randel, Eric
TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
FILE REFERENCE: 0575/54806
CURRENT APPLICATION NUMBER: US/08/997,685A
CURRENT FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,619
FILING DATE: 14-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REFERENCE/DOCKET NUMBER: P-LJ 9867
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.8; DB 1
Pred. No. 3e+03;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 ATTCGCGGAGCCAGACGGCACTGAAG 30
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08182619; Patent No. 5484710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                    ch 49.3%;
1 Similarity 73.1%;
19; Conservative (
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TELEPAX: (619) 535-8849
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 73.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 base pairs
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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Floppy disk
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MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS
                                                            San Diego
California
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US-08-607-269-4
                                                                                                      USA
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                                                                                                    COUNTRY:
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APPLICANT: Reed, John C.
APPLICANT: Miyashita, Toshiyuki
APPLICANT: Miyashita, Toshiyuki
APPLICANT: Harada, Macayoshi
APPLICANT: Hanada, Motol
TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores Lip
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
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Patent No. 5702897
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: Interaction of Proteins Involved in a
TITLE OF INVENTION: Cell Death Pathway
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/330,535A
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,619
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 1174
TELECOMMUNICATION INFORMATION:
                 GGAATTCGCGGAGCCAGACGCCACTG 27
                                                       1 ddaarrcccccrcarccaccccrcc 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 73.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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                                                                                                                                            US-08-330-535A-8
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Gaps
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APPLICANT: Rato, Takaaki
TITLE OF INVENTION: Interaction of Proteins Involved in a
TITLE OF INVENTION: Cell Death Pathway
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
49.3%; Score 14.8; DB 1
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/226,876
FILING DATE: 13-APR-1994
ATTORNEY-YAGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 91,915
REFERENCE/DOCKET NUMBER: 9-LJ 9882
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
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TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGAATTCGCGGAGCCAGACGCCACTG 27
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/226,876
FILING DATE: 13.APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: PCR primer Bax F
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                                                                                         ; Sequence 1, Application US/08616732A; Patent No. 5770690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bitler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGI.
MOLECULE TYPE: DN
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TILLE OF INVENTION: BAX Promoter Sequence and Screening
Patent No. 5744310
TITLE OF INVENTION: Assays for Identifying Agents that Regulate BAX Gene
TITLE OF INVENTION: Expression
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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se+03;
nes 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,145
FILING DATE:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9882
FELECOMMUNICATION INFORMATION:
FELEPHONE: (619) 535-9001
FELEPHONE: (619) 535-9001
FELEPA: (619) 535-9001
FELEPA: (619) 535-8049
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
FYPE: nucleic acid
STRANDEDNESS: single
FOROLOGY: linear
US-08-607-269-12
                                                                                                                                                                                                                                                                                                                                                                                                                        1 ddaarrcdcdgrdarddacddgrccd 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08688145
Patent No. 5744310
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 73.1*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 19; Conserv
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Gaps
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APPLICANT: Miyashita, Toshiyuki
APPLICANT: Harigai, Masayoshi
APPLICANT: Haradai, Motoi
TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 49.3%; Score 14.8; DB 1; Length 27; Best Local Similarity 73.1%; Pred. No. 3e+03; Matches 19; Conservative 0; Mismatches 7; Indels
APPLICANT: Bitler, Catherine Mastroni
APPLICANT: Bitler, Catherine Mastroni
APPLICANT: Bowersox, Stephen Scott
APPLICANT: Crea, Roberto
APPLICANT: Demo, Susan Duuham
APPLICANT: Horne, William A.
APPLICANT: Abou, Mei
TITLE OF INVENTION: Bax Omega Protein and Methods
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: PLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,732A
FILING DATE: 15-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/495,042
FILING DATE: 27-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/POCKET NUMBER: 5865-0017.30
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 73.12
Best Local Similarity 73.12
Conservative
                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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ANTI-SENSE: NO
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PCT-US95-04600-4
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THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
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                                                                                                                                                                                                                                                                                    CURENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/0818,844

FILING DATE: 11-APR-1997

CLASSIPICATION DATA:

APPLICATION NUMBER: US/08/182,619

FILING APPLICATION NUMBER: US/08/182,619

FILING DATE: 14-JAN-1994

PRIOR APPLICATION NUMBER: US/08/182,619

FILING DATE: 27-OCT-1994

ATONREY/AGENT INPORMATION:

NAME: Campbell, Cathyrn A.

REGISTRATION NUMBER: B-LJ 2520

FELEFAK: (619) 535-9001

TELEFAK: (619) 535-9001

TELEFAK: (619) 535-849

INPORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LUMCTH: 27 base pairs

LUMCTH: 27 base pairs

LUMCTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Bax Omega Protein and Methods NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: ADDRESSE: Dehlinger & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto STATE: CA
               TITLE OF INVENTION: DEATH
NUMBER OF SEQUENCES: 30
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 dcaarrcccccrcarccacccccc 26
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APPLICANT: Bowersox, Stephen Scott
APPLICANT: Crea, Roberto
APPLICANT: Demo, Susan Dunham
APPLICANT: Horne, William A.
APPLICANT: Zhou, Mei
                                                                                                                                                              COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09037742B Patent No. 6140484
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                  STREET: 4370 La Jo
CITY: San Diego
STATE: California
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Gaps
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04600
FILING DATE: 12-APR-1995
CLASSIFICATION:
ATTORNEY/ACEVIT
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Campbell and Flores
STREET: 4310 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application PC/TUS9504600
GENERAL INFORMATION:
APPLICANT: LA JOLILA CANCER RESEARCH FOUNDATION:
TITLE OF INVENTION: Interaction of Proteins In:
TITLE OF INVENTION: a Cell Death Pathway
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.3%; Score 14.8; DB 373.1%; Pred. No. 3e+03;
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKEY NUMBER: 5865-0017.30
TELECOMMUNICATION INFORMATION:
TELEFHOM: (415) 324-0880
TELEFAX: (415) 324-0880
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
REFERENCE/DOCKET NUMBER: FP-LJ 1361
TELECOMMUNICATION INFORMATION:
TELEPRAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE: PCR primer Bax F
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                                           US/09/037,742B
                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,732
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LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                COUNTRY: US
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: line
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                                                                                                                                                                                                                                                                           PCT-US95-04600-12
; Sequence 12, Application PC/TUS9504600
; GENERAL INFORMATION:
; APPLICANT: LA JOLIA CANCER RESEARCH FOUNDATION
; TITLE OF INVENTION: Interaction of Proteins Involved in TITLE OF INVENTION: a Cell Death Pathway
; TITLE OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; STREET: Campbell and Flores
; STREET: San Diego
; CITY: San Diego
; STATE: California
                                                                             DB 5; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.3%; Score 14.8; DB 5; Length 27; 73.1%; Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/07642734C
Patent No. 2824513
GENERAL INFORMATION:
APPLICANT: Katz, L
APPLICANT: Donadio, S
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMDUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMDUTER: IBM PC compatible
COMBUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION NUMBER: PCT/US95/04600
FILING DATE: 12-APR-1995
CLASSIFICATION NUMBER: PCT/US95/04600

ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
MAWE: Imbra, Richard J.
REFERENCE/DOCKET NUMBER: FP-LJ 1361
TELECOMMUNICATION INFORMATION:
TELEFHONE: (619) 535-9001
TELEFPAN: (619) 535-901
TELEFPAN: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
TENDERAL 27 base pairs
                                                                                                3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.1%; Pred. ...
                                                                           49.3%; Score 14.8; I
ilarity 73.1%; Pred. No. 3e+(
Conservative 0; Mismatches
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                                                                                                                                                           2 GGAATTCGCGGAGCCAGACGCCACTG 27
                                                                                                                                                                                                 1 GGAÁTTCGCGGTGATGGACGGGTCCG 26
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
                                                             Query Match
Best Local Similarity
                     linear
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TOPOLOGY:
PCT-US95-04600-12
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                ; TOPOLOGY:
PCT-US95-04600-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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MUDRESSEE, Ebbard H. Gorman

STREET, Abort Raidboractite D377/AP6D-2 One Abbott

CTTT. Abort Park

COMPUTER READALE PORM:

MORRITHER: 11

COMPUTER READALE PORM:

MORRITHER: 10

COMPUTER READALE PORM:

MORRITHER: 10

COMPUTER READALE PORM:

MORRITHER: 10

COMPUTER READALE PORM:

MORRITHER: 10

COMPUTER READALE PORM:

MORRITHER: 17-7M-91

COMPUTER READALE PORM:

MORRITHER: 17-7M-91

MORRITHER: 17-7M-91

MORRITHER: 17-7M-91

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                                                                                                 NAME/KEY: misc_feature

COCATION: (26)...(0)

OTHER INFORMATION: 2 of 2 allelic variants (939 is other entry);
NAME/KEY: misc_feature

COCATION: (25)...(26)

OTHER INFORMATION: nucleotide deleted between bases 25 and 26

NAME/KEY: misc_feature

COCATION: (0)...(0)

OTHER INFORMATION: Accession number cg43982025

US-09-443-199C-940
                                                                                                                                                                                                                                                                                                                                                                 Query Match 48.7%; Score 14.6; DB 4; Length 50; Best Local Similarity 69.0%; Pred. No. 3.9e+03; Matches 20; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.0%; Score 14.4; DB 4; Length 25; 93.8%; Pred. No. 4.4e+03; Live 0; Mismatches 1; Indels
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; Patent No. 6504083
; GENERAL INPORMATION:
; APPLICANT: Barbour, Eric
; APPLICANT: Barbour, Eric
; APPLICANT: Ed Saad, Mohammed
; TITLE OF INVENTION: No. 6504083el Maize Promoters
; FILE REFERENCE: 5718-72
; CURRENT APPLICATION NUMBER: US/09/410,935B
; CURRENT FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/107,201
; PRIOR APPLICATION NUMBER: US 60/107,201
; PRIOR PILING DATE: 1998-11-05
; PRIOR PILING DATE: 1998-11-06
; PRIOR FILING DATE: 1998-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL NO. 0811/24

GENERAL INTORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SCOTTARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 68465
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGAATTCGCGGAGCCAGACGCCACTGAA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGAAGGCGCATATCCTGGCGGCACAGCA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 68465, Application US/09396196G
; Patent No. 6821724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AGCTAGACGCCACTGA 19
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Best Local Similarity 93.8'
Matches 15; Conservative
                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-396-196G-68465
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            LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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Patent No. 6670464

GENERAL INFORMATION:

APPLICANT: Shawets, Richard A.

APPLICANT: Leach, Martin

TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof

TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof

FILE REFERENCE: 15966-34A

CURRENT APPLICATION NUMBER: US/09/443,199C

CURRENT APPLICATION NUMBER: 60/109,024

PRIOR APPLICATION NUMBER: 60/109,024

PRIOR FILING DATE: 1998-11-17

NUMBER OF SEQ ID NOS: 1272

SOFTWARE: Curaden Patent Formatter Version 0.9
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                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 68463, Application US/09396196G
Patent No. 6821724
GERREAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                            3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 4952.US.DI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                      Score 14.8;
Pred. No. 3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/396,196G CURRENT FILING DATE: 1999-09-15 PRIOR APPLICATION NUMBER: 60/100,678 PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 68463
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGAATTCGCGGAGCCAGACGCCACTG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CGCGGAGCCAGACGCCACTGA 28
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 73.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                          NAME/KEY: PCR primer 10b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA; ORGANISM: mus musculus
US-09-396-196G-68463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-396-196G-68463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-443-199C-940
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                                                                                                                                                                                                       ch 48.0%; Score 14.4; DB 4; Length 44; l. Similarity 75.0%; Pred. No. 4.7e+03; 18; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.0%; Score 14.4; DB 4; Length 44; larity 75.0%; Pred. No. 4.7e+03; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-951-200A-3/c

Sequence 3, Application US/08951200A

Sequence 3, Application US/08951200A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schwartz, Martin A.
APPLICANT: Takada, Yoshikazu
APPLICANT: Takada, Yoshikazu
APPLICANT: Languino, Lucia
ITILE OF INVENTION: METHODS OF USE FOR INTEGRIN BIC CELL
ITILE OF INVENTION: GROWTH INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCORMATION:
APPLICANT: Barbour, Eric
APPLICANT: Barbour, Eric
APPLICANT: Ed Saad, Mohammed
TITLE OF INVENTION: No. 6670467el Maize Promoters
FILE REFERENCE: 35718/208067
CURRENT APPLICATION NUMBER: US/09/784,403A
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/107,201
PRIOR PILING DATE: 1998-11-05
PRIOR PILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
                                                                                                                                     ; OTHER INFORMATION: Gene specific primer 3 for Gos-2 US-09-410-935B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Gene specific primer 3 for Gos-2
US-09-784-403A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Fichardson P.C.
STREET: 4225 Executive Square, Suite 1400
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15
LENGTH: 44
                                                                                                                                                                                                                                                                                                   2 GGAATTCGCGGAGCCAGACGCAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGAATTCGCGGAGCCAGACGCCAC 25
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US-09-784-403A-15/c
; Sequence 15, Application US/09784403A
; Patent No. 6670467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                           ORGANISM: Artificial Sequence
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California
                                                                                                                                                                                                                               Best Local Similarity
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Best Local Similarity
Matches 18; Conserv
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STATE: C
COUNTRY:
                                                                                                                                                                                                         Query Match
                                                                        TYPE: DNA
                                                                                                                   FEATURE:
                                              LENGTH:
                                                                                                                                                                                                                                                    Matches
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COMPUTE: 72037

COMPUTE: FLORM:
MEDIUM TYPE: Flory disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,200A
FLING DATE: 14-OCT-1997
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,118
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REPERENCE/POCKET NUMBER: 33,347
REPERENCE/POCKET NUMBER: 03300/026002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 88, Application US/08253155A
Patent No. 5691147
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDR4 Binding Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155A
FILING DATE: 02-UN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GAATTCGCGGAGCCAGACGCCACT 26
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REFERENCE/DOCKET NUMBER: MII-028
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-951-200A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO. 88:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (619) 678-5070
TELEPAX: (619) 678-5099
INPORMATION FOR SEO ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GYALIS, Jeno
APPLICANT: GYALIS, Jeno
APPLICANT: GYALIS, Jeno
APPLICANT: Lamphere, Lo.
APPLICANT: Danhere, Lo.
TITLE OF INVENTION: Cdc37 Cell-Cyle Regulatory Protein,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SUCHENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,209A
FILING DATE: 01-APR-1996
CLASSIFTCATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV048.02
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHAK: (617) 832-1000
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                            ; STRANDEDNESS: single
TOPOLOGY: linear
; MOLECUL TYPE: other nucleic acid
US-08-253-155A-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-853-733B-17
Sequence 17, Application US/08853733B
Patent No. 6015692
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/08625209A
Patent No. 5756671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 70.4
Matches 19; Conservative
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 35
US-08-625-209A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Bost
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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US-09-422-978-3058/c

i Sequence 3058, Application US/09422978

sequence 3058, Application US/09422978

sequence 3058, Application US/09422978

sequence 3058, Application US/09422978

sequence 3058, Application Using a Sequence 3058, Application and Application and Application and Applicant: Chumakov, Ilya Applicant: Chumakov, Ilya Applicant: Chumakov, Ilya Applicant: Chumakov, Ilya Applicant Chumakov, Ilya Applicant ON UNMBER: US/09/422, 978

CURRENT FILING DATE: 1999-10-20

EARLIER FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109, 732

EARLIER APPLICATION NUMBER: US 60/109, 732

EARLIER PILING DATE: 1998-04-21

MUMBER OF SEQ ID NOS: 11796

SEQ ID NO 3058

LENGTH: 47
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APPLICANT: Lamphere, Lou
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: Cdc37 Cell-Cycle Regulatory Protein,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag, & Bliot, LLP
SIREET: One Post Office Square
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 39;
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                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,733B
FILING DATE: 09-MAY-1997
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/625,209
FILING DATE: 10-APRIL-1996
ATTORNEY/AGENT INPORMATION:
NAME: Campbell, Paula A.
REGISTRATION NUMBER: 32,503
REGISTRATION NUMBER: 32,503
REGISTRATION NUMBER: 32,503
REGISTRATION INFORMATION:
TELEPHONE: (617)832-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
47.3%; Score 14.2; DB 3;
Best Local Similarity 70.4%; Pred. No. 5.7e+03;
Matches 19; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGAATTCGCGGAGCCAGACGCCACTGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 GGAATTCAAGGAGGACGCCGCGCGGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
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US-09-292-435A-8
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                                                                                       Query Match 47.3%; Score 14.2; DB 4; Length 47; Best Local Similarity 84.2%; Pred. No. 5.8e+03; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Yutaka, Takarada
APPLICANT: Hiroaki, Inoue
APPLICANT: Hiroaki, Inoue
APPLICANT: House
APPLICANT: Sobihisa, Kawamura
TITLE OF INVENTION: METHOD FOR AMPLIFYING AND DETECTING
TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: USING THERMOSTABLE ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 46.7%; Score 14; DB 2; Length 30; Best Local Similarity 77.3%; Pred. No. 6.7e+03; Matches 17; Conservative 0; Mismatches 5; Indels
; LOCATION: 24
; OTHER INFORMATION: 99-21916-359 : polymorphic base A or G
US-09-422-978-3058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM PC
OPERATING SYSTEM: Dos 5.0
SOFTWARE: MOTEDPETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,782
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Leydig, Voit & Mayer, Ltd.
Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Ahern, Paul L.
REGISTRATION NUMBER: 17020
REFERENCE/DOCKET NUMBER: 66425
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 TTCGCGGAGCCAGACGGCACTG 27
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,709
                                                                                                                                                                                                                                                                                               RESULT 38
US-08-821-782-8
; Sequence 8, Application US/08821782
; Patent No. 5981183
                                                                                                                                                                                11 GGAGCCAGACGGCACTGAA 29
                                                                                                                                                                                                                             43 GGAGCCATAAGGCACTGCA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic DNA
US-08-821-782-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: (25)3533
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Sequence - 981183

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yutaka, Takarada
APPLICANT: Hioaki, Inoue
APPLICANT: Shuji, Shibata
APPLICANT: Shuji, Shibata
APPLICANT: Shuji, Shibata
TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: USING THERMOSTABLE ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: Levigi, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 61601-6780
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM PC
COMPUTER: IBM PC
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APPLICANT: Yutaki, Inoue
APPLICANT: Shuji, Shibata
APPLICANT: Shuji, Shibata
APPLICANT: Yoshijisa, Kawamura
TITLE OF INVENTION: METHOD FOR AMPLIFYING AND DETECTING
TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: USING THERMOSTABLE ENZYME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14; DB 2; Length ov, Pred. No. 6.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCHIDEA: IDENTICATIONS
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WORDPEfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,782
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION NUMBER: 08/446,709
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Ahern, Paul L.
REGISTRATION NUMBER: 17020
REFERENCE/DOCKET NUMBER: 66425
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 TTCGCGGAGCCAGACGCCACTG 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.3%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic DNA
US-08-821-782-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: (25)3533
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two P
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RESULT 39 US-08-821-782-24

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COUNTRY: USA

ZITE: 6160-6790

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB

COMPUTER: IBM PC
COMPUTER: IBM PC
COMPUTER: Dos 5.0

CORENATING SYSTEM: Dos 5.0

CORENATING SYSTEM: Dos 5.0

CORENATING MARK: Dos 5.0

CORENATING MARK: US/09/292,435A

FILING DATE: WORDER: US/09/292,435A

FILING DATE: PROCRATION NUMBER: 08/446,709

FILING DATE: PROCRATION NUMBER: 17020

REGISTRATION NUMBER: 17020

REGISTRATION NUMBER: 66425

FILING DATE: PROCRATION:
MAME: Ahear PROCRATION:
CONTREPANCE (312) 616-500

TELEFRA: (22)353

INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 30

TYPE: double

TOPOLOGY: unknown

WOLECULE TYPE: Genomic DNA

US-09-292-435A-8

Query Match

Query Match

MATCHES 17; Conservative 0; Mismatches 5; Indels 0; Gaps
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Search completed: November 18, 2005, 11:22:01 Job time : 59.289 secs

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15, Appl 3, Appli 439430,

Sequence

Sequence

258513,

Sequence Sequence Sequence Sequence Sequence 24, Appl 35, Appl 784963,

Sequence Sequence

3, Appli 169041, 611467, 148502, 255015,

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

231991, 285782,

142021, 561534, 674828,

708626, 794581, 965123

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

Perfect score:

Sequence:

OM nucleic

Run on:

Minimum DB E Maximum DB E

Database

Searched:

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Sequence 805772,
Sequence 844398,
Sequence 804896,
Sequence 299133,
Sequence 14, Appl
Sequence 14, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35
Sequence 78
Sequence 25
Sequence 50
1 US-10-716-803-42
5 US-10-716-803-42
1 US-10-13-036-15
2 US-10-433-036-15
3 US-10-439-300-439430
6 US-10-098-263B-97474
6 US-10-098-263B-97474
6 US-10-098-263B-97774
6 US-10-719-956-258513
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6 US-11-036-317-21919
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10 US-10-035-833A-1888
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13 US-10-807-466-35
14 US-10-1036-317-503091
15 US-10-956-157-231991
15 US-10-956-157-231991
16 US-11-036-317-56128
17 US-10-956-157-231991
18 US-10-956-157-231991
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18 US-10-956-157-231991
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Publication No. US20030054343A1
GENERAL INFORMATION:
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: WATKINS, HUGH
APPLICANT: WATKINS, HUGH
APPLICANT: ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 510
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APPLICATION NUMBER: US/08/469,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 STATE STREET, Suite CITY: BOSTON STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02109
         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASCII
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-08-469-172-7
       Sequence 7, Appli
Sequence 28, Appl
Sequence 804897,
Sequence 203038,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Appl
                                                                                                                                                              November 18, 2005, 06:36:48; Search time 403.232 Seconds (without alignments) 615.265 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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:: /ggn2_6/ptodata1/l/pubpna/USO7_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO7_NEW_PUB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO6_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO6_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO7_NEW_PUB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO8_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO8_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO8_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO8_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO9_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO9_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO9_NEW_PUB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO9_NEW_PUB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO9_NEW_PUB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO9_NEW_PUB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO0P_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO0P_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USO0P_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/USOOP_PUBCOMB.seq:*

:: /ggn2_6/ptodata1/l/pubpna/US
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/cgn2_6/ptodata/1/pubpna/UB11_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/UB60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/UB60_NEW_PUB.seq:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-788-779-7

4 US-110-349-788-78

5 US-11-036-317-804897

5 US-110-956-157-203038
                                                                                                                                                                                                                                                                                                              1 GGGAATTCGCGGAGCCAGACGGCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                     9794790 segs, 4134909567 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                      nucleic search, using sw model
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Match Length
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seq length: 50
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score greater tha
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100.0
62.7
56.7
54.7
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Score

Result

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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10788779
Publication No. US20040152121A1
GENERAL INFORMATION:
APPLICANT: SEIDWAN, CHRISTINE
SEIDWAN, JOHN
WATKINS, HUGH
ROSENWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
DISBASE-ASSOCIATED MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/788,779
FILING DATE: 27-Feb-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA: US/08/469,172
FILING DATE: «Unknown»
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/ACENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: 34,505
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

21: 02.109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGAATTCGCGGAGCCAGACGGCACTGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGAATTCGCGGAGCCAGACGGCACTGAAG 30
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                    linear
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US-10-788-779-7
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Sequence 804897, Application US/11036317

Sequence 804897, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2005-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                            RESULT 3
US-10-349-780A-28
US-10-349-780A-28
Sequence 28, Application US/10349780A
Publication No. US20040146866A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: QUANTITATIVE MULTIPLEX DETECTION OF NUCLEIC ACIDS
TITLE OF INVENTION: QUANTITATIVE MULTIPLEX DETECTION OF NUCLEIC ACIDS
TITLE OF INVENTION: QUANTITATIVE MULTIPLEX DETECTION OF NUCLEIC ACIDS
CURRENT APPLICATION UNDER: US/10/349,780A
CURRENT FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 50
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                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Pred. No. 1.5e+03;
0; Mismatches 5;
                                                                                                     Query Match
100.0%; Score 30; DB 20;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                             1 GGGAATTCGCGGAGCCAGACGCCACTGAAG 30
                                                                                                                                                                                                                                         GGGAATTCGCGGAGCCAGACGCACTGAAG 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 dadahrrcdacdarccadercrcacrdaad 43
; MOLECULE TYPE: CDNA; SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-10-788-779-7
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ilarity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-349-780A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-804897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
Matches 23; Conserv
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US-10-956-157-203038
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Publication No. US20050048466A1
Publication No. US20050048466A1
Publication No. US20050048466A1
Publication No. US20050048466A1
Publication No. US20050048466A1
APPLICATION:
APPLICATION:
TITLE OF INVENTION: Antioncogene with high efficiency and the use of it.
FILE REFERENCE: IECO180408FUS
CURRENT APPLICATION NUMBER: US/10/483,289A
CURRENT FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 3
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide US-10-483-289A-3
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-13-036-15/c

| Sequence 15, Application US/10123036
| Sequence 15, Application US/10123036
| Publication No. US20030073656A1
| GENERAL INFORMATION:
| APPLICANT: Children's Hospital Research Foundation
| TITLE OF INVERTION: METHODS FOR THE TREATMENT OF HEPATIC DISORDERS
| FILE REFERENCE: 0010872/0483563
| CURRENT PAPLICATION NUMBER: US/10/123,036
| CURRENT FILING DATE: 2002-04-15
| PRIOR APPLICATION NUMBER: US 60/283,788
| PRIOR FILING DATE: 2001-04-13
| NUMBER OF SEQ ID NOS: 16
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                                                     Length 38;
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                                                                                                                                                                                                                                                                                                                                                                                 Indels
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       REGISTRATION NUMBER: 46,063
REFERENCE/DOCKET NUMBER: 03806.0054-04000
                                                                                                                                                                                                                                                                                                                                   Score 16.2; DB 21;
Pred. No. 3.2e+03;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.2; DB 15;
Pred. No. 3.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                         TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGAATTCGCGGAGCCAGACGCCACTG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 GSGAGTTCGCSGCSTGGGACGCCCG 37
                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CGCGGAGCCAGACGGCACTGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 cecedaaccadacececrea 6
                                                                                                               INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
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66.7%;
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.74
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                       US-10-716-803-42
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US-10-483-289A-3
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                                                                    APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLBIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 203038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zagorec, Monique
Zagorec, Monique
Debussche, Laurent
De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
Blosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/10/716,803
FILING DATE: 20-Nov-2003
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             54.7%; Score 16.4; DB 22; 94.4%; Pred. No. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/635,359
FILING DATE: 09-AUG-2000
APPLICATION NUMBER: US 09/231,818
FILING DATE: 15-07N-1999
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-5EP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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FILING DATE: 25-SEP-1992
Sequence 203038, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
Blanch, Francis
Crouzet, Joel
Jacques, Nathalie
Liacroix, Patricia
Thibaut, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Arrigo, Salvatore J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/10716803
Publication No. US20040229236A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-203038
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US-10-716-803-42
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Gaps

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4; Indels

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Sequence 258512, Application US/10719956
; Sequence 258512, Application US/10719956
; Publication No. US20040146910A1
; GENERAL IMPORMATION:
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11.20
; RIDER PRICK PILING DATE: 2003-11.20
; RUMBER: OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 258512
; LENGTH: 25
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; Bublication No. US20040146910A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; TITLE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; RICK APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.0%; Score 15.6; DB 24; Length 25; Best Local Similarity 81.8%; Pred. No. 6.1e+03; Matches 18; Conservative 0; Mismatches 4; Indels (
                             FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SEQ TO NO 128306
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                               Query Match 52.0%; Score 15.6; DB 16; Best Local Similarity 81.8%; Pred. No. 6.1e+03; Matches 18; Conservative 0; Mismatches 4;
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       TITLE OF INVENTION: Human Microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 GGAATTCGCGAACCAAGAGGGC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Rattus norvegicus
US-10-719-956-258512
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US-10-719-956-258513
                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapien
US-10-098-263B-128306
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US-10-719-956-258512
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; Publication Wo. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittenan, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; ENDOWN: 25474
Query Match 54.0%; Score 16.2; DB 22; Length 39; Best Local Similarity 72.4%; Pred. No. 3.2e+03; Matches 21; Conservative 0; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.0%; Score 15.6; DB 16; Length 25; Best Local Similarity 81.8%; Pred. No. 6.1e+03; Matches 18; Conservative 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                                                                                                                                                     APPLICANT Xee Mai Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 35.204
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR PILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 499430
LENGTH: 25
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89.5%; Pred. No. 4.9e+03;
ive 0; Mismatches 2;
                                                                                                       2 GGAATTCGCGGAGCCAGACGCCACTGAAG 30
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US-10-098-263B-128306/c
; Sequence 128306, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
                                                                                                                                                                                                                                                                                ; Sequence 439430, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAATTCGCGAACCAAGAGGGC 23
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-439430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-97474
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DB 24;

52.0%; Score 15.6;

Query Match

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Query Match
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General 10 10 1020050214823A1
General INFORMATION: US20050214823A1
GENERAL INFORMATION: US20050214823A1
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIOR APPLICATION UNMER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERSUCE: 3654.1
CURRENT PAPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01.13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 875174
LENGTH: 25
                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 991174
SOFTHARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 21919
LENGTH: 25
                     4; Indels
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Best Local Similarity 81.8%; Pred. No. 6.1e+03; Matches 18; Conservative 0; Mismatches 4
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Pred. No. 6.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 875174, Application US/11036317; Publication No. US20050214823A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 805772, Application US/10719900; Publication No. US20050026164A1; GENERAL INFORMATION:
                                                            8 CGCGGAGCCAGACGCCACTGAA 29
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81.8%;
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Matches 18; Conservative
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Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus
US-11-036-317-21919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-875174
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US-10-719-900-805772/c
                                                                                                                                                            RESULT 14
US-11-036-317-21919/c
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US-11-036-317-804896

| Sequence 804896, Application US/11036317
| Publication No. US/20050214823A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Alan
| APPLICANT: Blume, John
| TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
| FILE REFERENCE: 3664.1
| CURRENT FILING DATE: 2006-10-13
| PRIOR APPLICATION NUMBER: US/11/036,317
| PRIOR FILING DATE: 2004-01-13
| PRIOR FILING DATE: 2004-01-13
| NUMBER OF SEQ ID NOS: 991174
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| SEQ ID NO 804896
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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; Sequence 844398, Application US/10719900
; Publication No. US20050026164A1
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT PILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR PILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SEQ ID NO 844398
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                               Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.3%; Score 15.4; DB 22; Length 25; 94.1%; Pred. No. 7.4e+03; ive 0; Mismatches 1; Indels
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REPERENCE: 3528.1
FILE REPERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003.11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR APPLICATION NUMBER: 60/427,808
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 805772
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.4; DB 22;
Pred. No. 7.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AATTCGCGGAGCCAGACGCCACTGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 AAGACCCGGATACCGACGCCACTGA 1
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76.0%;
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Matches 19; Conservative
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Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus US-10-719-900-844398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-719-900-844398/c
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                                                                                                                                                                                                                                                                   LENGTH: 25
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Gaps

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APPLICANT: ROTH, CHARLES W.
APPLICANT: BREY, PAUL T.
APPLICANT: HOLM, INGE
APPLICANT: ACAILLES, MARINE
APPLICANT: RZHETSKY, ANDREY
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND
CURRENT APPLICATION NUMBER: US/10/667,891
CURRENT FILING DATE: 2003-09-23
PRIOR PAPLICATION NUMBER: 60/413,469
PRIOR FILING DATE: 2002-09-26
                                                                                                                                                                                                                                                                                                                                         Length 41;
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APPLICANT: Sekine, Akihiro
APPLICANT: Sekine, Akihiro
APPLICANT: Ida, Aritoshi
APPLICANT: Ida, Aritoshi
APPLICANT: Salto, Osamu
ITILE OF INVENTION: Detection of Genetic Polymorphisms
FILE REFERENCE: FORS-06904
CURRENT APPLICATION NUMBER: US/10/035,833A
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 7669
SOFTWARE: Patentin version 3.2
SEQ ID NO 4483
LENGTH: 41
              APPLICANT: Saito, Osamu
TITLE OF INVENTION: Detection of Genetic Polymorphisms
FILE REFERENCE: FORS-06804
CURRENT APPLICATION NUMBER: US/10/035,833A
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 7669
SOFFWARE: Patentin version 3.2
SEQ ID NO 1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.4; DB 19;
Pred. No. 7.1e+03;
1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                    Score 15.4; DB 19;
Pred. No. 7.1e+03;
1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-035-833A-4483/c
; Sequence 4483, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.3%;
70.4%;
                                                                                                                                                                                                                                                                                                                                      Query Match 51.3%;
Best Local Similarity 70.4%;
Matches 19; Conservative
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Best Local Similarity 70.49
Matches 19; Conservative
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 24
Iida, Aritoshi
                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                         US-10-035-833A-1888
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APPLICANT: PLAKSIN, Daniel
TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
FILE REFERENCE: 87534-2800
CURRENT APPLICATION NUMBER: US/09/858,349
CURRENT APPLICATION OF 15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SSOFTWARE: Patentin version 3.1
LENGTH: 34
                                                                                                                                                                                                                                                                               Sequence 299133, Application US/11060756
Publication No. US20502213541
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Woulds, William Martin
APPLICANT: Woulds, William Martin
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SSCPTWARE: Patentin version 3.2
LENGTH: 25
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                 51.3%; Score 15.4; DB 26; Length 25; 76.0%; Pred. No. 7.4e+03; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.3%; Score 15.4; DB 26; Length 25; Best Local Similarity 76.0%; Pred. No. 7.4e+03; Matches 19; Conservative 0; Mismatches 6; Indels (
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Pred. No. 7.2e+03;
0; Mismatches 6; Indels
                                                                                                                                              1 TGCACTGAGGGACACGGCCCTGAAG 25
                                                                                                                6 TTCGCGGAGCCAGACGCACTGAAG 30
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. Sequence 1888, Application US/10035833A

. Publication No. US20040072156A1

. GENERAL INFORMATION:
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Patent No. US20020012909A1
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Best Local Similarity 76.0%;
Matches 19; Conservative
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; ORGANISM: DET-21aVH3' XhOI
US-09-858-349-14
              Query Match
Best Local Similarity 76.0
Matches 19; Conservative
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; APPLICANT: Sekine, Akihiro
                                                                                                                                                                                                                                       RESULT 19
US-11-060-756-299133/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-299133
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US-09-858-349-14
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Gaps

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; ORGANISM: Mus musculus
US-10-719-900-784963
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US-11-036-317-611467
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                                                                                                                                                                                                                                                            RESULT 26
US-10-719-956-25613
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Publication No. US20040244066A1

GENERAL INFORMATION:
APPLICANT: ROTH, CHARLES W.
APPLICANT: BREY, PAUL T.
APPLICANT: HOLM, INGE
APPLICANT: REIETSKY, ANDREY
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND TITLE OF INVENTION WUMBER: US/10/807,466
CURRENT FILING DATE: 2004-03-24
PRIOR PILING DATE: 2003-09-23
PRIOR PILING DATE: 2003-09-24
PRIOR FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 139
SEQ ID NO 35
LENGTH: 24
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                                                                                                                                                                                                                    Gaps
                                                                               ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: primer US-10-667-891-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic; COTHER INFORMATION: primer US-10-807-466-35
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; Sequence 784963, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TILE REFERENCE: 3528.1
; CURRENT PAPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR RILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 784963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.7%; Score 15.2; DB 21; Length 24; 85.0%; Pred. No. 9.1e+03; ive 0; Mismatches 3; Indels (
                                                                                                                                                                       Length 24;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                       Score 15.2; DB 20;
Pred. No. 9.1e+03;
                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                            1 GGGAATTCGCGGAGCCAGAC 20
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                                                                                                                                                                         50.7%;
                  TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                  Query Match
Best Local Similarity. 85.07
Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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US-10-807-466-35
                                                               FEATURE:
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Sequence 503091, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
FITHE REPERENCE: 3654.1
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
FRIOR FILING DATE: 2004-01-13
SOFTWARE: Wicroarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 503091
LENGTH: 25
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  Length 25;
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CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR PILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 699466

SOFTHARE MICROAIRAY Probe Sequence Listing Generator V 1.1

LENGTH: 25
                                          Indels
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                                                                                                                                                                                                                                                                                                     APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
Query Match 50.7%; Score 15.2; DB 22; Best Local Similarity 85.0%; Pred. No. 9.1e+03; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.7%; Score 15.2; DB 26; Best Local Similarity 85.0%; Pred. No. 9.1e+03; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.7%; Score 15.2; DB 24;
85.0%; Pred. No. 9.1e+03;
vative 0; Mismatches 3;
                                                                                                                                                                                                                                      ; Sequence 25613, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
                                                                                   7 TCGCGGAGCCAGACGCCACT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 CGGAGCCAGACGGCACTGAA 29
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                                                                                                                   25 TTGCAGAGTCAGACGCCACT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Rattus norvegicus
US-10-719-956-25613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 85.04
Matches 17, Conservative
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CORGANISM: Mus musculus
US-11-036-317-503091
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Publication US/09759112A
Publication No. US20030100741A1
Publication No. US20030100741A1
Publication No. US20030100741A1
Publication No. US20030100741A1
APPLICANT: Mueller, Sybille
APPLICANT: Kohler, Heinz
APPLICANT: Kohler, Heinz
APPLICANT: Nonler, Heinz
APPLICANT: Nonler, Heinz
APPLICANT: Nonler, Heinz
APPLICANTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
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; Sequence 169041, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OP INVENTION:
; TITLE OP INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 05/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169041
                                                                                                                                             Length 25;
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                                                                                                                                          50.7%; Score 15.2; DB 26;
85.0%; Pred. No. 9.1e+03;
ive 0; Mismatches 3;
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85.0%; Pred. No. 8.9e+03;
tive 0; Mismatches 3;
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LOCATION: (1)..(33)

OTHER INFORMATION: 1F7 light chain 5' primer

US-09-759-112A-3
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Best Local Similarity 85.04
Matches 17; Conservative
                                                                                                                                       Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
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Best Local Similarity 78.3
Matches 18; Conservative
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US-10-719-900-169041
             ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-255015
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 31
US-09-759-112A-3
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US-11-060-756-255015

US-11-060-756-255015

Sequence 255015, Application US/11060756

Publication No. US20050221354A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William Martin

TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug

FILE REFERENCE: AM101083 (031896-042000)

CURRENT APPLICANT: AM101083 (031896-042000)

CURRENT FILING DATE: 2005-02-18

NUMBER OF SEQ ID NOS: 303284

SOFTWARE: Patentin version 3.2

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 148502, Application US/11060756
| Publication No. US20050221354A1 |
| GENERAL INFORMATION: |
| APPLICANT: Wyeth |
| APPLICANT: Wounts, William Martin |
| TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug |
| TITLE OF INVENTION: Target Genes |
| TITLE OF INVENTION: Target Genes |
| TITLE OF INVENTION: Target Genes |
| TITLE OF INVENTION: Target Genes |
| TITLE OF INVENTION: Target Genes |
| TITLE OF INVENTION NUMBER: US/11/060,756 |
| CURRENT APPLICATION DATE: 2005-02-18 |
| NUMBER OF SEQ ID NOS: 303284 |
| SOFTWARE: Patentin version 3.2 |
| SEQ ID NO 148502 |
| LENGTH: 25
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Sequence 611467, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Williams, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT APPLICATION NUMBER: US 60/536,639
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR PILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Midroarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 611467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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85.0%; Pred. No. 9.1e+03;
iive 0; Mismatches 3;
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Best Local Similarity 85.0°
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-611467
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; ORGANISM: probe
US-11-060-756-148502
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US-11-060-756-148502
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE SEFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 561534
LENGTH: 25
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Sequence 674828 Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, John
TITLE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
FRICE APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
FRICE APPLICATION NUMBER: US 60/536,639
FRICE REFERENCE: 2004-01-13
FRICE APPLICATION NUMBER: US 60/536,639
FRICE APPLICATION DATE: 2004-01-13
FRICE APPLICATION DATE: 2004-01-13
FRICE SEQ ID NOS: 991174
SOFTWARE OF SEQ ID NOS: 991174
SOFTWARE OF SEQ ID NOS: 991174
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                       NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 142021
LENGTH: 25
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Pred. No. 1.1e+04;
0; Mismatches 5;
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Pred. No. 1.1e+04;
0; Mismatches 5;
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; Sequence 561534, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        3 GAATTCGCGGAGCCAGACGGCAC 25
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ilarity 78.3%;
Conservative 0
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78.3%;
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Best Local Similarity 78.3
Matches 18; Conservative
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                                                                                                                                        ORGANISM: Mus musculus US-11-036-317-142021
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US-11-036-317-561534
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Best Local Similarity
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Best Local Similarity
Matches 18; Conserv
    PRIOR FILING DATE:
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LENGTH: 25
                                                                                                                     TYPE: DNA
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                                                                                                                                                                       APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wounts, William TITLE OF INVENTION: WUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES FILE REFERENCE: 031896-043000 (AM 101081) CURRENT APPLICATION WUMBER: US/10/956,157 CURRENT FILING DATE: 2004-10-04 NUMBER OF SEQ ID NOS: 319805 SOFTWARE: Patentin version 3.2 SOFTWARE: 231991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROFEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEG ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 285782
LENGTH: 25
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Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
CURRENT APPLICATION WUBBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
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Pred: No. 1.1e+04;
Sred: Tathes 5; Indels
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78.3%; Pred. No. 1...
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                             ; Sequence 231991, Application US/10956157; Publication No. US20050118625A1; GENERAL INFORMATION:
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24 GGTACTTTGTGGAGCCAGACTGC 2
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hes 18; Conservative
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US-10-956-157-231991
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US-10-956-157-285782
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Matches 18; Conserv
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US-11-036-317-142021
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; Sequence 708626, Application US/11036317
; Publication No. US20050214823A1
; GENERALI INFORMATION:
    APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFRENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 708626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 794581, Application US/11036317
; Sequence 794581, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Jan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFREENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; FRICR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 794581
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CGCGGAGCCAGACGGCACTGAAG 30
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                                        2 cacrgadcacacgcccrgaag 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-708626
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; ORGANISM: Mus musculus
US-11-036-317-794581
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Best Local Similarity
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US-11-036-317-830452
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US-11-036-317-794581
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; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT APPLICATION NUMBER: US 60/536,639
; FRIOR APPLICATION NUMBER: US 60/536,639
; FRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SCO ID NO 830452
; LENGTH: 25
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; ORGANISM: Mus musculus
US-11-036-317-830452
Query Match
Best Local Similarity 78.3%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps

Qy 6 TTCGCGGACCAGACCACTGA 28

Qy 6 TTCGCGAGCCACACGCCCTGA 25

Search completed: November 18, 2005, 15:41:07
Job time: 404.232 secs
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AX323399 Sequence A51711 Sequence 17

ARI6759 Sequence
ARI78100 Sequence
BD221995 Near infr
AR200195 Sequence
AX323182 Sequence
AX68852 Sequence
CQ628817 Sequence
CQ628818 Sequence
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AR275510 Sequence
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Run on:

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BD172395 24 bp DNA linear PAT 18-FEB-2003 Secreted and transmembrane polypeptides and nucleic acids encoding the same.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified.
1 (bases I to 26)
Seidman, C., Seidman, J., Matkins, H. and Rosenzweig, A.
Method for detecting hypertrophic cardiomyophathy associated
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 24)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: US 5429923-A 8 04-JUL-1995,
Location/Qualifiers
Location / Oxganism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="unassigned DNA"
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Sequence 8 from patent US 5429923.
112901
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AK178317
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AK16300
AK200395
AK263832
AK33382
AK363817
CQ628817
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AK469819
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JP 2002223786-A/168.
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  Similarity
                                                                                                mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
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                                                                                                            DEFINITION
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BD172395/c
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AUTHORS
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                                                                               November 18, 2005, 11:12:34; Search time 721.376 Seconds (without alignments) 1746.433 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
          GenCore version 5.1.6
(c) 1993 ~ 2005 Compugen Ltd.
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        4708233 segs, 24227607955 residues
                                                                                                                                 US-10-788-779-8
26
1 CCCTCCTTCTTGTACTCCTCCTGCTC
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Maximum Match 100%
Listing first 45 summaries
                                                         - nucleic search, using sw model
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BD173352
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Length 26;

AR120089 Sequence BD183077 Novel ins BD103248 Novel ins A35229 Synthetic p AR012257 Sequence

PR

AUTHORS

JOURNAL

COMMENT

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BD173033 24 bp DNA linear PAT 18-FEB-2003 Secreted and transmembrane polypeptides and nucleic acids encoding the same.
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                                                                                              Secreted and transmembrane polypeptides and nucleic acids encoding
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C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (C12N5/10,C12R1:91), (C12P21/02,C12R1:91), (C12P21/02,C12R1:645), (C12P21/02,C12R1:19), (C12P21/08,C12R1:91), C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic FH Key Location/Qualifiers
                                                 Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIANE PENNICA
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6 (0/052287, 17-OCT-1997 US

6 (0/052287, 17-OCT-1997 US

6 (0/05218, 12-OCT-1997 US

6 (0/053120, 24-OCT-1997 US

6 (0/053120, 24-NOV-1997 US

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6 (0/05513, 25-NOV-1997 US
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                              Patent: JP 2002238586-A 168 27-AUG-2002;
    other sequences; artificial sequences.
                                                                                                                                                                                                                                       27-AUG-2002
18-DEC-2001 JP 2001385205
17-SEP-1997 US 60/0591:
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                                                                                                                                                                                        Artificial Sequence
JP 2002238586-A/168
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WILLIAM I WOOD, AUSTIN
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ilarity 86.4%;
Conservative 0
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17-SEP-1997 US
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                                                                                                                                                                      GENENTECH INC
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Best Local Similarity
Matches 19; Conserv
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BD173033/c
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                                                                                              TITLE
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Secreted and transmembrane polypeptides and nucleic acids encoding
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C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21,
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Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
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/organism="synthetic construct"
/mol_type="genomic DNA"
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Pred. No. 2.4e+04;
); Mismatches 3
                                                                                         Patent: JP 2002223786-A 168 13-AUG-2002;
GENENTECH INC
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60/059113,17-SEP-1997
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18-DEC-2001 JP 2001385135
17-SEP-1997 US 60/0591:
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JP 2002238586-A/168.
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JP 2002223786-A/168
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JEAN YUAN
C12N15/09,C07K14/435,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
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PC C12P21/02//C12P21/08, (C12N1/19, C12R1:64S), (C12N1/21, C12R1:19),
PC C12P21/02/12.C12R1:91), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC
Description of Artificial Sequence: Synthetic FH Key
Location/Qualifiers
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1 (bases 1 to 24)
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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Location/Qualifiers
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Pred. No. 2.4e+04;
0; Mismatches 3;
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60/062897,17-0CT-1997 U
60/063486,24-0CT-1997 U
60/063120,24-0CT-1997 U
60/063120,24-0CT-1997 U
60/063329,24-0CT-1997 U
60/06354,28-0CT-1997 U
60/06354,28-0CT-1997 U
60/06354,28-0CT-1997 U
60/06354,28-0CT-1997 U
60/06354,28-0CT-1997 U
60/06354,28-0CT-1997 U
60/06354,29-0CT-1997 U

    .24
    ^24subism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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60/059119,18-SEP-1997
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OS Artificial Sequence
PN JP 2002238588-A/168
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385315
PR 17-SEP-1997 US 60/059115
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FT source 1. .24

/organism='Artificial Sequence'.
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                                          synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 24)
Mood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.
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llarity 86.4%; Pred. No. 2.4e+04;
Conservative 0; Mismatches 3;
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/organism="synthetic construct"
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17-SEP-1997 US 60/0591:
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AR473148/c
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C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19), (C12N5/10,
Secretory and transmembrane polypeptide and nucleic acid encoding
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1 (bases 1 to 24)
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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/organism='Artificial Sequence'
Location/Qualifiers

    .24
    Aorganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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OS Artificial Sequence
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                                                                           BD175386.1 GI:29121082
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  PAT 18-DEC-2003
                                                                                                                                             Unclassified.

1 (bases 1 to 24)

Ashkenazi,A., Botestein,D., Desnoyers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,B., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J.,
Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
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Pred. No. 2.4e+04;
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AR410764 24 bp DNA Sequence 204 from patent US 6635468.
AR410764
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/wol_type="genomic DNA"
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PAT 02-APR-2003

DEFINITION ACCESSION VERSION

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS

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buv/5535 24 bp DNA linear PAT 27-AUG-2002 Secretory and transmembrane polypeptide and nucleic acid encoding the same.
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        1 (bases 1 to 24)
Besnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding the same
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                                                                                                                                                                                                                          66.2%; Score 17.2; DB 6; Length 24; 86.4%; Pred. No. 2.4e+04; artive 0; Mismatches 3; Indels
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Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3;
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synthetic construct
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1 (bases 1 to 24)
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Genentech Inc. (US)
Location/Qualifiers
                                                                                  Patent: US 6767995-A 204 27-JUL-2004;
Location/Qualifiers
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Sequence 204 from Patent W00104311.
AX697613
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/db xref="taxon:32630"
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JP 2001516580-A/168.
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Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Mather, J.P., Williams, P.M. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
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                                                                                                                                                                                                                                                                 Patent: US 6686451-A 204 03-FEB-2004;
Location/Qualifiers
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AR566167
24 bp Di
Sequence 204 from patent US 6686451.
AR473148
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                                                               AR473148.1 GI:42708523
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DEFINITION ACCESSION VERSION

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KEYWORDS SOURCE

REFERENCE AUTHORS

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PAT 20-JUN-2002
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Nolan, G.P. and Rothenberg, S.Michael.
Methods for screening for transdominant effector peptides and RNA
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Davies, K.E. and Theodosiou, A.
MURINE GUANINE NUCLEOTIDE EXCHANGE FACTOR - (MNGEF) AND HUMAN
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80.0%; Pred. No. 2.7e+04;
tive 0; Mismatches 5; Indels
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Pred. No. 2.8e+04;
0; Mismatches 5;
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Patent: WO 9823743-A 10 04-JUN-1998;
MEDICAL RES COUNCIL (GB); DAVIES KAY
Location/Qualifiers
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Patent: US 6365344-A 12 02-APR-2002;
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1 .36
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Sequence 12 from patent US 6365344.
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Sequence 10 from Patent WO9823743.
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Unclability.
Unclaber 1 to 30)
Schalling, M., Hudson, T.J. and Housman, D.E.
Direct detection of expanded nucleotide repeats in the human genome Patent: US 5695933-A 4 09-DEC-1997;
Location/Qualifiers
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C12N15/09, C07K14/47, C07K14/705, C07K16/18, C07K16/28, C07K19/00,
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C12N15/00,C12N5/00
Description of Artificial Sequence: Synthetic
Location/Qualifiers
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60/059121,17-SEP-1997 US

60/059113,17-SEP-1997 US

60/059266,15-0CT-1997 US

60/062287,17-OCT-1997 US

60/063287,17-OCT-1997 US

60/063180,24-0CT-1997 US

60/063180,24-0CT-1997 US

60/063120,24-0CT-1997 US

60/063120,24-0CT-1997 US

60/063120,27-0CT-1997 US

60/063120,27-0CT-1997 US

60/063129,27-0CT-1997 US

60/063129,28-0CT-1997 US

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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PR 17-SEP-1997 US 60/0591:
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Canis familiaris mRNA for class IVb beta-tubulin, partial cds.
AB022058
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Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.
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Submitted (06-JAN-1999) Katsuhiko Arai, Tokyo University of
Submitted (06-JAN-1999) Katsuhiko Arai, Tokyo University of
Agriculture and Technology, Faculty of Agriculture; Salwai-cho,
3-5-8, Fuchu, Tokyo 183-8509, Japan (E-mail:karai@cc.tuat.ac.jp,
Tel:81-42-367-5789(ex.5106), Fax:81-42-367-5787)
On Mar 16, 2001 this sequence version replaced gi:8247713.
Location/Qualifiers
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Location/Qualifiers
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Expression of Class II (beta.Pribulin by Proliferative
Myoepithelial Cells in Canine Mammary Mixed Tumors
Vet. Pathol. 40 (6), 670-676 (2003)
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/product="class IVb beta-tubulin"
/protein_id="BAA96413.2"
/db_xref="GI:13365823"
/txanslation="AREEGGEFEERAEEEVA"
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/note="isotype-specific region"
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/mol_type="mRNA"
/db_xref="taxon:9615"
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       Mismatches
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Schälling,M., Hudson,T.J. and Housman,D.E.
Direct detection of expanded nucleotide repeats in the human genome
Patent: US 5695933-A 9 09-DEC-1997;
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Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular cloning of isotype-specific regions of five classes of canine beta-tubulin and their tissue distribution
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Submitted (06-JAN-1999) Katsuhiko Arai, Tokyo University of
Submitted (06-JAN-1999) Katsuhiko Arai, Tokyo University of
Agriculture and Technology, Faculty of Agriculture; Saiwai-cho,
3-5-8, Fuchu, Tokyo 183-8509, Facili Karail: karai@cc.tuat.ac.jp,
Tel:81-42-367-5789(ex.5106), Fax:81-42-367-5787)
On Mar 16, 2001 this sequence version replaced gi:8247707.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 6; Length 39;
Pred. No. 2.7e+04;
0; Mismatches 5; Indels
                                                                                                                     linear
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/product==class II beta-tubulin"
/protein_id="BAA96410.2"
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/wol_type="unassigned DNA"
                                                                                                                   184408 39 bp
Sequence 9 from patent US 5695933.
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/db_xref="taxon:9615"
Location/Qualifiers
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Matches 20; Conservative
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Unclassified.
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Best Local Similarity
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AB022055/c LOCUS

RESULT 18

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DEFINITION ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE

REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

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Gaps

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PAT 17-DEC-2001

linear

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BD223995 50 bp DNA linear PAT 17-JUL-2003 Near infrared chemiluminescent acridinium compounds and uses thereof.
BD223995.1 GI:33033765
                                                                                                                                                                                                                                   Unknown.
Unclassified.
Unclassified.
Crosset,J., Scheman,D. and Wils,P.
Purification of a triple helix formation with an immobilized oligonucleotide
Patent: US 6287762-A 17 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 50)
Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
Purification of a triple helix formation with an immobilized
oligonucleotide
Patent: US 6319672-A 17 20-NOV-2001;
Location/Qualifiers
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Sequence 17 from patent US 6287762.
AR167590
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/organism="unknown"
/mol_type="unassigned DNA"
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AR178300/c
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unclassified.
1 (bases 1 to 50)
Crouzet,J., Scherman,D. and Wils,P.
PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN IMMOBILIZED
OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                    Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B. Purification of a triple helix formation with an immobilized oligonucleotide
Patent: Wo 0192511-A 34 06-DEC-2001;
Aventis Pharma (FR)
Location/Qualifiers
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                                                  Length 48;
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                                               65.4%; Score 17; DB 6; I
llarity 80.0%; Pred. No. 2.6e+04;
Conservative 0; Mismatches 5;

    .48
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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    .50
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                  AX323399 48 bp
Sequence 34 from Patent WO0192511.
AX323399
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Sequence 17 from Patent WO9618744.
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A51711.1 GI:2304515
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synthetic construct
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Gaps

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PAT 20-APR-2002

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                Crouzet, J., Scherman, D., Wils, P., Blanche, F. and Cameron, B. Purification of a triple helix formation with an immobilized oligomucleotide
Patent: WO 0192511-A 17 06-DEC-2001;
Aventis Pharma (FR)
Location/Qualifiers
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Patent: EP 1281774-A 17 05-FBB-2003;
Aventis FP harma 8.A. (FR)
Location/Qualifiers
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"Organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="synthetic oligonucleotide"
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Pred. No. 2.6e+04;
0; Mismatches 5;
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Sequence 13556 from Patent WO0192524.
CQ628816.1 GI:41679034
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Sequence 17 from Patent EP1281774.
AX686852
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     AX323382.1 GI:18094144
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Best Local Similarity 80.00,
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Homo sapiens
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                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [7 [base] 1 to 50]
Natrajan, A., Jiang, Q., Sharpe, D. and Law, S.J.
Near infrared chemiluminescent acridinium compounds and uses
                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                 DS Homo sapiens (human)
PN JP 2002522530-A/4
PD 23-JUL-2002
PD 23-JUL-2003
PP 10-AUG-1999 US 60/096073
PP 10-AUG-1999 US 60/096073
PP ANAND NATRAJAN, QINGPING JIANG, DAVID SHARPE, SAY JONG LAW COTD219/04, COTD401/12, CO9K3/00, CO9K11/07, C12N15/09, C12Q1/68, 102011/76, C001013/58/C07K14/765, C07K16/26, G01N13/532, C12N15/00 CC VANCO B PMP-PROBE 496.20 (ON PMP) IN EXAMPLE 16 FH Key
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Natrajan, A., Jiang, Q., Sharpe, D. and Law, S.-J.
Near infrared chemiluminescent acridinium compounds and uses thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 65.4%; Score 17; DB 6; Length 50; Similarity 80.0%; Pred. No. 2.6e+04; 20; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                  Patent: JP 2002522530-A 4 23-JUL-2002;
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/organism="unknown"
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T misc_feature (223). .(223).
Location/Qualifiers
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Location/Qualifiers
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Sequence 17 from Patent WO0192511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
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JP 2002522530-A/4.
Homo sapiens (human)
Homo sapiens
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AR200395/c LOCUS

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Polynuclectide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 13556 03-FEB-2004;
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 25) Gu,Y.,\ Ji,Y.,\ Penn,S.G.,\ Hanzel,D.K.,\ Rank,D.R.,\ Chen,W.\ and\ Shannon,M.E.
                                                                                          Score 16.6; DB 6; Length 25;
Pred. No. 4.1e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.8%; Score 16.6; DB 6; Length 25; ilarity 82.6%; Pred. No. 4.1e+04; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                     25 bp DNA
Sequence 13556 from patent US 6686188.
AR469879
   /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/wol_type="genomic DNA"
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ilarity 82.6%;
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Matches 19;
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AR469879/c
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AR469880/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13556 06-DEC-2001;
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Shannon,M.E.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13558 06-DEC-2001;
Aeomica, Inc. (US)
10. 25
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Patent: WO 0192524-A 13557 06-DEC-2001;
                                                                                                                                                                                                                       Length 25;
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Pred. No. 4.1e+04;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                         25 bp DNJ Sequence 13557 from Patent W00192524. CQ628817. GI:41679035
                                                                                                                           /organism="Homo sapiens"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                    Aeomica, Inc. (US)
Location/Qualifiers
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Location/Qualifiers
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Best Local Similarity 82.6%;
Matches 19; Conservative 0
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Matches 19; Conserva
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CQ628817/c
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CQ628818/c
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REFERENCE AUTHORS

AR469881/c

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Hourz,R.L.
Cloning and developmental expression of pea
ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
N-methyltransferase
Patent: US 5723752-A 36 03-MAR-1998;
Locaion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 48)
Berlin, V., Chiu, M. Isabel., Cottarel, G. and Damagnez, V.
Immunosuppressant target proteins
Patent: US 6127521-A 7 03-OCT-2000;
                                                                                                                                                                                                                             Length 42;
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Berlin, V., Chiu, M.I., Cottarel, G. and Damagnez, V. Immunosuppressant target proteins
Patent: US 6464974-A 7 15-OCT-2002,
Location/Qualifiers
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Pred. No. 3.9e+04;
0; Mismatches 4;
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82.6%; Pred. No. 3.8e+04;
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/organism="unknown"
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ARII1808.1 GI:12828656
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Sequence 7 from patent US 6464974.
AR236256.1 GI:27280077
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/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 82.6%;
Matches 19; Conservative (
                                 (bases 1 to 42)
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                  Unclassified.
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Best Local Similarity
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AR111808/c
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AR236256/c
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                                                                                                                                                                                                                                                          Polynuclectide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 13558 03-FEB-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning and developmental expression of pea
ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
epsilon N-methyltransferase
Patent: US 58665944.A 36.D-FEB-1999;
Location/Qualifiers
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                                                                                                                                                                                          Unclassified.
1 (bases 1 to 25)
(Su,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shamon,M.E.
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Sequence 36 from patent US 5866394.
AR031676
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/mol_type="unassigned DNA"
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Sequence 36 from patent US 5723752.
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/organism="unknown"
/mol_type="genomic DNA"
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24 CTCCTTCTTGGCTTCCTCCAGCT
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Best Local Similarity
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DEFINITION ACCESSION VERSION

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AUTHORS TITLE

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RESULT 35 AR031676/c

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1 (bases 1 to 28)
Liotta, D.C., Petros, J.A., Wey, S.-J., Karr, J.F. and Pohl, J.
Polycationic oligomers
Patent: US 615356-A 2 28-NOV-2000;
Location/Qualifiers
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Unknown.

Unclassified.

E 1 (bases 1 to 48)

S Berlin, V., Chiu, M.I., Cottarel, G. and Damagnez, V.
Immunosuppressant target proteins

AL Patent: US 6509152-A 7 21-JAN-2003;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.8%; Score 16.6; DB 6; Length 48; Best Local Similarity 82.6%; Pred. No. 3.8e+04; Matches 19; Conservative 0; Mismatches 4; Indels
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/organism="unknown"
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                                                                                                                                       AR275530 48 bp
Sequence 7 from patent US 6509152.
AR275530 GI:29708948
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Sequence 2 from patent US 6153596.
AR120088.1 GI:14102787
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/organism="unknown"
/mol_type="genomic DNA"
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Search completed: November 18, 2005, 17:43:00 Job time : 723.476 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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OM nucleic - nucleic search, using sw model

November 18, 2005, 05:29:23; Search time 179.034 Seconds Run on:

(without alignments) 859.686 Million cell updates/sec

US-10-788-779-8 26

1 CCCTCCTTCTTGTACTCCTCCTGCTC 26 score: Perfect sc Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4167226 Total number of hits satisfying chosen parameters:

4390206 seqs, 2959870667 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:*geneseqn2002bs:* N Geneseq 16Dec04:* geneseqn1980s:* geneseqn1990s:* Database :

geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2003ds: geneseqn2004as:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqn2004bs:

SUMMARIES

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Score	26	26	56	18.6	18.6	18.4	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2
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24 9 ACD66957 24 9 ACD83118 24 9 ADA46240 24 9 ADA46240 24 9 ADA4385 24 9 ADA16664 24 9 ADA41961 24 9 ADA41308 24 9 ADA42811 24 9 ADA42811 24 10 ADB74866	
177.22.22.22.22.22.22.22.22.22.22.22.22.2	17.2 17.2 17.2 17.2 17.2 17.2 17.2 17.2

ALIGNMENTS

Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy; diagnosis; primer; mutation; detection; ss. Beta-cardiac myosin heavy chain PCR primer D' (HARD) HARVARD COLLEGE. (BGHM) BRIGHAM & WOMENS HOSPITAL. (GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA. AAQ91128 standard; cDNA; 26 BP 92US-00989160. 92US-00989160. 19-FEB-1996 (first entry) 11-DEC-1992; 11-DEC-1992; US5429923-A. 04-JUL-1995. Synthetic. AAQ91128; RESULT 1 AAQ91128

Watkins H, Rosenzweig Seidman C, Seidman J,

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WPI; 1995-245715/32.

Example 1; Col 10; 22pp; English

Non-invasive method for diagnosis of hypertrophic cardio-myopathy useful for testing asymptomatic individual(s).

AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hyperrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

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asymptomatic individuals suspected of having the disease. The method has a broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease and phenylketonuria
                                                                                                                                                                                                                                                                                                                                           Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC; familial hypertrophic cardiomyopathy; SHC; Gaucher's disease; sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia; buchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease; phenylketonuria; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting a presence or absence of a mutation associated with hypertrophic cardiomypathy, useful for diagnosing cystic fibrosis or hemophilia, by detecting a mutation in an amplified product of a beta cardiac myosin heavy-chain DNA.
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                                                                                                     DB 2; Length 26;
                                                                                                                            0; Indels
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                                                                            Seguence 26 BP; 1 A; 13 C; 2 G; 10 T; 0 U; 0 Other;
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SEIDMAN J.
WATKINS H.
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associated with hypertrophic cardiomyopathy (sporadic or familial, SHC and FHC) comprises detecting a mutation associated with hypertrophic cardiomyopathy in an amplified product of a beta cardiac myosin heavy chain DNA. The mutations associated with SHC/HC are detected in the myosin gene isolated from blood, by detecting mis-marched areas in RNA-DNA hybrid double strands (RNA from the normal gene, DNA from the suspect sample). FHC associated point mutation can be classified and used to determine life expectancy in affected individuals e.g. using a Kaplan-Meier curve for the classified type of FHC causing point mutation. Also included are an RNA probe comprising ribonucleotides arranged in a sequence which is complementary to at least a portion of beta-cardiac myosin heavy-chain DNA and a set of DNA oligonucleotide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

mutation

The invention relates to detecting the presence or absence of a

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oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain DNA. The method is useful for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. This method is especially useful for diagnosing SHC and FHC, as well as for determining the estimated the life expectancy of a person with familial hypertrophic cardiomyopathy. In particular, the method is useful for determining an individual's genetic information, and diagnosing e.g. Gaucher's disease, hacmophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Taysachs disease, heapth stronuria or cystic fibrosis. The present sequence is a nested PCR primer used to amplify a region of the beta cardiac myosin heavy chain cDNA containing an FHC-associated mutation
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                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC;
familial hypertrophic cardiomyopathy;
sporadic hypertrophic cardiomyopathy.
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95US-00469172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR05304 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                        26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROSENZWEIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-592586/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEIDMAN C.
SEIDMAN J.
WATKINS H.
                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR05304;
                                                                                                                                                                                                                                                                     Query Match
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(WATK/)
(ROSE/)
                                                                                                                                                                                                                                                                                         Best Local
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cardiomyopathy associated mitration in the beto of detecting a hypertrophic cardiomyopathy by being capable of detecting a hypertrophic cardiomyopathy cardiomyopathy (comprising the diagnosis of hypertrophic cardiomyopathy (comprising a first container diagnosis of hypertrophic cardiomyopathy (comprising a first container cardiomyopathy associated mutation, a second container of holding primers for amplifying beta-cardiac myosin heavy-chain DNA, and and the components of the kit to detecting a more cardiomyopathy-associated mutation, a second container cardiomyopathy-associated mutation in holding primers for amplifying beta-cardiac myosin heavy-chain DNA and instructions for using the components of the kit to detect the presence or absence of a hypertrophic cardiomyopathy cardiomyopathy cansociated mutation in amplified beta-cardiac myosin heavy-chain DNA). The method is used for detecting the presence or absence of a mutation associated with chypertrophic cardiomyopathy for facilitating the diagnosis of for hypertrophic cardiomyopathy relies on the presence of typical chypertrophic cardiomyopathy relies on the presence of typical chypertrophy. The present invention is une-invasive and based, at least in part, on the discovery that hypertrophic cardiomyopathy is caused by point mutations in the beta cardiac myosin heavy-chain gene. Prior art creveals that there are no extensive studies involving a large number of families which established that this particular disease or disorder was caused by point mutations in the beta cardiac myosin heavy-chain gene and in the beta cardiac myosin heavy-chain gene.

The present sequence is a PCR primer used to amplify a region of the beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiac myosin heavy chain having a disease-related point mutation.
amplify beta-cardiac myosin heavy-chain DNA (the set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 BP; 1 A; 13 C; 2 G; 10 T; 0 U; 0 Other;
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Gaps ö ch 100.0%; Score 26; DB 13; Length 26; Similarity 100.0%; Pred. No. 2.8; 26; Conservative 0; Mismatches 0; Indels CCCTCCTTCTTGTACTCCTCCTGCTC 26 1 CCCTCCTTCTTGTACTCCTCCTGCTC 26 Local Similarity Best Loca Matches ð

Polyanionic polymer related oligonucleotide #47. ABZ22093 standard; DNA; 50 (first entry) 11-MAR-2003 ABZ22093;

BP

Polyanionic polymer; bioactivity; water solubility; ss. WO200277036-A2. 03-0CT-2002 Synthetic.

21-MAR-2002; 2002WO-US008614. 21-MAR-2001; 2001US-0277705P

Lofquist A, Pietz GE, Bergman PA, (LEUN/) LEUNG D W. Waggoner DW; Leung DW,

WPI; 2003-058367/05.

Tompkins CK;

Producing monodispersed preparation of polyanionic polymer for therapy, by expressing vector comprising ligation product of oligonucleotides encoding glutamate/aspartate residues in host cell and isolating the product

Disclosure; Fig 5; 74pp; English

The present invention describes a method (M) for producing a monodispersed preparation of a polyanionic polymer (PP) larger than 10 CC Monodispersed preparation of a polyanionic polymer (EV) a ligation product formed by ligating together oligomuclectides that encode glutamate/aspartate residues, expressing EV in a host cell, and isolating compressing EV in a host cell, and isolating compressing EV in a host cell, and isolating compressing to the protein product (P) of EV, where (P) is PP and at least 80% of PP is approximately of the same molecular weight. Also described: (1) a compressing a polyanionic polymer and comprise to polyanionic polymer and at polyanionic polymer polyanionic polymer is polyanionic polymer is polyanionic polymer is polyanized and in a vector (III) comprising a polyanionic polymer is polyanized and at comprise a nucleotide sequence encoding a polyanionic polymer is polyanized and or polyanized sequence encoding a polyanionic polymer is polyanized acid or polyaspartic acid; (4) production of (I); (5) a cell (IV) comprising (III) or a vector that is larger than 10 kDa; and (6) a recombinantly-produced polyanionic polymer (V) that is of any molecular combinantly-produced polyanionic polymer (V) that is of any molecular combinatering (I) to the individual. (I) is also useful for delivering an effective amount of a pharmaceutically active agent, a therapeutic and ceffective amount of a pharmaceutically active agent, a therapeutic protein or a drug to a patient in need of it, or for diagnostic and testing or research purposes. ABZ22045 to ABZ22131 and ABB56374 to ABB56400 represent sequences used in the exemplification of the present invention 88999999999999999999999

Sequence 50 BP; 1 A; 24 C; 1 G; 24 T; 0 U; 0 Other;

Gaps ö Score 18.6; DB 10; Length 50; Pred. No. 1.5e+03; 0; Mismatches 4; Indels (71.5**%**; 84.0**%**; 21; Conservative Best Local Similarity Query Match datches

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2 CCTCCTTCTTGTACTCCTCCTGCTC 26 21 CCTCCTTCTTCTTCTCTCTTCTCTCTC

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45

ABZ22129 standard; DNA; 50 BP. 11-MAR-2003 (first entry) ABZ22129; RESULT 5 ABZ22129

Polyanionic polymer; bioactivity; water solubility; ss. Polyanionic polymer related oligonucleotide #83.

Synthetic.

WO200277036-A2. 03-OCT-2002

21-MAR-2002; 2002WO-US008614. 21-MAR-2001; 2001US-0277705P. (LEUN/) LEUNG D W.

Producing monodispersed preparation of polyanionic polymer for therapy, by expressing vector comprising ligation product of oligonucleotides encoding glutamate/aspartate residues in host cell and isolating the Tompkins CK; Pietz GE, Lofquist A, Bergman PA, WPI; 2003-058367/05. Waggoner DW; Leung DW,

Example 7; Fig 8; 74pp; English.

product

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The present invention describes a method (M) for producing a monodispersed preparation of a polyanionic polymer (PP) larger than 10 compodispersed preparation of a polyanionic polymer (EV) a ligation product (P) involves inserting into an expression vector (EV) a ligation product (P) of EV, where (P) is PP and at least 80% of PP is glutamate/aspartate residues, expressing EV in a host cell, and isolating comprising together coligonal product (P) of EV, where (P) is PP and at least 80% of PP is approximately of the same molecular weight. Also described: (1) a correct recombinant fusion protein (I) comprising a polyanionic polymerial and polyanionic polymer (II) comprising a polyanionic polymer and comprises a nucleotide sequence encoding a polyanionic polymer and at least one other nucleotide sequence encoding a polyanionic polymer and at least one other nucleotide sequence, where the polyanionic polymer is polygultamic acid or polyaspartic acid; (4) production of (I); (5) a cell (IV) comprising (III) or a vector that comprises a nucleotide sequence that is larger than 10 kDs; and is conjugated to another protein. (I) is useful for treating a disease or aliment in an individual by comprise than 10 kD, and is conjugated to another protein. (I) is useful for treating a disease or aliment in an individual by administering (I) to the individual. (I) is also useful for delivering and effective amount of a pharmaceutically active agent, a therapeutic protein or a drug to a patrient in need of it, or for diagnostic and the polyanion or research purposes. ABZ22045 to ABZ22011 and ABBS2014 to another process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP56400 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin heavy chain binding protein; BiP(78KD); chondrocyte;
autoantigen; rheumatoid arthritis; antiarthritic; antirheumatic; p78;
PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lanchbury JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human immunoglobulin heavy chain binding protein and encoding polynucleotide, useful for diagnosis and treatment of rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human BiP(78KD) forward PCR primer, derived from GenBank X87949.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50 BP; 1 A; 24 C; 1 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5e+03;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA30793 standard; cDNA; 32 BP.
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1 Similarity 84.0%;
21; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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arthritis.

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The invention relates to a human immunoglobulin heavy chain binding protein, BiP(78KD) (Y90693), having a 639 amino acid sequence, and to the protein, BiP(78KD) (Y90694). The invention also encompasses a BiP(78KD) protein of 633 amino acids (Y90694). The cDNA encoding BiP(78KD) also referred to as p78 in the specification, was isolated from human chondrosarcoma cell lines. The BiP(78KD) cDNA of this invention contains a number of differences compared with the published sequence (GenBank at number X87949), and has therefore has been deposited with genBank with the accession number AF188611). These differences comprise 6 single nucleotide substitutions and a codon insertion, and result in three amino acid substitutions and an arginine insertion at position 834-cc fire protein. The BiP(78KD) proteins react with matibodies present in the serum of rheumatoid arthritis patients, and is therefore a cutthritis. BiP(78KD) or peptides derived from the protein are useful as cragents to indicate the presence of rheumatoid arthritis, and can be used in prognostic or diagnostic tests of body fluids for rheumatoid arthritis by ELISA (enrywellinked immunosorbent assay) or Western blotting. The protein or the CDNA encoding it can also be used to test for rheumatoid arthritis by BiP(78KD) its peptides and polynucleotides are also useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutically. Sequences A30743-A30794 represent human BiP(78KD) PCR primers used in an exemplification of the invention for subcloning into a bacterial expression vector. The sequence of the primers are based on the previously published BiP(78KD) sequence (GenBank X87949)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zollinger Ellison syndrome; gastrointestinal ulceration; congenital microvillus arrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; transmembrane protein; human; enterocolitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 70.8%; Score 18.4; DB 3; Length 32; Local Similarity 95.0%; Pred. No. 1.7e+03; nes 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reverse PCR primer used to amplify cDNA encoding PRO263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32 BP; 13 A; 3 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wound healing; tissue repair; PCR primer; ss.
Example 2; Page 8; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CCTCCTTCTTGTACTCCTCC 21
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97US-0059115P.
97US-0059117P.
97US-0059119P.
97US-0059121P.
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17-SEP-1997;
17-SEP-1997;
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New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration.
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                                                9705-00621259-9705-0062285P-9705-0062287P-9705-0062814P-9705-0063812B-9705-0063121P-9705-0063128P-9705-0063128P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-006354P-9705-0063564P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-9705-0063733P-970
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970S-0064103P
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970S-0065809P
970S-0065846P
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970S-0066120P
970S-0066453P
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97US-0066511P.
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21-OCT-1997;
24-OCT-1997;
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28-OCT-1997
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24-0CT-19
27-0CT-19
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Yuan J; Chen J,

Example 33; Page 140; 320pp; English.

oligonuclectides AAX52276-532 represent PCR primers and probes used to isolate and amplify cDNA encoding secreted and transmembrane human proteins (see AAX52213-74 and AAY13144-403). The cDNA sequences are brain feetal brain, fetal liver and fetal retina. The cnocked polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and remaince of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriamis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's diseases, Alzheimer's diseases, Alzheimer's disease, Alzheimer's disease, PRO2533 may scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may

The polymetric state of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-Blisen syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal scarring and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple sclenosis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature aging, AIDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the PCR primer of the invention which was used to analyse the human PRO DNA of

Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.

Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;

(GETH) GENENTECH INC.

WPI; 2000-271434/23.

Chen J, Yuan J;

The invention relates to a novel nucleic acid encoding a PRO polypeptide.

Example 33; SEQ ID NO 204; 355pp; English.

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be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO267 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract
                                                                                                                                                                                                                                                                                                                                                                                   antinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic; neurotrophic; osteopathic; antiathmatic; antiarthritic; antirheumatic; antiatteriosclerotic; cardiant; antidiabetic; cerebroprotective; thrombolyric; immunomodulator; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease; Alzheimer's; ALS; neuropathy; dermal scarring; wound healing; asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder; atherosclerosis; cardiac injury; infertility; premature aging; AlDS; diabetes; stroke; gene therapy; transgenic; PRO; human; ss; primer; PCR.
                                                                                                                                              Gaps
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0
                                                                                                                Score 17.2; DB 2; Length 24;
                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                             Human PRO protein-related reverse PCR primer SEQ ID 204.
                                                                                      Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                                                              4.7e+03;
                                                                                                                               Pred. No. 4.7e
0; Mismatches
                                                                                                                                                                         S CCTTCTTGTACTCCTCCTGCTC 26
                                                                                                                                                                                         24 CCTACTACTACTCCTCCTGCTC 3
                                                                                                                                                                                                                                                                           ADC78524 standard; DNA; 24 BP.
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                                                                                                                  66.2%;
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                                                                                                                                             19; Conservative
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polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. poworlasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatorid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular phology, including use as hybridization probes, and in chromosome and gene mapping
one nucleic acids encoding novel secreted and transmembrane PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, 88; PCR; secreted protein; transmembrane protein; PRO; gene therapy; chromosome identification; chromosome marker; primer.
                                                                                                                                                                                                                                                                                                             Query Match 66.2%; Score 17.2; DB 4; Length 24; Best Local Similarity 86.4%; Pred. No. 4.7e+03; Matches 19; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                      Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
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97US-0059117P
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97US-0059124P
97US-0059263P
97US-0062287P
97US-0062287P
97US-0062281P
97US-0062814P
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97US-0063550P.
97US-0063564P.
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24-OCT-1997;
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21-0CT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory; antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antianglogenic; vasotropic; antiasthmatic; antirheumatic; cancer; antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation; PCR primer; ss.
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H, Gerritsen ME, Goddard A;
Hillan KJ, Kljavin IJ;
Stewart TA, Tumas D;
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                                                                           / Match 66.2%; Score 17.2; DB 3; Length 24; Local Similarity 86.4%; Pred. No. 4.7e+03; les 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO polypeptide gene PCR primer SEQ ID NO: 204.
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Fong S, Gao W, Gerber H, Gerritsen I,
Grimaldi CJ, Gurney AL, Hillan KJ,
Fan J, Paoni NF, Roy MA, Stewart TA,
Wood WI;
                                       Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                              99WO-US023089.
99WO-US028214.
99WO-US028564.
99WO-US028565.
99WO-US030095.
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99US-0146222P.
99WO-US020594.
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AZ
AAF72558;
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AAF72558;
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AAF72558;
XX
Human PRO polypeptide gene PC
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WHUMAN; PRO; dermatological; a
antiparkinsonian nootropic; n
Antiarthritic; antinifertili;
XX
MULianglogeni; vasotropic; n
Antiarthritic; antinifertili;
XX
MULianglogeni; vasotropic; n
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Homo sapiens.
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Homo sapiens.
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MOZ00104311-A1.
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MACO-USC-19999
MACO-US0201999

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  the invention
                                                                              Query Match
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New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, in generating probes and in tissue typing.
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                     970S-0063704P
970S-0063734P
970S-0063738P
970S-0063738P
970S-0064103P
970S-0064103P
970S-0064103P
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98WO-US019330.
98WO-US019437.
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99WO-US028564.
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Williams PM,
29-0CT-1997;
29-0CT-1997;
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20-MAR-2000;
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24-NOV-1997;
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17-SEP-1998;
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24-NOV-1997
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The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a PRO protein extracellular domain. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO

Ferrara N; n ME, Goddard A; Kljavin IJ; , Tumas D;

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polypeptide (by culturing the host cell for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture), cc an isolated PRO polypeptide (having at least 80% sequence identity to: (c a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence encoded by a nucleic acid molecule deposited with an ATCC number (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide acking its associated signal peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a RRO245 or PRO1868 in a sample suspected of containing the polypeptide, correctly a bloactive molecule to a cell expressing a PRO245 or PRO1868 in a sample suspected of containing the polypeptide, correctly and a least one biological activity of a cell expressing a PRO245 or PRO1868 in molecule to a cell expressing a PRO245 or PRO1868 in the molecule proced processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing processing a processing a processing a processing a processing processing a processing a processing a processing a processing a processing a processing a processing a processing a processing processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a processing a proc
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les 19; Conservative
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Goddard A;

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The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide comprising any of 61 sequences having 164-1119 amino acids fully defined in the Specification. The PRO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are capair, collateral blood vessel formation, canners (e.g. colorectal cancer), haemorrhage (or reduce risk for hemorrhage), rheumatoid arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs, cretenosis, dermal fibrotic conditions (e.g. keloids or scarring), cischaemia, strokes, hypertension, heart attacks, atherosclerosis, or infertility in mammals (e.g. humans, dogs, cats, atherosclerosis, or infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats, or rabbits) The PRO polypeptides are useful as targets for therpeutic intervention in these diseases, and diagnostic determination of the presence of these diseases, The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO cas molecular weight markers, or for chromosome identification. The PRO chuman cDNA, genomic DNA, mand. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene This sequence of therapy are also mand, and processed in the presence of therapy and permit a novel human secreted and transmembrane PRO polypeptide
                                                                                                    New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
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Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 66.2%; Score 17.2; DB 8; Length 24; Local Similarity 86.4%; Pred. No. 4.7e+03; nes 19; Conservative 0; Mismatches 3; Indels
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06-JAN-2000; 2000WO-US000219.
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The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) any one of 61 fully defined amino acid sequence glaven in the specification (appearing as ABU54347-ccc deposited under American Type Culture Collection (accession numbers CC listed in the specification); (c) any one of the PRO sequences which clisted in the specification); (c) any one of the PRO sequences which lacks its associated signal peptide; (d) an extracellular domain of the PRO polypeptide which lacks its associated signal peptide; or (e) an one correctly associated signal peptide; or (e) an an include are the nucleic acids encoding the PRO polypeptides, vectors, host cells and anti-PRO articodies. The PRO polypeptides and mucleic acids are useful in diagnosing or treating corrects such as squamous cell carcinoma, Alzheimer's disease, Parkinson's cancers such as squamous cell carcinoma, Alzheimer's disease, parkinson's cancers such as squamous cell carcinoma, Alzheimer's disease, e.g. cheuratoid arthritis, asthem or multiple sclerosis, organ fallure, catherosclerosis, cardiac injury, infertility, birth defects, premature disease, amyortrophic lateral sclerosis, inflammatory diseases e.g. crheuratoid arthritis, asthem or multiple sclerosis, organ fallure, catherosclerosis, cardiac injury, infertility, birth defects, premature also useful for wound repair and associated therapies concerned with re-growth of tissue. The nucleotide sequences may be used an hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules are also useful in the ergoperate transgenic animals or knockout animals, which in turn are useful in the adversagence and successing purposes. The anti-PRO antibodies may be used in electrophoresis purposes. The anti-PRO antibodies may be used in electrophoresis purposes. The anti-PRO antibodies may be breased electrophoresis purposes are com New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's Gaps Ferrara N; ME, Goddard A; ME, Goddard Kljavin IJ; ö Tumas D; 66.2%; Score 17.2; DB 8; Length 24; 86.4%; Pred. No. 4.7e+03; Live 0; Mismatches 3; Indels Botstein D, Desnoyers L, Eaton DL, 1 Fong S, Gao W, Gerber H, Gerritsen P Grimaldi JC, Gurney AL, Hillan KJ, 1 Pan J, Paoni NF, Roy MA, Stewart TA, Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other; Example 33; Page 99; 473pp; English. 2000WO-US005841. 2000WO-US007377. 2000WO-US014042. 2000WO-US01564. 2000WO-US015264. 2000WO-US015264. 2000WO-US005004 2000US-00665350 2000WO-US004414 Local Similarity 86.4 nes 19, Conservative Wood WI; (GETH) GENENTECH INC. WPI; 2003-147434/14. Pan J, 22-FEB-2000; 24-FEB-2000; 20-MAR-2000; 20-MAR-2000; 30-MAR-2000; 22-MAY-2000; 22-MAY-2000; 22-JUN-2000; 2 Ashkenazi A, Filvaroff E, Godowski PJ, Mather JP, Pa 18-SEP-2000; 28-JUL-2000; 24-AUG-2000; disease. Query Match Best Loca Matches

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Human; PCR; primer; abnormal bleeding; gynaecological disease; tumour; hysterectomy; anglogenesis; coronary ischaemic condition; skin disease; gastrointestinal mucosa disorder; acute mucosal lesion; neuropathy; ALS; chronic mucosal lesion; abnormal keratinocyte differentiation; psoriasis; parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; uncontrolled cell growth, cancer; blood coagulation cascade; thrombosis; haemorrhage; endometrial bleeding; anglogenesis; wound healing; asthma; tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing;
                                                                                       Human secreted/transmembrane polypeptide PRO263 reverse primer.
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97US - 0066840P
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(GETH) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-492258/46.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases

Example 33; Page 105; 478pp; English.

The invention relates to an isolated PRO polypeptide. PRO317 is useful in diagnosing or treating abnormal bleeding involved in gynecological diseases e.g. to avoid or lessen the need for hysterectomy. PRO317 may also be useful as an agent that affects angiogenesis and PRO317 is useful in anti-tumour indications or in treating coronary ischaemic conditions. PRO311 and PRO317 polypeptides are useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis).

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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
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                  Alzheimer's disease, amyorrophic lateral sclerosis (ALS), neuropathies and disease related to uncontrolled cell growth, e.g. cancer. PRO219 polypeptide plays a regulatory role in the blood coagulation cascade. PRO246 polypeptides which serves as tumour specific antigens may be exploited as therapeutic targets for anti-tumour drugs. PRO269 collypeptide is useful as an antithrombotic agent with reduced risk for haemorrhage as compared with hepatin. PRO317 polypeptide is useful in treating endometrial bleeding angiogenesis. PRO287 polypeptides and polypeptides are useful for treating asthma, rheumatoid arthritis, protain and multiple sclerosis. The polypeptide and its nucleic acid are useful for tissue typing. PRO antibodies are useful for tissue typing. PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity pursient sequence represents a human secreted/transmembrane PRO entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane entransmembrane en
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  PRO187 polypeptide is useful for treating Parkinson's disease,
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29-NOV-1999;
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16-DEC-1999
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21-NOV-1997
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  The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise and the nucleic acid encoding them. The polypeptide, for linking a bioactive molecule to a cell expressing a PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polymorleotides are also useful as pharmaceuticals, diagnostics, concerns or bioreactors, for detecting or treating e.g. hyperplasia, endometriosis, cancers (e.g. those involving solid tumours), ischaemia, coronary attertial disease, polycystic kidney disease, chronic or acute renal failure, or inflammatory responses (e.g. asthma, rheumatoid arthritis, psoriasis or multiple sclerosis) in mammals. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABX96017-ABX96378 are the genes encoding, the primers amplifying and the probes detecting the PRO polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                               ö
          New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245) and genes encoding them, useful for detecting or treating e.g. hyperplasia, endometriosis, cancers, ischemia, coronary arterial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease; postiasis; cancer; lung cancer; oclon cancer; nerve cell disease; Alzheimer's disease; Parkinson's disease; Usher syndrome; angiogenesis; atrophia areata; inflammatory disease; asthma; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                    Match 66.2%; Score 17.2; DB 8; Length 24; Local Similarity 86.4%; Pred. No. 4.7e+03; les 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                             Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein PRO263 reverse primer.
                                                                       Example 33; Page 105; 477pp; English.
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970S-0059117P.
970S-0059121P.
970S-0059122P.
970S-0059263P.
970S-0059266P.
970S-0062285P.
970S-0062287P.
970S-0062287P.
970S-0062287P.
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                                               or inflammations.
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17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
18-SEP-1997;
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21-OCT-1997;
24-OCT-1997;
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15-OCT-1997,
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970S-0059119P

970S-0059121P

970S-0059124P

970S-0059126P

970S-0063285P

970S-0063287P

970S-00632814P

970S-00632814P

970S-0063121P

970S-0063121P

970S-0063121P

970S-0063121P

970S-0063124P

970S-006312P

970S-006421SP

970S-006421SP

970S-006646E

970S-006646E

970S-006646E

970S-006645B

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970S-006646E

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98WO-US019437.
98US-0104080P.
98US-0109304P.
98WO-US025108.
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99US-0146222P.
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15-OCT-1997;
17-OCT-1997;
17-OCT-1997;
24-OCT-1997;
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17-SEP-1997;
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17-SEP-1997;
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28 OCT - 1997;
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                                                                                                                                                                                                                                                                                                                                                                               The invention relates to sixty one nucleic acids encoding PRO
polypeptides (secreted and transmembrane). The polynucleotide is useful
in molecular biology, including uses as hybridisation probes, in
chromosome and gene mapping, in generating antisense RNA and DNA, and in
gene therapy. The polynucleotide may also be used in preparing PRO
polypeptides by recombinant techniques, and in generating PRO
transgenic animals or knock-out animals which, in turn, are useful in the
development and screening of therapeutically useful reagents. The PRO
polypeptide or the antibody is used in preparing a medicament for
treating a condition responsive to the polypeptide or antibody, such as
mucosal lesions e.g. ulcars and enterocollitis, skin disease e.g.
psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease
e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,
atrophia areata, anglogenesis, inflammatory disease e.g asthma and
rheumatoid arthritis, ischaemia, and in various diagnostic assays. The
present sequence represents an PCR primer used in isolating a PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; 88; PCR; primer; gene therapy; tumour; tissue typing; obesity; diabetes; hypoinsulinaemia; hyperinsulinaemia; vascular permeability; cardiac insufficiency disorder; immune response; regeneration; cartilage; auditory hair cell; hearing loss; bone disorder; sports injury; arthritis.
                                                                                                                                                                                                                                                                       Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in treating cancer and Alzheimer's disease.
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                                                                                                                               Ferrara N;
ME, Goddard A;
Kljavin IJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.2%; Score 17.2; DB 8; Length 24; Best Local Similarity 86.4%; Pred. No. 4.7e+03; Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                        Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Frivaroff E, Fong S, Gao W, Gerber H, Gerritsen N Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, i Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
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02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US03328.
18-SEP-2000; 2000US-00665350.
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                                                                                       (GETH ) GENENTECH INC.
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5 CCTTCTTGTACTCCTCCTGCTC 26

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The invention relates to an isolated, secreted and transmembrane polypeptide, termed PRO polypeptide. The polypeptide is useful for identifying agonists or antagonists of the polypeptide, for preparing variants of the polypeptide. The polypeptide is useful for recombinantly electrophoresis purpose and the nucleic acid is useful for recombinantly expensing those markers. The polypeptide is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. The nucleic acid is useful as therapeutic acid is useful as therapeutic acid in the development and screening of therapeutically useful activolved in the development and screening of therapeutically useful activolates the PRO and for the generic analysis of individuals which encodes the PRO and for the generic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes for polymerase chain reaction (PCR), or useful in diagnostic assays for prolymerase chain reaction of PRO, is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of FRO from recombinant cell culture or natural sources. The polypeptide or its antibody is useful for the preparation of medicament for treating conditions which is responsive to the PRO polypeptide or anti-PRO antibody is useful for the preparation of medicament for treating obesity, diabetes or hypo- or hypor-insulinaemia and cardiac insulficiency disorders, for inhibiting tumour growth, enhances vascular permeability and immune response, for inducing regeneration of auditory hair cells and for reating bearing loss in mammals and for treating bone and/or cartilage represented bear and arthiring the present sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
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                                                        02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030095.
20-JAN-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US00565.
22-FEB-2000; 2000WO-US005641.
24-FEB-2000; 2000WO-US005641.
26-MAR-2000; 2000WO-US005841.
26-MAR-2000; 2000WO-US005841.
26-MAR-2000; 2000WO-US005841.
27-MAR-2000; 2000WO-US006841.
28-JUL-2000; 2000WO-US015264.
                   99WO-US028301
99WO-US028564
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Human; secreted and transmembrane protein; gene therapy; psoriasis; entercolitis; gastrointeetinal ulceration; skin disease; keratinocyte differentiation; epithelial cancer; Alzheimer's disease; squamous cell carcinoma; Parkinson's disease; inflammatory disease; amyotrophic lateral sclerosis; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; atherosclerosis; cardac injury; infertility; birth defect; premature aging; AIDS; cancer; diabetic complication; wound repair; tissue re-growth; PCR; primer; ss.
                                                                                                                                       Novel secreted and transmembrane protein associated primer #89.
CCTACTACTACTCCTCCTGCTC 3
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9705-0059115P

9705-0059115P

9705-0059121P

9705-0059122P

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9705-0062285P

9705-0062285P

9705-0062285P

9705-0062285P

9705-0062285P

9705-0062285P

9705-0062285P

9705-0063124P

9705-0063124P

9705-0063124P

9705-0063124P

9705-0063124P

9705-0063542P

9705-0063544P

9705-0063543P

9705-0063738P

9705-0063738P
                                                                    ACA54975 standard; DNA; 24 BP
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97US-0065186P.
97US-0065846P.
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                                                                                                                 05-JUN-2003 (first entry)
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17-NOV-1997;

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97US-0066120P
97US-0066364P
97US-0066418P
97US-006611P
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16-DEC-1999;
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski FJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-341586/32.

New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease.

Example 33; Page 99; 473pp; English.

The invention describes sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as squamous

27-OCT-1997

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Human; 88; PCR; primer; gene therapy; apoptosis; bleeding; tumour; ALS; ynaccological disease; hysterectomy; angiogenesis; skin disease; cancer; coronary ischaemic condition; gastrointestinal mucosa disorder; asthma; mucosal lesion repair; keratinocyte differentiation; psoriasis; parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; neuropathy; blood coaquiation cascade disorder; thrombosis; haemorrhage; neurodegenerative disease; endometrial bleeding; wound healing; tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral Socierosis, inflammatory diseases, e.g. rheumatorid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with regrowth of tissue. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This sequence represents a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted / transmembrane polypeptide PRO263 reverse primer.
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4.7e+03;
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Pred. No. 4.7e+
0; Mismatches
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970S-0063121P
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86.4%;
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18-SEP-1997;
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Goddard A; Kljavin IJ;

Gerritsen ME,

Tumas D;

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The invention relates to an isolated secreted and transmembrane PRO polypeptides are useful for modulating biological activity of a cell, in diagnosing or treating abnormal bleeding involved in gynaecological diseases e.g. to avoid or lessen the need for hysterectomy, for treating angiogenesis, tumour, coronary ischaemic condition, disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal elsions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), neuropathies, disease cascade disorders, neurodegenerative disease, thrombosis, haemorrhage, endometrial bleeding, wound healing, tissue repair, asthma, rheumatoid arthritis, multiple sclerosis. Nucleic acid encoding PRO polypeptides are useful in molecular biology including uses as hybridisation probes and in the generating transgenic animals or knockout animals. The PRO antibodies are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for pro affinity purification of PRO from recombinant cell culture or natural coursemenbrane PRO polypeptides a human secreted and course. The present sequence represents a human secreted and course.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal mucosa, mucosal lesion, skin disease, keratinocyte differentiation, psoriamis; Parkinson's disease, Alzheimer's diseases, amyotrophic lateral sclerosis; ALS, neuropathy; cell growth, cancer, tumour, viral infection, neurodegenerative disease, antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; kidney tissue, apptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
                                                                                                  Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.2%; Score 17.2; DB 9; Length 24; 86.4%; Pred. No. 4.7e+03;
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Codowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, F Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Williams PM, Wood WI;
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ADB29409 standard; DNA; 24
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2000WO-US015264. 2000WO-US020710. 2000WO-US023328. 2000US-00665350. 99WO-US028301. 99WO-US028564. 99WO-US028565. 99WO-US028214. 2000WO-US003565. 2000WO-US004414. 2000WO-US008439. 2000WO-US014042. 99WO-US030095 99WO-US030911 99WO-US030999 2000WO-US000219 2000WO-US005044 2000WO-US005841 2000WO-US007377 05-JAN-2000; 11-FEB-2000; 22-FEB-2000; 01-DEC-1999; 02-DEC-1999; 02-DEC-1999; 16-DEC-1999; 20-DEC-1999; 20-DEC-1999; 24-FEB-2000; 02-MAR-2000; 20-MAR-2000; 30-MAR-2000; 22-MAY-2000; 02-JUN-2000;

(GETH) GENENTECH INC.

Desnoyers L, Eaton DL, Ferrara N; W, Gerber H, Gerritsen ME, Goddard A; Gurney AL, Hillan KJ, Kljavin IJ; NP, Roy MA, Stewart TA, Tumas D; Ashkenazi A, Botstein D, Des Filvarcff E, Fong S, Gao W, Godowski PJ, Grimaldi JC, Gu Mather JP, Pan J, Paoni NF, Williams PM, Wood WI;

WPI; 2003-765473/72.

Novel isolated native PRO polypeptide useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration, Alzheimer's disease, amyotrophic lateral sclerosis, Usher syndrome.

Example 33; Page 96; 469pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for Inking a bloactive molecule to a cell expressing a PRO polypeptide, for Inking a conscience molecule to a cell expressing a PRO polypeptides are useful for catecting other PRO polypeptides in a sample and for linking a conscience molecule to a cell expressing a PRO polypeptides are useful for modulating the biological activity of a cell expressing PRO polypeptides. PRO polypeptides are also useful conflict antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. PRO polypeptides are also useful conflictestinal mucosa and the repair of acute and chronic mucosal of gastrointestinal mucosa and the repair of acute and chronic mucosal conflictestinal mucosa and the repair of acute and chronic mucosal estimates, skin disease related to uncontrolled cell growth, e.g. cancer. Conflictestinally, disease related to uncontrolled cell growth, e.g. cancer. PRO polypeptides at herapeutic trargets for anti-tumour druggs, and are also employed therapeutically in vivo for lessening the effects of viral intection. The PRO polypeptides can be also used in assays to determine intection. The PRO polypeptides can be also used in assays to determine intervention of antithrombotic agent with reduced risk for haemorrhage as compared with heapearing other PRO-associated diseases or their reversal, as an antithrombotic agent with reduced risk for haemorrhage as compared with heapearing other PRO-associated diseases or their reversal, as an entithrombotic agent with reduced risk for haemorrhage as compared to generating other and angeled and their portions affect the expression of commertial bleeding angiogenesis, and may also have an effect on kidney to isolate the full-length PRO cDNA or to isolate other cDNAs, in concludation and gene mapping, in the generation of antisense and gene mappi

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98WO-US019330.
98US-0100858P.
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           28-0CT-1997;
28-0CT-1997;
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28-0CT-1997;
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05-JAN-2000;
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          therapeutic agents, for screening compounds to identify those that minic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists) rhe polymucleotides and proteins are useful for tissue typing. PRO antibodies are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to amplify a PRO polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                           Human; PCR; primer; ss; PRO; secreted; transmembrane; gastrointestinal mucosa; mucosal lesion; skin disease; skratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
are useful as molecular marker for protein electrophoresis purposes, as
                                                                                                                                                                                                         Gaps
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                                                                                                                                                                               Query Match 66.2%; Score 17.2; DB 9; Length 24; Best Local Similarity 86.4%; Pred. No. 4.7e+03; Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Human secreted/transmembrane protein, #40, PCR primer #3.
                                                                                                                                                         Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
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970S-0059117P
970S-0059121P
970S-0059122P
970S-0059184P
970S-0059263P
970S-0063263P
970S-0062285P
970S-0062287P
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970S-0063486P
970S-0063486P
970S-0063120P
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970S-0063120P
970S-0063120P
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ADA18265/C
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ACD66957 standard; DNA; 24 BP.

17-SEP-2003 (first entry)

ACD66957;

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the invention distillation that the polypoptides can be used to raise and the muclat acid encoding them. The polypoptides can be used to raise and the muclate that specifically bind to the PRO polypeptide for linking a bioactive molecule to a cell expressing a PRO polypeptide for inking a conflower that specifically bind to the PRO polypeptide. The PRO polypeptides are useful a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. PRO polypeptide are also useful for reducing disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal estimates, skin diseases associated with abnormal keratinocyte differentiation (e.g. peortasis) Parkinson's disease, amyotrophic lateral sclerosis (ALS), neuropathies and additionally, disease related to uncontrolled call growth, e.g. cancer. Company and the properties as tumour specific antiques which may be exploited as therapeutic lateral sclerosis (ALS), neuropathies and additionally disease related to uncontrolled call growth, e.g. cancer. Company at the PRO polypeptides can be also used in assays to determine infection. The PRO polypeptides can be also used in assays to determine infection. The PRO polypeptides can be also used in assays to determine infection. The PRO polypeptides can be also used in assays to determine infection. The PRO polypeptides can be also used in acreased of company of the properties as tumour specific antithrombotic agant with reduced risk for haemorrhage as compared with here a role in apportoins. The polymeticetical sclenar which have a role in apportoins. The polymeticetical and proteins are useful and may also have an effect on kindle concentary briefly and protein and for chromosome and gene mapping, in the generation of antisense RNA and concentary of individual which have a role in apportoines, and protein and concentary of re
                                                                                                                                                                                                                                                                                                                                                                  The invention discloses isolated PRO secreted/transmembrane polypeptides
                                                                                                                                                                                                                       New secreted and transmembrane polypeptides useful for treating skin, neurodegenerative diseases, asthma, rheumatoid arthritis, psoriasis and
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                                      Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; an J, Paoni NP, Roy MA, Stewart TA, Tumas D;
                                                                                                                                                                                                                                                                                                                   Example 33; SEQ ID NO 204; 471pp; English.
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Ashkenazi A, Boter,
Filvaroff E, Fong S, Gau-
Godowski PJ, Grimaldi JC,
Fer JP, Pan J, Paoni
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                                   66.2%; Score 17.2; DB 9; Length 24; 86.4%; Pred. No. 4.7e+03; ive 0; Mismatches 3; Indels
Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
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                                                      86.4%;
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Best Local Similarity 86.4
Matches 19; Conservative
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RESULT 21 ACD66957/c

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rheumatoid arthritis; psoriasis; multiple sčlerosis; atherosclerosis; infertility; blth défect; premature aging; malignancy; cancer; stroke; heart attack; hypertension; gastrointestinal ulceration; Parkinson's disease; Alzheimer's disease; AIDS; cholesterol uptake;
                                                                  Human; 88; PRO; secreted and transmembrane protein; inflammation;
                                                 Human secreted/transmembrane protein PRO263 PCR primer #3.
                                                                                                           wound healing; tissue repair; gene therapy.
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97US-0063486P
97US-0063414P
97US-0062814P
97US-0063120P
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97US-0066772P.
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99WO-US028564.
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99WO-US030095.
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98US-0100262P.
98WO-US019177.
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99US-0145698P.
99US-0146222P.
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2000WO-US014042.
2000WO-US015264.
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Ferrara N; ME, Goddard A; Kljavin IJ; Tumas D; Botstein D, Desnoyers L, Eaton DL, Fong S, Gao W, Gerber H, Gerritsen Grimaldi JC, Gurney AL, Hillan KJ, Pan J, Paoni NF, Roy MA, Stewart TA, Wood WI; Ashkenazi A, Botste Filvaroff E, Fong S Godowski PJ, Grimal Mather JP, Pan J, Williams PM,

WPI; 2003-512316/48.

New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO1868), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, AIDS or multiple sclerosis in mammals.

Example 33; Page 100; 476pp; English.

The invention relates to an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nuclectide encoding any of 61 PRO (secreted and transmembrane protein) polypeptides appearing as ABO32756-ABO32816, or (b) any of 61 nuclectide sequences having 50-4053bp fully defined in the specification; or the full length coding sequence of polypeptide (lacking its associated signal peptide or an extracellular peptide (lacking its associated signal peptide or an extracellular peptide, a vector comprising the nucleic acid molecule. A host cell comprising the vector (used to produce the PRO polypeptide), a chimaeric acid sequence, an anti-PRO anti-PRO anti-PRO proposed to a heterologous amino acid sequence, an anti-PRO anti-PRO, decerting PRO245 or PRO1868 polypeptide in a sample suspected of containing any of these PRO polypeptides, linking a bioactive molecule to a cell expressing a PRO245

24-OCT-1997; 24-OCT-1997; 24-OCT-1997;

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or PRO1868 polypeptide and modulating at least one biological activity of a cell expressing the PRO245 or PRO1868 polypeptide. The PRO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for diagnostics, biosensors or bioreactors. These are particularly useful for diagnostics, biosensors e.g. inflammations, rheumatoid arthritis, psoriasis, multiple sclerosis, atherosclerosis, infertility, birth defects, premature aging, malignancy (e.g. cancers), strokes, heart attacks, hypertension, gastrointestinal ulcerations, Parkinson's diseases, Alzheimer's disease, or AIDS in mammals. These are also useful for modulating cholesterol uptake in the cody, and in wound healing or tissue repair. The PRO polypeptides are useful in drug screening. The PRO polypeptides are also useful as hybridisation probes, or for screening libraries of human contains the replacing a defective gene. The present charapy, particularly for replacing a defective gene. The present sequence is an oligonucleotide (PCR primer or probe) used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; PRO; primer; ss; secreted polypeptide; transmembrane polypeptide; abnormal bleeding; gynaecological disease; hysterectomy; mucosal lesion; coronary ischaemic condition; gastrointestinal mucosa; skin disease; ALS; keratinocyte differentiation; psortiasis; Parkinson's disease; asthma; Alzhaimer's disease; rheumatoid arthritis; multiple sclerosis; cancer; amyotrophic lateral sclerosis; neuropathy; uncontrolled cell growth; PCR.
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Best Local Similarity 86.4
Matches 19; Conservative
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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynucleotides encoding them. The PRO polypucleotides and be used in diagnosing or treating abnormal bleeding involved in gynaecological diseases e.g. to avoid or lessen the need for hysterectomy. They can also be used in treating coronary ischaemic conditions, disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis), Parkinson's disease, Alzaheimer's disease, asthma, rheumatoid arthritis, multiple sclerosis, amyotrophic lateral sclerosis (ALS), neuropathies and diseases related to uncontrolled cell growth, such as cancer. This sequence represents a PCR primer used to isolate a human PRO polynucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fcs; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinaulinaemia; hypoinsulinaemia; hypoinsulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
                                                                                                                                                                                   Novel secreted and transmembrane PRO polypeptides and polynucleotides encoding them, useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.
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                                                     ME, Goddard A;
Kljavin IJ;
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                                       Ferrara N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted/transmembrane protein, #40, PCR primer #3.
                                 Botstein D, Desnoyers L, Eaton DL, Fong S, Gao W, Gerber H, Gerritsen I, Grimaldi JC, Gurney AL, Hillan KJ, Pan J, Paoni NF, Roy MA, Stewart TA, Wood WI;
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                   Desnoyers L, E
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(GETH ) GENENTECH INC
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                                 Ashkenazi A,
Filvaroff E,
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2000WO-US015264.
2000WO-US020710.
2000WO-US023328.
2000US-00665350.
               2000WO-US003565.
2000WO-US004414.
2000WO-US005004.
                           2000WO-US005841.
2000WO-US007377.
2000WO-US008439.
           2000WO-US000219
        99WO-US030999
               11-FEB-2000;
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24-FEB-2000;
                          02-MAR-2000;
20-MAR-2000;
30-MAR-2000;
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20-DEC-1999;
           05-JAN-2000;
                                       22-MAY-2000;
                                           02-JUN-2000;
                                              28-JUL-2000;
24-AUG-2000;
                                                      18-SEP-2000;
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(GETH) GENENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Allavin IJ; Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Ashkenazi A, Botstein D, Filvaroff E, Fong S, Gao Godowski PJ, Grimaldi JC, Williams PM, Wood WI; Pan J Mather JP,

WPI; 2003-521801/49.

New genes encoding for secreted and transmembrane PRO polypeptides, useful for treating e.g. cardiac insufficiency disorders, wounds, cancers, obesity, diabetes, hyperinsulinemia, hypoinsulinemia, or arthritis.

Example 33; SEQ ID NO 204; 476pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the mucloid scid encoding them. The polypeptides contributing a cartibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a call expressing a PRO polypeptide, for linking a bioactive molecule to a call expressing a PRO polypeptides. The PRO polypeptides are useful cortive and productive modelcule to a call expressing a PRO polypeptides. The PRO polypeptide antibodies are useful for modulating the biological activity of a call expressing a PRO polypeptides or polymental activity of polypeptide artibodies are useful as pharaccuticals, diagnostics biosensors or polymucleotides are useful as pharaccuticals, diagnostics biosensors or polymucleotides are useful as pharaccuticals, diagnostics biosensors or polymucleotides are useful for stimulating hypertrophy of monatal heart, inhibiting vascular endothelial cells, modulating proliferation of for proliferation of chondrocytes, enhancing the proliferation of control for etinal neurons or rod photoreceptor cells, inducing c-fos in endothelial cells, modulating glucose or PRA uptake, inducing proliferation of chondrocytes, enhancing the proliferation of chondrocytes, enhancing the proliferation of chondrocytes, enhancing cells, modulating processor or practiles to be proportially due to cretinal incurrences or practiles of the proportial city and the control of the proportial city of the proportial city of the proportial city of the proportial city of the proportial city of solate the full-length PRO cDNA or to isolate other control of solate control of control of solate the full-length PRO cDNA, in chromosome and gene mapping, in the generation of antisense RNA are useful in molecular biology including use as hybridiatation process of creening combinantly expressing the protein and for chromosome and gene mapping, in the generation of genetic analysis of individuals with genetic disorders as well for the propertied canagonic and propertied analysis of indiv

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Novel PRO polypeptides useful for treating Parkinson's disease,
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PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to amplify a PRO polynucleotide of the invention.
                                                                                                                                                                                                                  Human; PCR; primer; ss; PRO; secreted; transmembrane; gastrointestinal mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunobistochemical staining; sene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
                                                                     Gaps
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                                                    24;
                                                                    3; Indels
                                                                                                                                                                                                   Human secreted/transmembrane protein, #40, PCR primer #3
                                               / Match 66.2%; Score 17.2; DB 9; Length Local Similarity 86.4%; Pred. No. 4.78+03; les 19; Conservative 0; Mismatches 3; Indels
                                  Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                   5 CCTTCTTGTACTCCTCCTGCTC 26
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
9705 0063734P
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Wood WI;
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Alzheimer's disease, enterocolitis, Zollinger-Ellison syndrome, psoriasis, epidermoid carcinoma of the vulva and gliomas, gynecological diseases

Example 33; SEQ ID NO 204; 479pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides can define muclate acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a thiodites that specifically bind to the PRO polypeptide, for linking at least one biological activity of a cell. PRO polypeptide are useful for determine the properties are useful controlled activity of a cell. PRO polypeptide are useful for determine the properties are useful controlled and the repeat of activity of a cell expressing a PRO polypeptide and antichance of gastrointesinal mucosa and the repair of actual model in again with the area actual actual mucosa and the properties, and may also have an effect on kidner of antisens RNA and DNA, for prepairing PRO polypeptides and thair portions affect the actual mucosa and actual mucosa and for the generation of antisens RNA and DNA, for prepairing PRO polypeptides and may also have an effect of the formation of genes which have a role in apoptodis. The polymucleotides are useful in chargentically useful acagenesis, and may also have an effect of the formation of contentions are useful in the development and accordance and generation of antisens RNA and mucosa are useful as molecular mar

Seguence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Gaps ö 66.2%; Score 17.2; DB 9; Length 24; 86.4%; Pred. No. 4.7e+03; ive 0; Mismatches 3; Indels Query Match Best Local Similarity 86.4%

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ACD23296 standard; DNA; 24 BP 26-AUG-2003 (first entry) Human PRO PCR primer #83. ACD23296; ACD23296/ SEXEXEXEX

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Human; PRO; primer; ss; Parkinson's disease; Alzheimer's disease; ALS; amyotrophic lateral sclerosis; neuropathy; cancer; viral infection; ALDS; Usher's syndrome; haemorrhage; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; psoriasis; standasese; andometrial bleeding; anglogenesis; ischement condition; asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disease; atherosclerosis; infertility; birth defect; premature aging; stroke; PCR;
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                                                           diabetic complication
                                                                                            JS2003064367-A1.
                                                                             Homo sapiens.
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The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are used for treating diseases related to growth or survival of nerve cells such as Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS) and neuropathies, diseases related to uncontrolled cell growth such as cancer, viral infections, Usher's syndrome, paemorrhage, enterocolitis, Calinger-Ellison syndrome, gastrointestinal ulceration, congenital microvillus atrophy, skin diseases such as psoriasis and epithelial cancers, endometrial bleeding, angiogenesis, ischaemic conditions, asthma, rheumatoid arthritis, multiple sclerosis, inclammatory diseases, atherosclerosis, cardiac injury, infertility, birth defects, premature eqing, ALDS, stroke and diabetic complications. The polymucleotides are also useful in chromosome and gene mapping. This sequence represents a per primer used in isolation of a human PRO polymucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Botstein D, Desnoyers L, Eaton DL, Ferrara N;
, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
, Mon J, Paoni NF, Roy MA, Stewart TA, Tumas D;
, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated PRO polypeptides e.g. PRO245 and PRO1868, useful for treating e.g. Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
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            98US-0100858P.
98WG-0100408P.
98US-010408P.
98WG-0103025108.
98WG-0113296P.
99US-0145698P.
99US-0145698P.
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99WO-US021090
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22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
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Filvaroff E,
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gastrointestinal mucosa, mucosal lesion, skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; kidney tissue; apptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
                                                                                                                                 Human secreted/transmembrane protein, #40, PCR primer #3
                                                                                                                                                      Human; PCR; primer; 88; PRO; secreted; transmembrane;
CCTTCTTGTACTCCTGCTC 26
          24 CCTACTACTACTCCTCCTGCTC 3
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97US-0059113P.
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Query Match 66.2%; Score 17.2; DB 9; Length 24; Best Local Similarity 86.4%; Pred. No. 4.7e+03; Matches 19; Conservative 0; Mismatches 3; Indels

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97US-0065693P.
97US-0066120P.
97US-0066364P.
97US-0066463P.
97US-0066511P.
                                                   97US-0066772P.
97US-0066840P.
97US-0069425P.
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99WO-US021090.
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ME, Goddard A; Kljavin IJ; Ferrara N; rilvaroff E, Fong S, Gao W, Gerber H, Gerritsen Godowski PJ, Grimaldi JC, Gurney Ab, Hillan KJ, Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Williams PM, Wood WI; Ashkenazi A, Botstein D, Filvaroff E, Fong S, Gao

WPI; 2003-503391/47.

New secreted and transmembrane PRO polypeptides e.g. PRO187, which is a member of the epidermal growth factor-8 (EGF-8) family of proteins, useful for treating cancer.

Example 33; SEQ ID NO 204; 471pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modularing

c for detecting other PRO polypeptides in a sample and for linking a bioach can bological activity of a cell expressing a PRO polypeptides. The PRO polypeptides are also bioacical activity of a cell expressing a PRO polypeptides. The PRO polypeptides are also bioacical activity of a cell expressing PRO polypeptides. PRO polypeptides are also useful computation that are also useful computed by the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal diseases, amyotrophic lateral sclerosis (ALS), neuropathies and additionally disease related to uncontrolled cell growth, e.g. cancer. Rev polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also exploited as therapeutic diseases as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also exploited as therapeutic diseases or their reversal, as an antithrombotic agent with reduced risk for haemorrhage as compared with hepatin, in treating other PRO-associated disorders, in modulating capture. PRO polypeptides and their portions affect the expression of candometrial bleeding angiogenesis, and may also have an effect on kidney tissue. PRO polypeptides and their portions affect the expression of candometrial bleeding angiogenesis, and may also have an effect on kidney tissue. PRO polypeptides and their portions affect the expression of connecting PRO polypeptides and their portions affect the expression of the commonwer and gene mapping, in the generating transgenic animals of therapeutically useful reagents, as probes and for the generatic analysis of therapeutically useful reagents, as probes and for the generatic analysis of therapeutically useful reagents, as probes and for the generatic analysis of individuals which are useful in the generating transgenic analysis of therapeutically useful reagents, or prevent the effect of the PRO polypeptide (agonists) or prevent the reference typing PRO anti ö one biological activity of a cell. PRO polypeptides are useful recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to amplify a PRO Gaps . 0 66.2%; Score 17.2; DB 9; Length 24; 86.4%; Pred. No. 4.7e+03; 3; Indels Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other; 0; Mismatches s correracionica se CCTACTACTCCTCCTGCTC 3 polynucleotide of the invention. ВР ADA13093 standard; DNA; 24 Local Similarity 86.4 Query Match RESULT 27 ADA13093/c Matches à 셤

ADA13093;

06-NOV-2003 (first entry)

Human secreted/transmembrane protein, #40, PCR primer #3.

gastrointestinal mucosa; mucosal lesion; skin disease; seratinocyte differentiation; psoriaais; Parkinson's disease; Alstheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithromobcic agent; haemorrhage; endometrial bleeding anglogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; neuroprotective; immunohistochemical staining; gene therapy; nootropic; neuroprotective; Human; PCR; primer; ss; PRO; secreted; transmembrane;

cytostatic; virucide; anticoagulant.

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970S-0059113P.
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Homo sapiens.
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99WO-US020594. 99WO-US020944. 99WO-US021090. 99WO-US021547. 99WO-US023089. 99WO-US028214. 99WO-US028313. 99WO-US028301. 99WO-US028564. 99WO-US028565. 2000WO-US003565. 2000WO-US004414. 2000WO-US005004. 2000WO-US020710. 2000WO-US023328. 2000US-00665350. 99WO-US030095 99WO-US030911 2000WO-US007377, 2000WO-US008439, 99WO-US030999 2000WO-US000219 2000WO-US005841 20-MAR-2000; 30-MAR-2000; 22-MAY-2000; 22-FEB-2000; 24-FEB-2000; 02-MAR-2000; 05-OCT-1999; 29-NOV-1999; 30-NOV-1999; 01-DEC-1999; 02-DEC-1999; 02-DEC-1999; 16-DEC-1999; 11-FEB-2000; 20-DEC-1999; 05-JAN-2000; 15-SEP-1999

(GETH) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Baton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AJ, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-521802/49.

New secreted and transmembrane PRO polypeptides, useful for treating cancer, skin disorders, neurodegenerative diseases, and for lessening the effects of viral infection.

Example 33; SEQ ID NO 204; 473pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise and the nucleic acid encoding them. The polypeptides can be used to raise catical that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for inking a unicative molecule to a cell expressing a PRO polypeptides are useful for of acell expressing a PRO polypeptides. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal ferentiation (e.g. psoriated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal diseases, amyotrophic lateral sclerosis (ALS), neuropathies and diseases, amyotrophic lateral sclerosis (ALS), neuropathies and diseases, amyotrophic lateral sclerosis (ALS), neuropathies and calso diseases, amyotrophic lateral sclerosis (ALS), neuropathies and cancer. PRO polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also capped the preparin, in treating other PRO-associated disorders, in modulating antifection. The PRO polypeptides can be also used in assays to determine if it has a role in neurodegenerative diseases or their reversal, as an antifection. The PRO polypeptides and their portions affect the expression of engenes which have a role in apoptosis. The polymuclectices in modulating enes and their portions affect the expression of to solate the full-length PRO colypeptides, and may also have an effect on Nidney to solate the full-length PRO polypeptides, and may also have an effect on the commence and gene mapping, in the generation of antisense RNA and DNA, for preparing PRO polypeptides, or generating transgenic animals which are useful in the d

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         therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis purposes, as the PRO polypeptide (agonists) or prevent the effect of the PRO colypeptide (antagonists) or prevent the effect of the PRO colypeptide (antagonists) or prevent the effect of the PRO colypeptide (antagonists). The polymucleotides and proteins are useful for tissue typing. PRO antibodies are useful contissue typing. PRO antibodies are useful contissue typing. PRO antibodies are useful contissue typing and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO eg detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to amplify a PRO proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PCR; primer; ss; PRO; secreted; transmembrane; gastrointestinal mucosa; mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunobistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                       / Match 66.2%; Score 17.2; DB 9; Length 24; Local Similarity 86.4%; Pred. No. 4.78+03; nes 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted/transmembrane protein, #40, PCR primer #3.
                                                                                                                                                                                                                Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                          ADA41961 standard; DNA; 24 BP.
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970S-0059113P.
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970S-005912P.
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970S-005285P.
970S-0062285P.
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17-SEP-1997;
17-SEP-1997;
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Matches
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Human; PCR; primer; 88; PRO; secreted; transmembrane; gastrointeetinal mucosa, mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding anglogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.

US2003017498-A1. Homo sapiens.

Human secreted/transmembrane protein, #40, PCR primer #3.

20-NOV-2003 (first entry)

ADA17308;

ADA17308 standard; DNA; 24 BP.

ADA17308/

us-10-788-779-8.rng

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(GETH ) GENENTECH INC.
  Ashkenazi A,
Filvaroff E,
Godowski PJ,
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The invention discloses isolated PRO secreted/transmembrane polypeptides and the nutcleic acid encoding then. The polypeptides can be used to raise antichedies that specifically bind to the PRO polypeptide; for linking a carichedies that specifically bind to the PRO polypeptide. The PRO polypeptide antibodies are useful for a cell expressing a PRO polypeptide are useful for detecting other PRO polypeptides are useful for modulating the biological activity of a cell. PRO polypeptide are as also useful for detecting other PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. PRO polypeptide are also includes in an expension of gastrointestinal mucosa and the repair of gastrointestinal mucosa and the repair of seasons, skin diseases associated with the preservation and maintenance of gastrointestinal mucosa and the repair of seasons, skin diseases related to uncontroiled call growth. e.g. cencer. Gifferentiation (e.g. psoriasis), Parkinson's disease, anyotrophic lateral sclerosis (ALS), neuropathies and call tental sclerosis (ALS), neuropathies and call the properties are called to uncontrolled call growth. e.g. cencer. PRO polypeptides also serves as turniturolled call growth. e.g. cencer. PRO polypeptides can be also used in assays to determine infection. The PRO polypeptides can be also used in assays to determine controlled as role in neurodegenerative diseases or their reversal, as an antitrombotic agent with reduced risk for haemorrhage as compared with here a role in apoptosis. The polymuclectides are useful in apoptosis and presented disorders, in mucoderial percent with the development and screening of crissue. PRO polypeptides and their portions affect the expression of content of the proporties are useful in the development and screening of content and serversal, and the percent and serversal and proteins are useful in the respective (againsts). The polymuclectides are useful in the PRO polypeptide (againsts). The polymuc New PRO polypeptides useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration, Alzheimer's disease, amyotrophic lateral sclerosis and Usher syndrome. , Botstein D, Desnoyers L, Eaton DL, Ferrara N; , Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, , Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; , Paon J, Paoni NF, Roy MA, Stewart TA, Tumas D; , Wood WI; Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other; Example 33; SEQ ID NO 204; 468pp; English. WPI; 2003-755103/71. Mather JP, Pa Williams PM,

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Best Local Similarity

Query Match Matches

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98US-0100262P.
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25-NOV-1997;
12-DEC-1997;
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24-NOV-1997;
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13-OCT-1998;
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Baton DL, Ferrara N; Gerritsen ME, Goddard A; Hillan KJ, Kljavin IJ; Tumas D; Botstein D, Desnoyers L, Baton DL, Fong S, Gao W, Gerber H, Gerritsen Grimaldi JC, Gurney AL, Hillan KJ, Paoni NF, Roy MA, Stewart TA, Wood WI; Pan J, Ashkenazi A, Filvaroff E, Godowski PJ, Williams PM, JP, Mather

WPI; 2003-531434/50.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Example 33; SEQ ID NO 204; 475pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides.

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Correction discusses associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal diseases, anyotrophic lateral sciences; (ALS), neuropathies and diseases, anyotrophic lateral sciences; (ALS), neuropathies and diseases, anyotrophic lateral sciences; (ALS), neuropathies and diseases, anyotrophic lateral sciences; (ALS), neuropathies and acade additionally, disease related to uncontrolled cell growth, e.g. cancer. Pro polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also employed therapeutically in vivo for lessening the effects of viral antifection. The PRO polypeptides can be also used in assays to determine if it has a role in neurodegenerative diseases or their reversal, as an antifection with reating other PRO-associated disorders, in modulating anticophic proportions and may also have an effect on kidney tissue. PRO polypeptides and their portions affect the expression of genes which have a role in apoptosis. The polymucleotides are useful in chromosome and gene mapping, in the generation probes for cDNA library to isolate the full-length PRO cDNA or to isolate other cDNAs, in chromosome and gene mapping, in the generation of antisense RNA and DNA, for preparing PRO polypeptides, for generating transgenic animals or therapeutically useful reagents, for generating transgenic animals or therapeutically useful reagents, for spreaders as well as for recombinantly are useful as molecular marker for protein electrophoresis purposes, as the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (agonists) or the proteins are useful conting and/or assay of sample fluids. Anti-PRO antibodies are useful in approximated the processing the protein and for chromosome processing the protein or proteins are useful second and processing the protein and effect
treating disorders associated with the preservation and maintenance
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Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Gaps ; 0 66.2%; Score 17.2; DB 9; Length 24; 86.4%; Pred. No. 4.7e+03; ive 0; Mismatches 3; Indels Conservative Local Similarity les 19; Conserv Query Match Best Loc Matches

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ADA42811/c ID ADA42811 standard; DNA; 24 20-NOV-2003 (first entry) ADA42811; RESULT 30

Human secreted/transmembrane protein, #40, PCR primer #3.

gastrointestinal mucosa; mucosa; lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; Kidney tissue; apptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant. Human; PCR; primer; ss; PRO; secreted; transmembrane;

Homo sapiens

US2003054351-A1.

20-MAR-2003

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97US-0059115P.
97US-0059117P.
97US-0059121P.
97US-0059121P.
97US-0059122P.
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97US-0059266P.
97US-0062125P.
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9703-0062287P-
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2000WO-US007377. 2000WO-US008439. 2000WO-US014042. 2000WO-US015264. 2000WO-US020710. 99WO-US028313. 99WO-US028313. 99WO-US028301. 99WO-US028564. 99WO-US028565. 99WO-US030095. 99WO-US030911. 2000WO-US004414. 2000WO-US005004. 2000WO-US005841. 2000WO-US000219. 99WO-US030999 2000WO-US023328 18-SEP-2000; 2000US-00665350 01-DEC-1999; 02-DEC-1999; 16-DEC-1999; 16-DEC-1999; 20-DEC-1999; 20-DE 28-JUL-2000;

(GETH) GENENTECH INC.

Ferrara N; n ME, Goddard A; Kljavin IJ; Tumas D; Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, I Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen I Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, I Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Williams PM, Wood WI;

WPI; 2003-755052/71.

Novel isolated secreted and transmembrane PRO polypeptide, useful for tissue typing, treating Parkinson's disease, Alzheimer's disease, birth defects, cancer.

Example 33; SEQ ID NO 204; 464pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptides, for linking a broactive molecule to a cell expressing a PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a collective molecule to a cell expressing a PRO polypeptides are useful for medulating the biological activity of a cell expressing a PRO polypeptides are also useful cor recently and the properties are also useful activity of a cell expressing which the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal effects of gastrointestinal mucosa associated with the preservation and maintenance of gastrointestinal mucosa associated with the preservation and maintenance of gastrointestinal mucosa associated with the more and chronic mucosal effects of gastrointestinal mucosa associated with abnormal kerationcyte and the repair of acute and chronic mucosal distinguishing the effects of gastrointestinal ly, disease related to uncontrolled cell growth, e.g. cancer. Consolides also serves as tumour specific antigens which may be exploited as therapeutically in vivo for lessening the effects of viral infection. The PRO polypeptides can be also used in assays to determine comployed therapeutically in vivo for lessening the effects of viral candemetrial bleeding anglogenesis. The polymore and comparing of the parin, in treating other PRO-associated disorders, in modulating endomer and gase mapphylay, in the generating orber other connections are useful in a generating transgenic antisens of the full-length PRO polypeptides, for generating transgenic and propertical or construction probes for condemetrically useful reagents as probes and for the generating of the reagentic and so ortering complements of individuals with generic disorders as well as for recom

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WPI; 2003-567190/53
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the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). The polymucleotides and proteins are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to amplify a PRO polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; PRO, primer; 88; secreted polypeptide; transmembrane polypeptide; leukocyte homing; rheumatoid arthritis; psoriasis; multiple sclerosis; mucosal lesion; enterocolitis Zollinger Ellison syndrome; asthma; PCR; antiasthmatic; antirheumatic; antiarthritic; neuroprotective.
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ACD23658 standard; DNA; 24
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NP, Roy MA, Stewart TA, Tunas D;
97US-0063704P.
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11-FEB-2000; 2000WO-US003565
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21-NOV-1
24-NOV-1
     The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The polypeptides are useful for detecting PRO polypeptides and for linking a bioactive molecule to a cell expressing the polypeptides, where the bioactive molecule is a toxin, radiolabel or an antibody. The bioactive molecule is a toxin, radiolabel or an antibody. The bioactive molecule is a toxin, radiolabel or an antibody. The bioactive molecule is a toxin, radiolabel or an antibody. The bioactive polypeptides are useful for modulating at least one biological activity of a cell expressing the polypeptides or antibodies. The biological activity of a cell expressing the polypeptides. The copy polypeptides are useful for modulating and multiple copy as as than a sathma, rheumatoid arthritis, psoriasis and multiple collinger Ellison syndrome and for identifying agonists or antagonists of the polypeptides. The polymucleotides are useful as hybridization probes, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptides and for generating probes for polymerase chain reaction (PCR), Northern analysis, southern analysis and Western analysis. This sequence represents a PCR. primer used in isolation of a human PRO polymucleotide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal mucosa; mucosa lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; tidney tissue; appptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
                  Novel secreted and transmembrane polypeptide for modulating biological
                               activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 66.2%; Score 17.2; DB 9; Length 24; Best Local Similarity 86.4%; Pred. No. 4.7e+03; Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted/transmembrane protein, #40, PCR primer #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                    Example 33; Page 98; 471pp; English.
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97US-0059117P.
97US-0059117P.
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ADB77730 standard; DNA; 24 BP.
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The invention discloses isolated FVO Secreed/Tabmsemprash polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide for including a bloactive molecule to a cell expressing a PRO protein and for modulating a bloactive molecule to a cell expressing a PRO protein and for modulating a bloactive molecule to a cell expressing a PRO protein and for inking a bloactive molecule to a cell expressing a pRO polypeptide. The PRO polypeptide must be considered with abnormal Roral including a consideration of a cell expressing PRO polypeptide and maintenance of a cell expressing PRO polypeptides. PRO polypeptide are also useful for treating disorders associated with abnormal Recratinocyte mucosal eleanors. Sain diseases associated with abnormal Recratinocyte differentiation (e.g. poortiasis), Parkinson's disease, Alzheimer's differentiation (e.g. poortiasis), Parkinson's disease, Alzheimer's differentiation (e.g. poortiasis), Parkinson's disease, Alzheimer's differentiation (e.g. poortiasis), Parkinson's disease, Alzheimer's differentiation (e.g. poortiasis), Parkinson's disease, Alzheimer's disease related to uncontrolled cell growth, e.g. cancer. Celeases, amyorrophic laceral sclerosis (ALS), neuropathies and additionally, disease related to uncontrolled cell growth, e.g. cancer. Ce mployed therapeutically in vivo for lessening the effects of viral infection. The PRO polypeptides can be also used in seasys to determine if it has a role in neurodegenerative diseases or their reversal, as an entithronomic agent with reduced risk for haemorinage are useful in mendomeric agent with reduced risk for haemorinal series of the molecular biology including uses as hybridisation probes for chomosome and gene mapping, in the generating transgenic animals which are useful in the development and screening chromosome and gene mapping, in the generating to prevent the effect of the protein and for chromosome independent and protein electrophoresis purposes, as therapeutically weighted (antagonists) rheadome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated secreted and transmembrane polypeptide, useful for treating diseases, e.g. Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
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Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, I
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA,
Williams PM, Wood WI;
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22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US008439.
30-MAR-2000; 2000WO-US014042.
02-MAY-2000; 2000WO-US014042.
02-UIN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US01538.
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Eaton DL, Ferrara N; Gerritsen ME, Goddard A; Hillan KJ, Kljavin IJ; Tumas D;

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gastrointestinal mucosa; mucosal lesion; skin disease; keratinocyte differentiation; psoriaeis; Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth, cancer; tumour, viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
                                          Gaps
                                           .
                    Length 24;
                                                                                                                                                                                                           Human secreted/transmembrane protein, #40, PCR primer #3.
                                          Indels
                                                                                                                                                                                                                                  primer; 88; PRO; secreted; transmembrane;
Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
                  Score 17.2; DB 10;
Pred. No. 4.7e+03;
0; Mismatches 3;
                                                              CCTTCTTGTACTCCTCCTGCTC 26
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97US-0063121P.
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97US-0063735P.
97US-0063738P.
                    66.2%;
86.4%;
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                                                                                                                                          ADB74866 standard; DNA; 24
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                  Query Match
Best Local Similarity 86.4
Matches 19; Conservative
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29-OCT-1997;

Example 33; Page 101; 475pp; English.

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9705 0064248P.
9705 0064809P.
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9705 006634P.
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99US-0143048P.
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2000WO-US005004.
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(GETH) GENENTECH INC.

Goddard A; Gerber H, Gerritsen ME, Goddard Gurney AL, Hillan KJ, Kljavin IJ;
 Roy MA, Stewart TA, Tumas D; Ferrara N; Eaton DL, Botstein D, Desnoyers L, Filvaroff E, Fong S, Gao W, Godowski PJ, Grimaldi JC, Gur Mather JP, Pan J, Paoni NF, Williams PM, Wood WI, Ashkenazi A, Filvaroff E, Mather JP, P

WPI; 2003-765412/72.

Novel isolated native PRO polypeptide useful for tissue typing, modulating biological activity of cell, as molecular weight markers in protein electrophoresis, for treating enterocolitis, Zollinger-Ellison syndrome

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The invention discloses isolated PRO secreted/transmembrane polypeptides and the muclate acid encoding them. The polypeptides can be used to raise and the muclate acid encoding them. The polypeptides not be used to raise and the trape and for modulating the biological activity of a cell. PRO polypeptide are useful for modulating at least one biological activity of a cell. PRO polypeptides are useful for modulating the biological activity of a cell. PRO polypeptides are useful for modulating the biological activity of a cell expressing a PRO polypeptides are useful for modulating the biological activity of a cell expressing a PRO polypeptide and maintenance of garcronnessinal mucosa and the repair of activation and maintenance of garcronnessinal mucosa and the repair of activation and maintenance of garcronnessinal mucosa and the repair of acted and all nemance of garcronnessinal mucosa and the repair of acted foronic mucosal lenoms, skin disease related to uncontrolled cell growth, e.g. cancer. RRO polypeptides also serves as tumour specific antigens which may be disease, mayortophic leared sclerosis (ALS), neuropathics and additionally, disease related to uncontrolled cell growth, e.g. cancer. RRO polypeptides also serves as tumour specific antigens which may be employed therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutically in vivo for personal and part with reduced risk for associated disorders as effect the expression of gress which have a role in apoptosis. The polymucleotides are useful in charpentically useful aced in apoptosis, and may also the protein and dor charpentic and disorders as well as
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tissue typing; immunohistochemical staining; gene therapy;
neonatal heart; vascular endothelial growth factor; VBGF; proliferation;
endothelial cell; stimulated T-lymphocyte; retinal neuron;
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rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
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97US-0059117P.
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                                                               Homo sapiens.
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98US-0113296P.
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2000WO-US015264.
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Ferrara N; ME, Goddard A; W, Gerber H, Gerritsen ME, Goddarr Gurney AL, Hillan KJ, Kljavin IJ; F, Roy MA, Stewart TA, Tumas D; Eaton DL, Desnoyers L, Botstein D, Desno Fong S, Gao W, O Grimaldi JC, Gurn Pan J, Paoni NF, 1 Mather JP, Pan J, Pac Williams PM, Wood WI; Pan J Ashkenazi A, Filvaroff E, Godowski PJ, JP, Mather

WPI; 2003-540670/51.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating skin, neurodegenerative diseases, as an antithrombotic agent and for inducing endothelial cell apoptosis. encoding

Example 33; SEQ ID NO 204; 470pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating a confidencial order of a cell expressing a PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide are useful for modulating the biological activity of a cell expressing a PRO polypeptide or cell expressing as paramaceuticals, diagnostics, biosensors or polymedicotides are useful for stimulating the biological activity of polymedicotides are useful for stimulating hypertrophy of neonatal continuity inhibiting vascular endothelial growth factor (VEGP)-stimulated proliferation of endothelial cells, modulating the proliferation of stimulated T-lymphocytes, enhancing the survival or proliferation of chondrocytes. In particular, these are useful for efficientiation of chondrocytes. In particular, these are useful for detecting or treating cardiac insufficiency disorders, wounds, cancerous tumours, retinal disorders or injuries (e.g. loss of sight due to the propingulinaemia, or bone or cartilage disorders (e.g. sports injuries or arthritis) in mammals. PRO polypeptides and their portions affect the expression of genes which have a role in cell death. The polynucleotides

us-10-788-779-8.rng

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97US-0062814P.
97US-0063121P.
97US-0063122P.
97US-0063122P.
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           are useful in molecular biology including uses as hybridisation probes
for cDNA library to isolate the full-length PRO cDNA or to isolate other
cDNAS, in chromosome and gene mapping, in the generation of antisense RNA
and DNA, for preparing PRO polypeptides, for generation of antisense RNA
and DNA, for preparing PRO polypeptides, for generation standsgenic
animals or knockout animals which are useful in the development and
screening of therapeutically useful reagents, as probes and for the
screening of therapeutically useful reagents, as probes and for the
screening of therapeutically useful reagents, as probes and for the
screening of therapeutically useful reagents, as probes and for the
screening of therapeutically with genetic disorders as well as for
recombinantly expressing the protein and for chromosome identification.
The proteins are useful as molecular marker for protein electrophoreais
those that mimic the PRO polypeptide (agonists) or prevent the effect of
the PRO polypeptide (antagonists). The polymucleotides and proteins are
useful for tissue typing. PRO antibodies are useful for
immunohistochemical staining and/or assay of sample fluids. Anti-PRO
antibodies are useful in diagnostic assays for PRO e.g. detecting its
expression in specific cells, tissues or serum and for affinity
complexed of PRO from recombinant cell culture or natural sources. The
PRO genes may also be used in gene therapy, particularly for replacing a
defective gene. The sequence presented is a PCR primer which was used to
amplify a PRO polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; tosonatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; hom disorder; cartiage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
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                                                                                                                                                                                                                                                                                                                                        Query Match 66.2%; Score 17.2; DB 10; Length 24; Best Local Similarity 86.4%; Pred. No. 4.7e+03; Matches 19; Conservative 0; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted/transmembrane protein, #40, PCR primer #3.
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970S-005912P.
970S-0059263P.
970S-0059266P.
970S-0052266P.
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17-SEP-1997;
17-SEP-1997;
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Botstein D, Desnoyers L, Eaton DL, F
Fong S, Gao W, Gebber H, Gertitsen N
Grimaldi JC, Gurney AL, Hillan KJ, F
Pan J, Paoni NF, Roy MA, Stewart TA,
                                                                                                                      Example 33; SEQ ID NO 204; 477pp; English.
    22-MAY-2000; 2000WO-USG14042.
02-UUN-2000; 2000WO-USG15564.
28-JUL-2000; 2000WO-USG2710.
24-AUG-2000; 2000WO-USG3328.
18-SEP-2000; 2000US-00665350.
2000WO-US008439
                                                                       Wood WI:
                                       (GETH ) GENENTECH INC.
                                                 Ashkenazi A, Botste
Filvaroff E, Fong S
Godowski PJ, Grimal
Mather JP, Pan J,
Williams PM, Wood W
                                                                                     WPI; 2003-540675/51.
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Human; PCR; primer, 88; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neconatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinaulinaemia; hypoinsulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnezary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
                                                                                                                                   Human secreted/transmembrane protein, #40, PCR primer #3.
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9705-0063121P.
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97US-0064248P.
97US-0064809P.
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                     ADC40226 standard; DNA; 24
                                                                                               (first entry)
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28-0CT-199;
28-0CT-1997;
28-0CT-1997;
9-0CT-190-
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29-OCT-1997;
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ADC40226/
                                       The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide. For linking a cariotative for a cell expressing a PRO polypeptide. The PRO polypeptide are useful for detecting other PRO polypeptides. The PRO polypeptides are useful for modulating the biological activity of a cell. PRO polypeptides or the PRO polypeptides or the PRO polypeptides or the PRO polypeptides or polymorpetide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or polymorlectides are useful for modulating the proliferation of a cell expressing PRO polypeptides. The PRO polypeptides or polymorlectides are useful for stimulating hypertrophy of mennaral control profile antibodical activity of a cell spreasting PRO polypeptides. The PRO polypeptides or polymorlectides are useful for stimulated or lymphocytes, enhancing the survival or proliferation of endothelial cells, modulating uppoliferation addition or red phocyces, inducing proliferation of chondrocytes. In particular, these are useful for cells, modulating glucose or FPO uppea. Inducing proliferation of chondrocytes or injuries (e.g. loss of sight due to capture to the properties or injuries (e.g. loss of sight due to control properties or injuries (e.g. sports injuries or arthritis) in mammals. PRO polypeptides and their portions affect the arthritis on mammals. PRO polypeptides and their portions affect the crown properties or injuries (e.g. sports injuries or survival information of genes which have a role in cell death. The properties or injuries (e.g. sports injuries or the combinant problem and provides are useful in molecular bology including uses as hybridisation probes are useful in molecular bology including uses as hybridisation of genetic analysis of individuals with genetic also benefil and genetic assays for PRO expension in specific cells, insurance or serve and 
                                                                                                                                                                                                          Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating skin, neurodegenerative diseases, as an antithrombotic agent and for inducing endothelial cell apoptosis.
                                                         Ferrara N;
ME, Goddard A;
                                                                           ME, Goddard
Kljavin IJ;
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Best Local Similarity 86.4
Matches 19; Conservative
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03-NOV-1997;

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Gaps

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97US-0066770P.
97US-0066772P.
97US-006840P.
97US-006942SP.
98US-0099803P.
98WG-US018824.
     97US-0065846P.
97US-0065693P.
97US-0066120P.
                       97US-0066364P.
97US-0066453P.
97US-0066466P.
97US-0066511P.
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99US-0146222P.
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                       21-NOV-1997;
24-NOV-1997;
24-NOV-1997;
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11-FEB-2000;
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02-JUN-2000;
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21-NOV-1997
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24-NOV-1997
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29-NOV-1999
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20-DEC-1999;
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Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mood WI; Roy MA, Stewart TA, Tumas D; Ashkenazi A, Filvaroff E, Williams PM, Godowski PJ, Mather JP.

WPI; 2003-540676/51.

as an Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating skin, neurodegenerative diseases, antithrombotic agent and for inducing endothelial cell apoptosis.

Example 33; SEQ ID NO 204; 473pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO protein and for modularing

cc at least one biological activity of a cell. PRO polypeptides are useful for inhiting a bloadtive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide the PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or for ell expressing PRO polypeptides. The PRO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or provide actors. These are useful as pharmaceuticals, diagnostics, biosensors or provideration of endothelial cells, modulating hyperprises or provideration of endothelial cells, inducing proliferation of criminal neurons or rod photoreceptor cells, inducing proliferation of diafferentiation of chondrocytes. In particular, these are useful for cells, modulating glucose or FRA upgake, inducing proliferation of diafferentiation of chondrocytes. In particular, these are useful for differentiation of chondrocytes. In particular, these are useful for cells, modulating glucose or FRA upgake, inducing proliferation of thomerows. The properties of the survival or proliferation of chondrocytes. In particular, these are useful for cells, inducing proliferation of chosen or carrilage discorders (e.g. sports injuries or thomeromal or properties and their portions affect the are useful in molecular biology including uses as hybridisation probes or corribinal properties and their portions and corrections are useful as molecular biology including uses as hybridisation probes or comminal or knockout animals which have a useful as probes and for the general properties of animals which are useful as properties and proteins are useful as molecular marker for protein electrophoresis or proteins of therapeutically useful respented search general proteins are useful as molecular marker for protein electrophoresis or purposes as therapeutical general with generic discomplication or protein are useful and diagnostic assays defective gene. The sequence presented is a PCI amplify a PRO polynucleotide of the invention.

Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Gaps ; 66.2%; Score 17.2; DB 10; Length 24; 86.4%; Pred. No. 4.7e+03; ive 0; Mismatches 3; Indels (Best Local Similarity 86.4 Matches 19; Conservative Query Match

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ADC19050/c ID ADC19050 standard; DNA; 24 BP. 18-DEC-2003 (first entry) ADC19050; RESULT 37

Human secreted/transmembrane protein, #40, PCR primer #3.

Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nenonatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinaulinaemia; hypoinsulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological;

Homo sapiens

Page 40

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Mon Nov 21 10:29:03 2005
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970S-0059119P.
970S-0059121P.
970S-0059122P.
970S-0059184P.
970S-0059263P.
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970S-0063814F
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                            2001US-00909204
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                            18-JUL-2001;
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24-0CT-1997;
24-0CT-1997;
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24-0CT-1997;
27-0CT-1997;
28-0CT-1997;
28-0CT-1997;
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28-OCT-1997;
28-OCT-1997;
29-OCT-1997;
29-OCT-1997;
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22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US006343.
30-MAR-2000; 2000WO-US004343.
22-MAY-2000; 2000WO-US015264.
02-UNN-2000; 2000WO-US015264.
24-AUG-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US020328. 99WO-US021090. 99WO-US021090. 99WO-US021547. 99WO-US023089 99WO-US028214 99WO-US028313 99WO-US028301 99WO-US028564 99WO-US028565 99WO-US030095 99WO-US030911 US030999 2000WO-US003565 2000WO-US000219 -0M66 05-OCT-1999; 29-NOV-1999; 30-NOV-1999; 01-DEC-1999; 02-DEC-1999; 16-DEC-1999; 20-DEC-1999; 13-SEP-1999; 15-SEP-1999; 15-SEP-1999; 20-DEC-1999

(GETH) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski DJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Marther JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; William PM, Wood WI;

WPI; 2003-615762/58.

Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Example 33; SEQ ID NO 204; 476pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antitodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a call expressing a PRO protein and for modulating at the state of the protein and for modulating at loadctive molecule to a call expressing a PRO polypeptides are useful controlled to a call expressing a PRO polypeptides are useful for modulating the biological activity of a call expressing a PRO polypeptides. The PRO polypeptide antibodies are useful for modulating the biological activity of a call expressing a PRO polypeptides. The PRO polypeptides or activity of polymethed antibodies are useful for modulating the biological activity of polymethed antibodies are useful for stimulating hypertrophy of meonatal protectors. These are useful for stimulating hypertrophy of meonatal confideration of endothelial calls, modulating hypertrophy of retinulated T-lymphocytes, enhancing the survival or proliferation of formatorytes, enhancing the survival or proliferation and/or retinal meurons or rod photoreceptor calls, inducing proliferation and/or reciples, modulating glucose or PPA uptake, inducing proliferation and/or detecting or treating cardiac insufficiency disorders, wounds, cancerous tumours, retinal disorders or injuries (e.g. loss of sight due to detecting or treating cardiac insufficiency disorders, wounds, cancerous continities pigmentosum), obesity, diabetes, hyperinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or arthritis) in mammals. PRO polypeptides and their portions affect the expression of genes which have a role in call death. The polymucleotides are useful in molecular biology including uses as hybridisation probes of conda DNA, for preparing PRO polypeptides, for generating of therapeutically useful reagents, as probes and for the generation. Condannessing the protein and for chromosome and gene mapping, in the generation of antisense RNA a

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97US-0063329P.
97US-0063541P.
97US-0063542P.
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97US-0063549P.
97US-0063564P.
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970S-006642P-
970S-006672P-
980O-US019819-
980O-US019304P-
980S-0103294P-
990S-0145698P-
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2000WO-US005841.
2000WO-US007377.
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99WO-US028301
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2000WO-US014042
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11-FEB-2000;
22-FEB-2000;
                           28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
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29-0CT-1997;
29-0CT-1997;
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20-MAR-2000;
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31-OCT-1997;
03-NOV-1997;
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05-OCT-1999;
29-NOV-1999;
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24-NOV-1997;
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The proteins are useful as molecular marker for protein electrophoresis purposes, as therapeutic agents for screening compounds to identify those that mimic the RNO polypepide (agonists) or prevent the effect of the PRO polypepide (antagonists). The polymucleotides and proteins are useful for tissue typing. PRO antibodies are useful for assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity butification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to amplify a PRO polymucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                   Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; atimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FRA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
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                                                                                                                                                                           Match 66.2%; Score 17.2; DB 10; Length 24; Local Similarity 86.4%; Pred. No. 4.7e+03; les 19; Conservative 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                              Human secreted/transmembrane protein, #40, PCR primer #3.
                                                                                                                                                    Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
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970S-0059113P.
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970S-005912P.
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17-SEP-1997;
18-SEP-1997;
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18-DEC-2003 (first entry)

ADC29405;

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The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide. For Illuting a carbodies that specifically bind to the PRO polypeptide. The PRO polypeptide are useful for a cell sepressing a PRO polypeptide. The PRO polypeptide are useful for modulating the biological activity of a cell. PRO polypeptides are useful for modulating the biological activity of polypeptide antibodies are useful for seimulating hypertrophy of neonatal control of a cell expressing PRO polypeptides. The PRO polypeptides or polymuclectides are useful for seimulating hypertrophy of neonatal carbon of a cell expressing PRO polypeptides. The PRO polypeptides or polymuclectides are useful for seimulating hypertrophy of neonatal carbon of endothelial cells, modulating the proliferation of polymuclectides are useful for seimulated properties. The propertrophy of neonatal carbon of a cell seimulated properties are useful in modulating glucose or FRP uptake, inducing proliferation of chondrocytes. In particular, these are useful for cells, modulating glucose or FRP uptake, inducing proliferation of chondrocytes. In particular, these are useful for detecting or treating cardiac insufficiency disperent, and or red phorocytes. The particular, these are useful for certains in particular, these are useful in molecular bology including uses as hybridisation probes tumours, retinal disorders or injuries (e.g. loss of sight due to the consonal results and prolifers and their portions affect the are useful in molecular bology including uses as hybridisation probes are useful in molecular bology including uses as hybridisation properties or only the protein and so recombinantly expressing the protein and for chromosome and gene mapping, in the generation of antimals or knockout animals which are useful in diagnosic assetules are useful in diag
                                                                                                                                                                                                Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancers, asthma, rheumatoid arthritis, neurological diseases, and skin diseases.
  Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                         Example 33; SEQ ID NO 204; 478pp; English.
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                                                Query Match 66.2%; Score 17.2; DB 10; Length 24; Best Local Similarity 86.4%; Pred. No. 4.7e+03; Matches 19; Conservative 0; Mismatches 3; Indels (
Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
                                                                                                                                                        5 CCTTCTTGTACTCCTCCTGCTC 26
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24 CCTACTACTACTCCTCCTGCTC 3 29405/c ADC29405 standard; DNA; 24 BP. RESULT 39 ADC29405/ 셤

97US-0066466P. 97US-0066511P.

24-NOV-1997;

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Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; dlabete; hyperinaulineamia; hypoinsulineamia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
                                                     Human secreted/transmembrane protein, #40, PCR primer #3.
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9705-0059121P

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9705-0059265P

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9705-0062814P

9705-0062814P

9705-0063121P

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97US-0066120P.
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24-0CT-1997;
24-0CT-1997;
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The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO potypeptide, for linking at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides are useful for modulating the biological activity of a cell expressing PRO polypeptides or bolypeptides or bioreactors. These are useful for stimulating hypertrophy of neonatcal heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated PRO polypeptides e.g. PRO234 (useful for treating rheumatoid arthritis, psoriasis and multiple sclerosis) and PRO187 (useful for treating Alzheimer's disease, cancer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fong S, Gao W, Gerber H, Gerritsen ME, Goddard
Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
an J, Paoni NF, Ann Roy M, Stewart TA, Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 33; SEQ ID NO 204; 451pp; English.
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97US-0066772P.
97US-0066840P.
97US-0068840P.
97US-0069842EP.
98US-009802EP.
98US-009803P.
98WG-US01824.
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98US-0113296P.
99US-0143048P.
99US-0145698P.
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98WO-US019437.
98US-0104080P.
98US-0109304P.
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Godowski PJ, Grime
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Williams PM,
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Filvaroff E,
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11-FEB-2000;
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proliferation of endothelial cells, modulating the proliferation of stimulated T-lymphocytes, enhancing the survival or proliferation of cretinal neurons or rod photoreceptor cells, inducing c-fos in endothelial cells, modulating glucose or FFA uptake, inducing proliferation and/or redifferentiation of chondrocytes. In particular, these are useful for detecting or treating cardiac insufficiency disorders, wounds, cancerous tumours, retinal disorders or injuries (e.g. loss of sight due to cretinitis pigmentosum), obesity, diabetes, hyperinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or arthritis) in mammals. PRO polypeptides and their portions affect the expression of genes which have a rolle in cell death. The polymicleotides are useful in molecular biology including uses as hybridisation probes of are useful in molecular biology including uses as hybridisation probes of or cDNA library to isolate the full-length PRO cDNA or to isolate other consens and gene mapping, in the generating transgenic and DNA, in chromosome and gene mapping, in the generating transgenic and DNA, for preparing PRO polypeptides, for generating transgenic conformantly expressing the protein are useful in the development and screening of therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for those that mimic the PRO polypeptide (angenists). The polymucleotides and proteins are useful for tissue typing PRO antibodies are useful for tissue typing PRO antibodies are useful for insuential reagens or serum and for affinity conserment and secreting its expression in specific cells, tissues or serum and for affinity of propose or popurationally entered in deagnostic and case and an area and an area of the propose and an area of the propose and propose and in dense the remained in diagnostic assay of sample floor recondinant or proving and an area of the propose and an area of the propose and in gene in specific cells, transverse or an artical sources. The 
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0; Mismatches 3
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Goddard A;

Eaton DL, Ferrara N; Gerritsen ME, Goddan

Eaton DL,

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20-MAR-2000; 2000WO-US007377. 30-MAR-2000; 2000WO-US018439. 22-MAY-2000; 2000WO-US014042. 02-UUN-2000; 2000WO-US01564. 28-UUL-2000; 2000WO-US023328. 18-SEP-2000; 2000US-00665350. 99WO-US028564. 99WO-US028565. 99WO-US030095. 2000WO-US004414. 2000WO-US005004. 2000WO-US005841. 99WO-US030911 2000WO-US000219. 02-DEC-1999; 02-DEC-1999; 16-DEC-1999; 20-DEC-1999; 20-DEC-1999; 24-FEB-2000; 02-MAR-2000; 05-JAN-2000; 11-FEB-2000; 22-FEB-2000;

(GETH) GENENTECH INC.

Botstein D, Desnoyers L, Baton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; an J, Paoni NF, Roy MA, Stewart TA, Tumas D; Ashkenazi A, Botstein D Filvaroff E, Fong S, G Godowski PJ, Grimaldi J Mather JP, Pan J, Paon Williams PM, Wood WI;

WPI; 2003-615797/58.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating skin, neurodegenerative diseases, as an antithrombotic agent and for inducing endothelial cell apoptosis.

Example 33; SEQ ID NO 204; 470pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the mucled acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO polypeptide are useful as beauting a bioactive molecule to a cell expressing a PRO polypeptides are useful corrected and acidity of a cell. PRO polypeptides are useful corrected and beautiful as parametericals, diagnostics, biosensors or polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or polypeptides are useful as pharmaceuticals, diagnostics, biosensors or polyucalcotides are useful as pharmaceuticals, diagnostics, biosensors or polyucalcotides are useful for stimulating the proliferation of endothelial cells, inducing proliferation of proliferation of endothelial cells, inducing proliferation of cells, modulating diagnostics. In particular, these are useful for retinal neurons or rod phocroceptor cells, inducing proliferation and/or refiferentiation of chondrocytes. In particular, these are useful for detecting or treating cardiac insufficiency disorders, wounds, cancerous tumours, retinal disorders or injuries (e.g. loss of sight due to rethints pignentosum), obesity, diabetes, hyperinaliania, in mammals are bone or cartilage disorders (e.g. sports injuries or rethints pignentosum), obesity, diabetes, hyperinaliania, in mammals. PRO polypeptides and their portions affect the expression of genes which have a role in cell death. The polyuncleotides are useful in molecular biology including uses as hybridisation of entisense RNA and DNA, for preparing PRO polypeptides, for generating transgenic animals or knockout animals which have a role in cell death. The polyment and screening of therapeutic apents, is proper and processing the protein and for themosome identification. The proteins are useful in diagnostic assays for proper an minitarial and proteins are useful in

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purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to amplify a PRO polynucleotide of the invention.
888888
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Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

ô 0; Gaps Query Match 66.2%; Score 17.2; DB 10; Length 24; Best Local Similarity 86.4%; Pred. No. 4.7e+03; Matches 19; Conservative 0; Mismatches 3; Indels (

S CCTTCTTGTACTCCTCCTGCTC 26

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Search completed: November 18, 2005, 11:52:33 Job time: 181.034 secs

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Perfect score:

Sequence:

OM nucleic

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Run

Scoring table:

Searched:

Database

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Was musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (Dases 1 to 49)

1 (Dases 1 to 40)

1 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

L Contact: Robert B. Weiss

University of Utah Genome Center
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1M0178H1SF Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0178H15 F, genomic survey sequence.
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(http://www.jax.org/resources/documents/dnares/). The DNA
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muscullus C57BL/6J (male) was obtained from the Jackson
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84112, USA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0178 row: H column: 15
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 49.
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(c) 1993 - 2005 Compugen Ltd.
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophorasis. Vector DNA was prepared from a derivative of pwM92 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus (house mouse)

Mus musculus (burdata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musiner (bases 1 to 33)

E (bases 1 to 33)

Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Unpublished (2000)

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                     was hydrodynamically sheared by repeated passage through
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/noce="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.2%; Score 18; DB 8; Length 27;
80.8%; Pred. No. 1.8e+04;
Mismatches 5; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Brror: 0.00
Plate: 0222 row: E column: 03
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 33.
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/strain="C57BL/6J"
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/clone="UUGC1M0222E03"
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AZ435186/c
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KEYWORDS
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ESM Mus musculus (house mouse)

ENKaryora, Metzaca; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryora; Metzaca; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinacia; Lo 27)

Estato (house in to 27)

SS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederinausern,A. and Wright,D.,Waiss,R.

Nouse whole genome scaffolding with paired end reads from 10kb

Dlasmid inserts

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Hal. 801 585 506

Fax: 801 585 7177

Tel: 801 585 506

Fax: 801 585 7177

Email: ddunm@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0079 row: M column: 16

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 27.

High quality sequence stop: 27.
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732.114 [gb] AR12.9072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to damptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ345323 AZ345323 GI:10424560
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/lab_host="B. Coli strain XLI0-Gold, T1-resistant, F-"
/lab_host="B. Coli strain XLI0-Gold, Iibrary"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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o.005 inch orifice at constant by lepeacu passage unlough a was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM92 (gi|4732114|gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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E. (bases 1 to 35)
E. Dum, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diasmid inserts
D. Unpublished (2000)
C. Unpublished (2000)
C. Ontact: Robert B. Weiss
University of Utah Genome Center
University of Utah
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at concern the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the sta
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0199 row: J column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 35.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0199J13"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CE 1 (bases 1 to 36)
RS Junn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nicderhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
Tel: 801 585 5606
Fax: 801 585 5606
Fax: 801 585 5606
Fax: 801 585 5006
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerses and T4 polymurcleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWMD42 (gil4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-GOld (Stratagene) cells and selected for ampicillin resistance."
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Pred. No. 4.3e+04;
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Insert Length: 10000 Std Error: 0.00
Plate: 0300 Tow: P column: 16
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UUGC1M0300P16"
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Best Local Similarity 80.0%;
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E. Longacze, Marber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacze, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
D. Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
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/clone_lib="Mouse_lokb plasmid_UUGCIM library"
/note=""Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL6 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="UUGC1M0460M16"
/sex="Male"
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GSS.
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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TITLE

COMMENT

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rallam, L., Longacre, S., Mahmoud, M., Menent, E., Pedersen, T., Reilly, M., Rose, M., Rose, R. & Stokes, R. & Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Dingey, A., von Duse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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80.0%; Pred. No. 4.3e+04;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0240 row: J column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0240J20"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nede, M., Rose, M., Ro
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2M0142022F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Insert Length: 1000 Std Error: 0.00
Plate: 0142 row: O column: 22
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC2M0142022"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
Email: ddunn@qenet
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified, The sheared, adaptored mouse DNA was annealed to
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**Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

**Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

**Bukaryota; Metazoa; Chordata; Sciurognathi; Murinae; Mus.

**Bun,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

**Silly,M., Rose,M., Mahmoud,M., Meenen,E., Pedersen,T.,

**Reillly,M., Rose,M., Mose,R., Stokes,R., Tingey,A., von

**Niederhausern,A. and Wright,D., Weiss,R.

**Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

**Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah Bolvwers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ397298 50 bp DNA linear GSS 03-OCT-2000 1M0162A13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0162A13 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                  adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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80.0%; Pred. No. 4.4e+04;
tive 0; Mismatches 5;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0162 row: A column: 13
Seq primer: CGTYCTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 50.
High quality sequence
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0162A13"
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clone UUGC1M0249D13 F, genomic survey sequence.
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase and T4 polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil49132114 gpl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Kato, K. and Matoba, R. Generation of expressed sequence tags from mouse brain Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="brain"
/clone_lib="3'-directed mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                    65.4%; Score 17; DB 8; Length 50; 80.0%; Pred. No. 4.4e+04;
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URL:http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
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Graduate School of Biological Sciences
Nara Institute of Science and Technology
1916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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/clone="BED0008949"
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AU256766.1 GI:20320746
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AU256766/c
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musculus C57BL/61 (male) was obtained from the Jackson Laboratory Mouse DNA Resource (from the Jackson Laboratory Mouse DNA Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was but end repaired with T4 DNA polymerses and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0129P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 41)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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84112, USA
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0249 row: D column: 13
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 41.
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0249D13"
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                                                              Mus musculus (house mouse)
AZ450486.1 GI:10605322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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GSS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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/clone lib="Gm-cloids"
//note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
Xhof; This cDNA library was constructed from mRNA isolated
from mature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR cDNA library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XLIO-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Figure 1.1 Set@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. Trace
considered overall poor quality Possible reversed clone: similarity
on wrong strand This clone is available through: Biogenetic
Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                    Shoemaker, R., Kein, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khama, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCant, R., Waterston, R. and Wilson, T., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Glycine max"
/organism="Glycine max"
/mol type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-1293"
/tissue_type="Mature flowers, field grown plants"
/lab_nose="XL10-Gold"
      Gm-c1015-1293 5' similar to TR:004132 004132 SRC1. ;, mRNA
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Pred. No. 8.4e+04;
0; Mismatches 3;
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Location/Qualifiers
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85.7%;
                                                                                                                                                             Glycine max (soybean)
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Best Local Similarity
                                                                                                                                                                                             Glycine max
                                                                                                   AI966611.1
                                                                ACCESSION
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                             Mis musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (basas 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R.,
Muse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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clone UUGC2M0129P09 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0129 row: P column: 09
Seq primer: GGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
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/mol type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC2M0129P09"
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                                                                                                                             Mus musculus (house mouse)
                                                         AZ835139.1 GI:13005047
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Fax: 801 585 7177
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84112, USA
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Length 37;

GSS 06-JUL-2004

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LOCUS DEFINITION RESULT 13 A1966611/c

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                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 50) Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A. Davies, M. Hinxton, Cambridgeshire, Cabnited (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tr91a09.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2226424 3' similar to TR:015320 015320 MEA6. ;contains MSR1.t3 MSR1 repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: crapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN312f06, genomic survey sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATional Gancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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/tissue_type="adenocarcinoma"
/lab_host="DH108"
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Insert Length: 1126 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 1
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                                  CR235166
CR235166.1 GI:50014015
GSS; genome survey sequence; MICER.
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/organism="Mus musculus"
/organism="Mus musculus"
/ol_xref="taxon:10090"
/clone="MHRN112f06"
/clone_lib="MHPN"
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/db_xref="taxon:9606"
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Homo sapiens
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Best Local Similarity
Loca 19; Conserva
                                                                                                                  Mus musculus
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AUTHORS
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JOURNAL
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|472114|gla) [All 19.5] a copy-number inducible derivative of plasmid R1. The vector was ligated
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sall; Site 2: Not1; Cloned unidirectionally. Primer: OTigo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 31)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Railly, M., Roose, R., Stokes, R.,

Reilly, M., Rose, M., Rose, R., Stokes, R.,

Niederhaussern, A. and Wright, D., Weiss, R.
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1M0338A14F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0338A14 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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0
                                                                                                                                                                                                     Score 15.6; DB 1; Length 43;
Pred. No. 1.4e+05;
0; Mismatches 4; Indels
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clone lib="NCI CGAP Pan1"
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Class: plasmid ends
High quality sequence stop: 31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0338A14"
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Insert Length: 10000 Std Erro
Plate: 0338 row: A column: 14
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81.8%;
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Unpublished (2000)
                                                                                                                                                                                                                                                                      18; Conservative
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Fax: 801 585 7177
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SOURCE
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse lokb plasmid UUGCIM library"
/note="Weetor: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/nttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114 gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XLI0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ792853 32 bp DNA linear GSS 16-FEB-2001 2M0045C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0045C07 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Wouse, W., Stokes, R., Tungey, A., von Wouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact Robert B. Weiss
University of Utah Genome Center
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                                                                                                                                                                                    Score 15.4; DB 8; Length 31; Pred. No. 1.6e+05; 0; Mismatches 6; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: C column: 07
Seg primer: CACACAGGAAACAGCTAATGACC
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/strain="C57BL/6J"
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clone="UUGC2M0045C07"
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High quality sequence stop: 32.
Location/Qualifiers
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                                                                                                                                                                                  Query Match
Best Local Similarity 76.0%;
Matches 19; Conservative 0
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Fax: 801 585 7177
Email: ddunn@genet
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ORGANISM
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AZ792853/c
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COMMENT
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KEYWORDS
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0025B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0025B05 F, genomic survey sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
1 (bases 1 to 33)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The
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                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                           Length 32;
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                                                                                                                                                                                                  Score 15.4; DB 8;
Pred. No. 1.6e+05;
0; Mismatches 6;
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Fax: 801 585 7177
Email: ddunm@enetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0025 row: B column: 05
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0025B05"
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Best Local Similarity 76.00,
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84112, US
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0155 row: P column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                    1. .37
/organism="Mus musculus"
                                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0155P13"
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GSS.
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Best Local Similarity 76.0°
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                                                                                                        JOURNAL
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KEYWORDS
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                                                               TITLE
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Ciona intestinalis

Bukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,

Phlebobranchia; Cionidae, Ciona.

1 (bases 1 to 34)

Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Bryressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Satoh

Department of Zoology
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musi
1 (bases 1 to 37)
Eunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dev stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
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                                                                                                                                          Query Match 59.2%; Score 15.4; DB 8; Length 33; Best Local Similarity 76.0%; Pred. No. 1.66+05; Matches 19; Conservative 0; Mismatches 6; Indels
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Ciona intestinalis"
/mol_type="mkna"
/db_xref="taxon:719"
/clone="rcieg09f14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sákyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Matches 19; Conservative
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Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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84112, USA
                                  Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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(http://www.nduer.DNA kesources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM92 (gilfa732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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84112, USA
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/clone l1b="Mouse 10kb plasmid UGCIM library"
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musculus C57BL/6J (male) was obtained from the Jackson
                          Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
        islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606

Pax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 05
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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/ Jab host= Cocinosebue.
/ Jab host= Cocinosebue.
/ Jab host= Lib. Coli strain Xil0-Gold, Tl-resistant, F-"
/ Clone lib. Mouse loke plasmid UGCIM library
/ Inote= Weetcr: PWD4Zuv; Purified genomic DNA from
Musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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polynuclectide kinase. Adaptor oligonuclectides were
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of pwD42 (gil 4732114 [gp] AR129072.1), a copy-number
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adaptored vector DNA, and transformed into
chemically-competent B. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                          Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0556 row: D column: 02
Seg primer: CACACAGGAACAGGTATGACC
Class: plasmid ends
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                                                                                                            plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                          AI088341 46 bp mRNA linear EST 05-OCT-1
qb07a07.x1 Soares pregnant_uterus NbHPU Homo sapiens cDNA clone
IMAGE:1695540 3' similar to TR:Q19985 Q19985 F40E10.6;, mRNA
                                                     Gaps
                                                   .
0
Length 40;
                                                   6; Indels
  Score 15.4; DB 8;
Pred. No. 1.7e+05;
                                                0; Mismatches
                                                                                                                             8 CCTCCTCTCTCTTCTTTT 32
                                                                                                    1 CCCTCCTTCTTGTACTCCTCCTGCT 25
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
A-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Yv. Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU102295 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone LNG04811, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.2%; Score 15.4; DB 1; Length 49; 76.0%; Pred. No. 1.7e+05; ive 0; Mismatches 6; Indels
Trace considered overall poor quality Possible reversed clone: similarity on wrong strand
                                                                                                          organism="Mus musculus"
                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:789921"
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                                      High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                     /sex="pooled"
/tissue_type="embryo"
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                                                                                                                               /mol_type="mRNA"
/strain="C57BL/6J"
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AU102295/c
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Marray.M., Hillier, J., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
/lab_host="DH108"
/clone lib="Scares pregnant uterus NbHPU"
/note="Organ: uterus, Vector: p17T3-Pac; Site 1: Not 1;
Site 2: ECO RI; lst strand cDNA was primed with a Not I
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 988 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructed by M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1695540"
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                                                                                                                                                                                                                                                                                                                                                                                             sex="female"
                                        Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                       1. .46
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Best Local Similarity
Matches 19; Conserv
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Best Local Simi
Matches 18;
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AZ537227/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                     AZ854411 29 bp DNA linear GSS 21-FEB-2001 2M0158B05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0158B05 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Wector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 29)

Dunn, D., Acyagi, A., Barber, W., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                      Gaps
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                     /mol_type="mRNA"
/db_xref="texaon:9606"
/dcone="LM004811"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                       59.2%; Score 15.4; DB 1; Length 50; larity 94.1%; Pred. No. 1.7e+05; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0158 row: B column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
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organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
1. .29
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/clone="UUGC2M0158B05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ854411.1 GI:13043500
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                                                                                                                               Query Match
Best Local Similarity
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli Xil0-Gold (Stratagene) calls and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ537227 40 bp DNA linear GSS 06-NOV-2000 AST-2P03013 Genetrap PC-3 Human Prostatic Carcinoma Library Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomytoin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomytin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAmp-1 and used to transform DH5-alpha competent
by splice donor from the trapping construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Henkel, G. Liyanage, M., Pratt, E., Huang, D., Riley, M., Bernardino, A., Durick, K. and Pollok, B. Exon-trap tags from a PC-3 GenomeScreen(TM) Library Unpublished (2000)
                                                                                                                                                                                                    Score 15; _____Pred. No. 2.3e+05;
                                                                                                                                                                                                    Score 15; DB 8; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.7%; Score 15; DB 8; Length 40; 78.3%; Pred. No. 2.3e+05; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens genomic 5', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Adenocarcinoma"
/cell_type="Epithelial"
/cell_line="PC-3"
                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                      4 TCCTTCTTGTACTCCTCCTGCTC 26
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                              ch 57.7%;
1 Similarity 78.3%;
18; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Greg Henkel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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AZ456843/c
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VERSION
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COMMENT
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KEYWORDS
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/clone="1024-019-K13"
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/tissue_type="storage root"
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/note:"vector: pCMVSPORT6; Site 2: Not1;
/not
                                                                                                                                                     EST 06-DEC-2002
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2M0202C09F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0202C09 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          Beta vulgaris
Mukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 45)
Hervig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7;
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7;
Sequencing granted in the context of the GABI-Beet
project, local P1: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                              612843-024-019-K13-T7 MPIZ-ADIS-024-storage root Beta vulgaris CDNA clone 024-019-K13 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 45
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Best Local Similarity 72.0%; Pred. No. 2.4e+05;
Matches 18; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAx-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 45 Std Error: 0.00
Plate: 19 row: K column: 13
Seq primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
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                                                                                                                                                                                                                                                            BQ590260
BQ590260.1 GI:26119843
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12472698
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AZ942099/c
                                                                                                                                      LOCUS
                                                                                                          BQ590260/c
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VERSION
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PUBMED
COMMENT
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                                                               RESULT 28
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

1 (bases 1 to 26)

1 (bases 1 to 26)

1 (lam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Mehmoud, M., Meenen, B., Pedersen, T.,

Reilly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah

Rm. 300. Elomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCCTCCTTCTTGTACTCCTCCTGCTC 26
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Location/Qualifiers
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Mus musculus (house mouse)
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AZ456843.1 GI:10614968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 56.9%;
Best Local Similarity 73.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                          USA
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5

ORGANISM

KEYWORDS

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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39 bp mRNA linear EST 11-AUG-2004 AT794161 Antirrhinum majus cDNA clone 018 3 04 h20, mRNA sequence. AJ794161. GI:51109489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 Ubase; 1 to 50.

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0566 row: G column: 21
Seg primer: CGTTGTAAAACGACGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="UUGC1M0566G21"
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Location/Qualifiers
                                Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 32
AJ794161/c
LOCUS
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                                                                                                                                                       REFERENCE
AUTHORS
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KEYWORDS
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                                          "Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalais; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Lo 44)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Reilly,M., Rose,M., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wiright,D., Weiss,R. Tingey,A., von Diasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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AZ767297.1 GI:12885248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="B. Coli strain XLIO-Gold, Tl-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Famil: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 0259 row: J column: 24 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .44
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="taxon:10090"
'clone="UUGC1M0259J24"
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                             Mus musculus (house mouse)
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source

FEATURES

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Gaps ;

VERSION

DEFINITION

ACCESSION

VERSION

RESULT 31 AZ767297

Matches

8

ORIGIN

us-10-788-779-8.rst

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/...c.= invace.avarious...
/tissue_type="adenocarcinoma"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC_39"
/clone="Degan: pancreas; Vector: poTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: poTB7; Site_1: XhoI;
Site_2: BcoRI; cDNA made by oligo-dT priming.
Directionally cloned into BcoRI/KhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies)."
                                                                                                                                                                                                                                                                                     38 bp mRNA linear EST 15-SEP-2000 601306513F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640802 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 15-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Concentium/LLNL at:
Clone distribution: MGC Concentium/LLNL at:
http://image.llnl.gov
Plate: LLCM345 row: j column: 03
High quality sequence stop: 38.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 38)

NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HD--09-H17.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-H17, mRNA sequence.
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                                                               Score 14.6; DB 7; Length 50; Pred. No. 3.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                            4; Indels
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                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3640802"
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75.0%;
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81.0%;
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Best Local Similarity 75.09
                                                                                                              Conservative
    RT-PCR."
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hes 17; Conserv
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                                                                   Query Match
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CF319095/c
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                 BE736376/c
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JOURNAL
COMMENT
                                                                                                            Matches
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SOURCE
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 50)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                  Antirrhinum majus (snapdragon)
Antirrhinum majus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="proliferated callus on 2N6 media for 30 days" /lab_host="proliferated callus plasmid conditions in a callus plasmid cond library (NACL)" /note="Weetor: pCR4-TOPO; Site 1: Ecokl; mRNA was capped with oligoribonucleotides and then used as templates for
                                                                                                                                                                    Zachgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z.
Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GreenGene Biotech Inc.; Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NACL--05-B16.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-B16, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech In
Genomics and Genetics Institute, GreenGene Biotech In
of Bloscience and Bioinformatics, Myongdi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.2%; Score 14.6; DB 1; Length 39;
larity 81.0%; Pred. No. 3.3e+05;
Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                          Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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    .39
    /organism="Antirrhinum majus"

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/clone="NACL--05-B16"
/tissue_type="callus"
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/cultivar="Nackdong"
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CF329688.1 GI:33807590
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                                                                                                                                Antirrhinum.
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (basel to 48)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ443723
1M0238D11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0238D11 F, genomic survey sequence.
AZ443723
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                                                                       (organism="Oryza sativa (japonica cultivar-group)"
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0
                                                                                                                                                                                                                                                                                                                                                                                                       Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
    bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.4%; Score 14.4; DB 7; Best Local Similarity 75.0%; Pred. No. 3.9e+05; Matches 18; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0238D11"
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  Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                     SM Oryza sativa (apponica cultivar_group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoddeae; Oryzae; Oryza.
Enthartoddeae; Oryzae; Cheong, T., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:19947"
| Clone="MpD-09-H17"
| tissue_type="callus" | dev_stage="proliferated callus on 2N6 media for 2 weeks" | dev_stage="proliferated callus on 2N6 media for 2 weeks" | dev_stage="rs.coli DH108" | clone lib="0sHhAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF292564 43 bp mRNA linear EST 14-AUG-2003 30DGS--01-G23.gl Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--01-G23, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
I (base; I to 43)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(120un) for Ihr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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|mol_type="mRNA"
|cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
                                                                       Oryza sativa (japonica cultivar-group)
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerses and T4 polymurclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complamentary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana T-DNA flanking sequence GK-272H06-015096, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Subchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.

Details on the protocols used for generation of the sequence are
described in References 1-3. Re-examination of the source from
which this sequence has been produced indicates that the sequence
is of low reliability. Therefore, no information on a potential
insertion site is deduced. The sequences are generated at the MPI
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Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.4%; Score 14.4; DB 8; Length 48; 75.0%; Pred. No. 3.9e+05; 1ve 0; Mismatches 6; Indels
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8

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/note-rpcR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ645664 21 bp DNA linear GSS 14-DEC-2000 1M0511C13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0511C13 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                      /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="columbis 0"
/db xref="taxon:3702"
/clone="GK-272H06-015096"
/clone="GK-272H06-015096"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Talminates, December 1, 1 (Dases I to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Nouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T-DNA derived sequences were removed."
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Best Local Similarity 75.0%; Pred. No. 3.9e+05;
Matches 18; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0511C13"
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Fax: 801 585 7177
Emall: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
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                                                                                                                                                                                                                                                                                                                    /ecotype="Col-0"
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GSS.
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AUTHORS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwaptot (gqi 4712114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CU/838U3 39 bp mRNA linear BST 05-AUG-2004 BL279A_A01 6-Day Axolotl Tail Blastema (6DAxBL) Ambystoma mexicanum cDNA 57 similar to hypothetical protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/cell type="regenerating tail blastema" (coll type="regenerating tail blastema" (formellib="c-bay Axolot! Tail Blastema (formellib="c-bay Axolot! Tail Blastema (formellib="c-bay Axolot!")"
/note="Vector: pCMVSport6; Site!: NotI; Site_2: Sall;
Unnormalized coDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into NotI-Sall site of pCMVSport6. Bacterial host is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                               /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mi-cbg.de
Blate: BLZ79A row: 01 column: A
Seg primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .39
/organism="Ambystoma mexicanum"
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/db xref="taxon:8296"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ambystoma mexicanum (axolot1)
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Contact: Elly M. Tanaka
Tanaka Lab
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KEYWORDS
SOURCE
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CO783803/c
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DEFINITION
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EMDH10B-TONA. Average insert size is 1.67 kB TAG_LIB=6DAXBL"
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ORIGIN

Score 14.2; DB 7; Pred. No. 4.6e+05; 0; Mismatches 3; Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative C

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Gaps

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3 CICCIICITGIACICCICC 21 20 CrrcrrcrrArgcrccrcc 2 ઠે . G

Search completed: November 18, 2005, 21:12:54 Job time : 1246.65 secs

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Sequence Sequence 3

Sequence

Sequence Sequence

Sequence s

Sequence

Sequence

Sequence 13555, 7 Sequence 13559, 7 Sequence 62750, 7

Sequence 22, App]

Sequence Sequence 1

Scoring table:

Database

Perfect score:

Sequence:

OM nucleic

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DB 1; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: SEIDMAN, JOHN
APPLICANT: WATKINS, HUGH
APPLICANT: WATKINS, HUGH
APPLICANT: ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
COTIV: BOSTON
US-08-993-008A-2

US-08-993-008A-3

US-08-361-920-41

US-08-479-939-41

US-08-479-939-52

US-08-479-939-52

US-08-479-939-52

US-08-483-432-41

US-08-324-001-19

US-08-324-001-10

US-08-324-001-11

US-09-366-108A-13555

US-09-866-108A-13559

US-09-966-108A-13559

US-09-966-108A-13559

US-08-999-367-10

US-08-899-367-10
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Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
CLASSIPTCATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GML-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCCTCCTTCTTGTACTCCTCCTGCTC 26
                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   Massachusetts: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: cDNA
US-07-989-160-8
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                                                                                                                                                                                                                                                                                                                                                                                                             US-07-989-160-8
                                                   STATE:
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Sequence 4, Appli
Sequence 13556, A
Sequence 13557, A
Sequence 13557, A
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9, Appli
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                                                                                                             November 18, 2005, 00:26:13 ; Search time 50.5171 Seconds (without alignments) 842.154 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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Sequence 1
Sequence 1
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-905-125A-204

US-09-906-705-204

US-09-906-700-204

US-09-906-700-204

US-09-909-904-204

US-09-909-906-618-204

US-09-906-618-204

US-09-906-618-204

US-08-906-747-4

US-08-906-747-4

US-08-589-109A-12

US-08-580-923-34

US-09-580-923-34

US-09-580-923-34

US-09-580-923-17

US-09-866-108A-13556

US-09-866-108A-13558
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                                                                                                                                                                                                                                                                                                        1202784 segs, 818138359 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 - nucleic search, using sw model
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26
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Match Length
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Score

Reģult No.

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Gaps

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Indels

Gaps

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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thums, Thums, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                 FEATURE:
JOTHER INFORMATION: Description of Artificial Sequence: Synthetic
JOTHER INFORMATION: oligonucleotide probe
US-09-907-794A-204
                                                                                                                                                                                                                                                                  Query Match 66.2%; Score 17.2; DB 4; Length 24; Best Local Similarity 86.4%; Pred. No. 9.1e+02; Matches 19; Conservative 0; Mismatches 3; Indels
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CURRENT APPLICATION NUMBER: US/09/905,125A

CURRENT APPLICATION NUMBER: US/09/905,125A

CURRENT APPLICATION NUMBER: US/09/905,125A

PRIOR PELING DATE: 2000-02-22

PRIOR PELING DATE: 1909-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 204, Application US/09905125A Patent No. 6664376
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Grimaldi, Christopher J.
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                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
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Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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SEQ ID NO 204
LENGTH: 24
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUCREMY APPLICATION NOMBER: US/09/30//794A

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2001-02-22

PRIOR PELING DATE: 1999-07-28

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PELING DATE: 1999-07-28

PRIOR PELING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR PELING DATE: 1999-09-13

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PRIOR PELING DATE: 1999-11-20
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CURRENT APPLICATION NUMBER: US/09/907,794A
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FILING DATE: 1999-12-16
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
1 CCCTCCTTCTTGTACTCCTCCTGCTC 26
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                 US-09-907-794A-204/c
; Sequence 204, Application US/09907794A
; Patent No. 6635468
                                                                                                                                                                                                                                                                                                                                                                                 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Giang
Gerber, Hangpeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT

PRIOR FILI PRIOR APPL

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Paoni, Nicholas F
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide probe US-09-905-125A-204
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-00
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR PILING DATE: 1999-12-00
PRIOR PILING DATE: 1999-12-00
PRIOR FILING DATE: 1999-12-00
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 24
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CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
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ORGANISM: Artificial Sequence
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Gerritsen, Mary E
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Paoni, Nicholas F.
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Best Local Similarity 86.4%
Matches 19.% Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: oligonucleotide probe
                        PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-13

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PRIOR FILING DATE: 1999-12-07

PRIOR PRIOR FILING DATE: 1999-12-07

PRIOR PRIOR FILING DATE: 1999-12-07

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; 0 Length 24; Indels Query Match 66.2%; Score 17.2; DB 4; Best Local Similarity 86.4%; Pred. No. 9.1e+02; Matches 19; Conservative 0; Mismatches 3; 5 CCTTCTTGTACTCCTGCTC 26 cchachachachcchchachc 3

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Sequence 204, Application US/09906700 Patent No. 6723535 Godowski, Paul J. Grimaldi, Christopher J. Hillan, Kenneth, J Kljavin, Ivar J. Mather, Jennie P. Ferrara, Napoleone Filvaroff, Ellen Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Gurney, Austin L. Genentech, Inc. Botstein, Avi Desnoyers, Luc Eaton, Dan L. Sherman Goddard, A.

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APPLICANT: Tumas, Daniel,
APPLICANT: Tumas, Daniel,
APPLICANT: William, P. Mickey
APPLICANT: William, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT APPLICATION NUMBER: PCT/US0/04414
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
RIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
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PRIOR PLING DATE: 1999-09-13
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COTHER INFORMATION: Description of Artificial Sequence: Synthetic;
COTHER INFORMATION: Oligonucleotide probe
US-09-903-603A-204
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US09/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 204
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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FILING DATE: 1999-11-29
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
                 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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ORGANISM: Artificial Sequence
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Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT:
                                                          APPLICANT: Stewart, Timocny A.
APPLICANT: Exerwart, Timocny A.
APPLICANT: Tunas, Daniel
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
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FILE REPERENCE: 10466-14
FRIOR FILING DAME: 2000-02-2
FRIOR FILING DAME: 1999-07-7
FRIOR FILING DAME: 1999-07-7
FRIOR FILING DAME: 1999-07-8
FRIOR FILING DAME: 1999-09-18
FRIOR FILING DAME: 1999-09-18
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FRIOR FILING DAME: 1999-10-3
FRIOR FILING DAME: 1999-11-3
FRIOR APPLICATION NUMBER: PCT/US99/2099
FRIOR FILING DAME: 1999-11-3
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US-09-903-603A-204/c
; Sequence 204, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Generatech, Inc.
; APPLICANT: Ashkenazi, Avi
. APPLICANT: Botstein, David
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Roy, Margaret Ann
crewart, Timothy A.
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                                                   Stewart, Timot
Tumas, Daniel
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Query Match 66.2%; Score 17.2; DB 4; Length 24; Best Local Similarity 86.4%; Pred. No. 9.1e+02; Matches 19; Conservative 0; Mismatches 3; Indels

Desnoyers, Luc Eaton, Dan L.

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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, I.
APPLICANT: William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT FILING DATE: 2001-07-18
FRICH APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2000-02-22
FRICH APPLICATION NUMBER: PCT/US00/04414
FRICH APPLICATION NUMBER: US 60/145,698
FRICH RILING DATE: 1999-07-06
FRICH RILING DATE: 1999-07-06
FRICH RILING DATE: 1999-07-08
FRICH RILING DATE: 1999-07-08
FRICH RILING DATE: 1999-07-08
FRICH RILING DATE: 1999-09-08
                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence PEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-904-920A-204
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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-09-15
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FILING DATE: 1999-10-05
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 204
LENGTH: 24
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Sao, Wei-Qiang
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APPLICANT: Wood, William, I.
LITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
LITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT AFILIALION NUMBER: DCJ/USO/04141
PRIOR APPLICATION NUMBER: DCJ/USO/04414
PRIOR PLILING DATE: 2000-02-22
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-06
PRIOR PLILING DATE: 1999-07-06
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PRIOR PLILING DATE: 1999-09-13
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PRIOR PLILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLILING DATE: 1999-09-15
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PRIOR PLILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLILING DATE: 1999-11-20
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PRIOR PLILING DATE: 1999-12-02
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CURRENT FILING DATE: 2001-07-13
                                                                                                                  RESULT 7
US-09-904-920A-204/C
; Sequence 204, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
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Paoni, Nicholas F.
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Mather, Jennie P.
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Eaton, Dan L.
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Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P
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Best Local Similarity 86.4%
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Botstein, David
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Gao, Wei-Qiang
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Eaton, Dan L.
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APPLICANT: Genentech, Inc.
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US-09-906-618-204/c
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APPLICANT:
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-908-064-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
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CURRENT APPLICATION NUMBER: US/09/905,381A
CURRENT FILING DATE: 2001-07-13
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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8-09-905-381A-204/c
; Sequence 204, Application US/09905381A
; Patent No. 6818746
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan, James
Paoni, Nicholas F.
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Gerritsen, Mary E.
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goddard,
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APPLICANT:
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Gaps
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ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-905-381A-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                       PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-8
PRIOR FILING DATE: 1999-09-13
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PRIOR PRIOR DATE: 2000-01-05
PRIOR PRIOR DATE: 2000-01-05
PRIOR PRIOR DATE: 2000-01-05
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
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Sequence 12, Application US/08589109A
; Sequence 12, Application US/08589109A
; Patent No. 6365344
; GENERAL INFORMATION:
; APPLICANT: No. 6365344an, Garry P.
APPLICANT: No. 6365344an, Garry P.
TITLE OF INVENTION: Methods for Screening for Transdominant;
TITLE OF INVENTION: Effector Peptides and RNA Molecules
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; CATREET: CA
      Direct Determination of Expanded
Nucleotide Repeats in the Human Genome
TITLE OF INVENTION: Direct Determination of Expanded TITLE OF INVENTION: Nucleotide Repeats in the Human NUMBER OF SEQUENCES: 11
CORRESPONDERS: ADDRESS: ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                       CURRANTE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEFRAX: 617-861-6240
TELEFRAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,109A
FILING DATE: 23-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SILVa, Robin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.4%; Score 17; DB 1; Best Local Similarity 80.0%; Pred. No. 1.1e+03; Matches 20; Conservative 0; Mismatches 5
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DESCRIPTION: /desc = "Synthetic"
                                                                                                                                                                                                                                                                                                                              COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING EVERN
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                             CITY: Lexington
STATE: Massachusett
COUNTRY: USA
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                                                                  APPLICANY: Recwart, Innochy APPLICANY: APPLICANY: APPLICANY: APPLICANY: APPLICANY: APPLICANY: APPLICANY: APPLICANY: APPLICANY: APPLICANY: APPLICANY: William, P. Mickey APPLICANY: William, P. Mickey APPLICANY: William, P. Mickey CHING COF INNOCH APPLICANY: William, P. Mickey CHING COF INNOCH APPLICANY: Model and Transmembrane Polypeptides and Nucleic CIRRENT APPLICATION: Acids Encoding the Same CIRRENT APPLICATION: NUMBER: US/09/906,618
PRIOR FILING DATE: 2000-00-16
PRIOR FILING DATE: 1999-00-00
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
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Patent No. 5695933
GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.
                                                     Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                               Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 CCTTCTTGTACTCCTCC
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US-08-068-747-4/C
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Best Local 8
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Gaps

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Length 30; 5; Indels

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APPLICANT: Crouzet, Joel
APPLICANT: Scherman, Daniel
APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Wils, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELLX FORMATION WITH AN
TITLE OP INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
FILE REPERENCE: 03804.0138-01
CURRENT PILING DATE: 2000-05-26
CURRENT PILING DATE: 1997-06-09
PRIOR PILING DATE: 1997-06-09
PRIOR PLING DATE: 1997-06-09
PRIOR PLING DATE: 1997-06-09
PRIOR PLING DATE: 1997-06-09
PRIOR PLING DATE: 1997-06-36
PRIOR PLING DATE: 1997-06-36
PRIOR PLING DATE: 1997-06-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: oligonucleotide
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 3; 1
Pred. No. 1.2e+03;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STRREET: 500 Arcola Road, Malistop 3C43
CITY: Collegeville
              1 CCICCICCICCICCICCICCICCIC 72
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ZIF: 19426
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION UNMER: FR 94/15162
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-860-038-17/c
; Sequence 17, Application US/08860038
; Patent No. 6287762
; Patent No. 6287762
                                                                                                                                                                          Sequence 34, Application US/09580923
Patent No. 6319672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: WILE, Pierre
TITLE OF INVENTION: PURIFICAT
TITLE OF INVENTION: WITH AN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 80.0%;
Matches 20; Conservative
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                                                                                                                                             US-09-580-923-34/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΡÀ
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| Sequence 9, Application US/08068747
| Patent No. 5695933
| GENERAL INFORMATION:
| APPLICANT: Shealling, Martin APPLICANT: Hudson, Thomas J. APPLICANT: Hudson, David E. TILLE OF INVENTION: Direct Determination of Expanded TITLE OF INVENTION: Nucleotide Repeats in the Human Genome NUMBER OF SEQUENCES: 11
| CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STREET: Laxington STREET: Laxington STREET: Massachusett
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 1.1e+03;
0; Mismatches 5; Indels
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RECISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-64259/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRRANDENNESS: unknown
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DESCRIPTION: /desc = "Synthetic"
US-08-068-747-9
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0%;
Matches 20; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 39 base pairs
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown;
MOLECULE TYPE: cDNA
US-08-589-109A-12
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Best Local Similarity
Matches 20; Conserv
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Gaps . 0

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Query Match
Best Local Similarity 80.0
Matches 20; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN TITLE OF INVENTION: IMPOBLIZED OLIGONUCLECTIDE
FILE REFERENCE: 03804.0138-01
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Pred. No. 1.2e+03;
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; OTHER INFORMATION: oligonucleotide
US-09-580-923-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 06/860,038
PRIOR RILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/FR95/01468
PRIOR PILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 50
APPLICATION NUMBER: "C
FILING DATE: 08-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Oligonucleotide"
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Patent No. 6319672
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Patent No. 6355803
                                                                                                            REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST94
TELECOMMUNICATION INFORMATION:
TELEPRAN: (610) 454-3816
TELEPRAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 80.0%;
Matches 20; Conservative
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STRANDEDNESS: single
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GENERAL INFORMATION
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ઠે g APPLICANT: Anand Natrajan

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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR PELING DATE: 2000-10-36

PRIOR PLILING DATE: 2000-10-04

PRIOR PELING DATE: 2000-10-04

PRIOR PELING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
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MAMB/KEY: misc_feature
LOCATION: (223) ...(223)
OTHER INFORMATION: VANCO B PMP-PROBE 496.20 (ON PMP) IN EXAMPLE 16
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APPLICANT: David Sharpe
APPLICANT: Say-Jong Law
TITLE OF INVENTION: NEAR INFRARED CHEMILUMINESCENT
TITLE OF INVENTION: ACRIDINIUM COMPOUNDS AND USES THEREOF
FILE REFERENCE: CCDLT-258XX
CURRENT APPLICATION NUMBER: US/09/371,489
CURRENT PILLING DATE: 1999-08-10
EARLIER PILLING DATE: 1998-08-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: ON 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.4%; Score 17; DB 3; Length 50;
80.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 5; Indels
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CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
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US-09-866-108A-13556/c
; Sequence 13556, Application US/09866108A
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SEQ ID NO 13556
LENGTH: 25
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RESULT 21
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APPLICANT: GU, Yizhong

APPLICANT: JI, Yongqang

APPLICANT: PENN, Sharron G.

APPLICANT: RANK, David K.

APPLICANT: RANK, David R.

APPLICANT: SHANNON, Wark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7
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CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-010-04

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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                                                                                                                                             Query Match 63.8%; Score 16.6; DB 4; Length 25; Best Local Similarity 82.6%; Pred. No. 1.5e+03; Matches 19; Conservative 0; Mismatches 4; Indels
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US-09-866-108A-13558/c
; Sequence 13558, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-866-108A-13557/c
; Sequence 13557, Application US/09866108A
; Patent No. 6686188
                                                                                                                                                                                                                                                                                               3 CTCCTTCTTGTACTCCTCCTGCT 25
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13556
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ORGANISM: Homo sapiens
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Best Local Similarity
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-00-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
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Patent No. 6686188
SEQ ID NO 13558
LENGTH: 25
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JI, Yonggang
PENN, Sharron G.
HANZEL, David K.
RANK, David R.
CHEN, Wensheng
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Sequence 7, Application US/09012515A

Patent No. 6127210

GENERAL INFORMATION:
APPLICANT: Berlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Cottarel, Guillaume
TITLE OF INVENTION: IMMUNSUPPRESSANT TARGET PROTEINS
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
                                                                                               4; Indels
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ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,515A
                    Score 16.6; DB 2;
Pred. No. 1.6e+03;
0; Mismatches 4;
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Best Local Similarity 82.6%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-036.02
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: FOLEY, HOAG & ELLOT LLP
STREET: One Post Office Square
CITY: Boston
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/360,144
FILING DATE: 20-DEC-1994
ATTORNEY/AGENT INFORMATION:
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Patent No. 6150137
GENERAL INFORMATION:
APPLICANT: Berlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
                                                                                                                                                            4 TCCTTCTTGTACTCCTCCTGCTC 26
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                              63.8%;
82.6%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                         Best Local Similarity 82.6
Matches 19; Conservative
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STRANDEDNESS: single
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US-08-360-144A-7/c
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Sequence 36, Application US/08741931

Patent No. 586634

GENERAL INFORMATION:
APPLICANT: HOUTZ, Robert L.
TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF
TITLE OF INVENTION: SUBUNIT N-METHYLTRANSPERASE
TITLE OF INVENTION: SUBUNIT N-METHYLTRANSPERASE
TITLE OF INVENTION: SUBUNIT N-METHYLTRANSPERASE
CORRESPONDENCES: 41

CORRESPONDENCE ADDRESS:
ADDRESSES: Burns, Doane, Swecker & Mathis
CORRESPONDENCE ADDRESS:
ADDRESSES: Burns, Doane, Swecker & Mathis
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER REABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER REABALE FORM:
COMPUTER REABALE FORM:
COMPUTER REABALE FORM:
COMPUTER SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
COMPUTER: DEM PC compatible
COMPUTER: DEM PC COMPATIBLE
COMPUTER: DEM PC COMPATIBLE
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,931
FILING DATE: 31-0CT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/391,000
FILING DATE: 1-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Metth, Donna M.
REGISTRATION NUMBER: 028750-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-201
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/391,000
FILING DATE: 21-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 028750-123
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-5021
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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EDNESS: single
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STRANDEDNESS:
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| Sequence 7, Application US/09012504A |
| Patent No. 6464974 |
| Patent No. 6464974 |
| Patent No. 6464974 |
| Patent INFORMATION |
| APPLICANT: Berlin, V. APPLICANT: Cottant Octant Octant Octant Octant Octant Octant Octant Octant Octant APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Octant APPLICANT: APPLICANT: NUMBER: 08/09/012,504A |
| TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS |
| TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS |
| TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS |
| FILE REFERENCE: APPLICATION NUMBER: 08/360,144 |
| PRIOR APPLICATION NUMBER: 08/360,144 |
| PRIOR APPLICATION NUMBER: 08/250,795 |
| PRIOR FILING DATE: 1994-05-27 |
| SEQ ID NO 7 |
| SEQ ID NO 7 |
| CLENGTH 48 |
| CLENGTH 48 |
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| CLENGTH 48 |

TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES
ADDRESSES: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FLING DATE: US/08/360,144A

FLING DATE: US/08/360,144A

CLASSIFICATION: 435

ATTONREY/AGENT INPORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REGISTRATION NUMBER: 36,709

REGISTRATION INPORMATION:

TELEPHONE: 617-832-1000

INPORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LEMETHER CHARACTERISTICS:

LEMETHER CHARACTERISTICS:

LEMETHER CHARACTERISTICS:

LEMETHER CHARACTERISTICS:

LEMETHER CHARACTERISTICS:

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                                                                                                                                                                                                                                                                                                                      STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TCCTTCTTGTACTCCTCCTGCTC 26
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 82.0-
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                        STREET: One E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-360-144A-7
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US-09-012-399A-7/c
; Sequence 7, Application US/09012399A
; Patent No. 6509152
; GENERAL INFORMATION:
; APPLICANT: Berlin, Vivian
; APPLICANT: Chiu, Maria Isabel
; APPLICANT: Cottarel, Guillaume
; APPLICANT: Cottarel, Guillaume
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLOT LLP
; STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Immunosuppressant Target Proteins NUMBER OF SEQUENCES: 25
MOMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,399A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/360,144
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matchew, Nathew PREJESTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-832-1000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TTELENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 82.6
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
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Length 28;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 33-95
TELECOMMUNICATION INFORMATION:
                                                                                        63.1%; Score 16.4; DB 3; 76.9%; Pred. No. 1.9e+03; tive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
63.1%; Score 16.4; DB 3;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08993008A
Patent No. 6153596
GENERAL INFORMATION:
APPLICANT: Liotta, Dennis C.
APPLICANT: Petros, John A.
APPLICANT: Wey, Shiow-Jyi
APPLICANT: Rarr, Joan F.
TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Greenlee, Winner and Sullivan STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                  1 CCCTCCTTCTTGTACTCCTCCTGCTC 26
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303-499-8080
                                                                         Query Match
Best Local Similarity 76.9%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
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STATE: CO
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HYPOTHETICAL:
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US-08-361-920-41/c
                       ; ANTI-SENSE:
US-08-993-008A-2
                                                                                                                                                                                                                                                                                                  RESULT 29
US-08-993-008A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIPICATION S14
PRIOR APPLICATION 514
PRIOR APPLICATION DATE: 34-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan Sally A.
REGISTRATION NUMBER: 32,064
REFRENCE/DOCKET NUMBER: 33-95
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10F0809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08993008A
PETENT NO. 6153596
GENERAL INFORMATION:
APPLICANT: Liotta, Dennis C.
APPLICANT: Wetros, John A.
APPLICANT: Wetros, John A.
APPLICANT: War, Joan F.
APPLICANT: War, Joan F.
TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
STREET: S370 Manhattan Circle, Suite 201
                                                      CIASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDRER:
THING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION WOMBER: US 08/250,795
FILING DATE: 20-DEC-1994
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDENNES: single
                APPLICATION NUMBER: PCT/US95/06722 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 TCCTTCTTGTACTCCTCCTGCTC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 Trcracrigracrecreere 20
                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: other nucleic acid PCT-US95-06722-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 28 base pairs TYPE: nucleic acid STRANDEDNESS: double
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 28
US-08-993-008A-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Bor
STATE: CC
COUNTRY:
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Gaps

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,939
                    405 Lexington Avenue, 62nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERNICE/DOCKET NUMBER: 3435.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCCTCCTTCTTGTACTCCTCCTGCTC 26
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-361-920-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.99
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212-867-0298
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                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 32
US-08-479-939-41/c
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                                        APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hastrup
TITLE OF INVENTION: Or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS: ADDRESSE NO. 54570460 NO. 54570460th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hagen, Frederick
APPLICANT: Hagen, Frederick
APPLICANT: Hagen, Frederick
APPLICANT: Sven, Hastrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 54570460 No. 5457046disk of No. 5457046th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Par Poppy disk
COMPUTER: Poppy disk
COMPUTER: Par Poppy disk
COMPUTER: Par Poppy disk
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REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
TELECHONE: 212-867-0123
TELEPHONE: 212-867-0123
INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-0CT-1992
APPLICATION NUMBER: DK 1158/90
PRIOR APPLICATION NUMBER: DK 1158/90
PRIOR APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCCTCCTTCTTGTACTCCTCCTGCTC 26
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Sequence 41, Application US/08361920
Patent No. 5457046
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 52, Application US/08361920
Patent No. 5457046
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-361-920-52/c
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ADDRESSEE: No. 56865930 No. 5686593disk of No. 5686593th America, Inc. STREET: 405 Lexington Avenue, 62nd Floor CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Patent No. 5686593
GENERAL INFORMATION:
APPLICANT: Woeldike, Helle F.
APPLICANT: Hjort, Caraten M.
APPLICANT: Hjort, Caraten M.
APPLICANT: Sven, Hastrup
TITLE OF INVENTION: An Baryme Capable of Degrading Cellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.1%; Score 16.4; DB 1; Length 40; 76.9%; Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
STATE: New York
CUUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PENDY disk
COMPUTER: PENDY disk
COMPUTER: PENDY disk
COMPUTER: PENDY disk
COMPUTER: PENDY DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-CT-1992
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-CT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 08-MAY-1990
PRICA APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATPLICATION NUMBER: DK 158/90
FILING DATE: 08-MAY-1991
ATPLICATION NUMBER: PCT/DK91/00124
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APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Syen, Hastrup
TITLE OF INVENTION: Or Hemicellulose
TITLE OF INVENTION: Or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57632540 No. 5763254th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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COUNTRY: United States of America
ZID: 10174-6201
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
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COMPUTER: TEM PC COMPUTER: TEM PC COMPUTER: TEM PC COMPUTER: TEM PC COMPUTER: PAPLICATION DATA:
APPLICATION NUMBER: US/08/483,432
FILING DATE: OT-JUN-1995
RILING DATE: OT-JUN-1995
PRILING DATE: OT-JUN-1995
APPLICATION NUMBER: US 07/940,860
FILING DATE: OT-PUT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: OT-JUN-1992
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: OT-JUN-1990
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FILING DATE: OT-JUN-1990
FILING DATE: OT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCCTCCTTCTTGTACTCCTCCTGCTC 26
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
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; Sequence 41, Application US/08483432
Patent No. 5763254
; GENERAL INFORMATION:
                                                                                               ATTORNEY/AGENT INCOMES OF NAME: Lamblitis, Elias J.
NAME: Lamblitis, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0298
TELEFAX: 212-867-0298
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-479-939-52
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
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Patent No. 5686593

Patent No. 56865930

Patent No. 56865930

Patent No. 56865930

Patent No. 56865930

Patent No. 56865930

Patent No. 56865930

TITLE OF INVENTION: An Enryme Capable of Degrading Cellulose

TITLE OF INVENTION: An Enryme Capable of Degrading Cellulose

TITLE OF INVENTION: An Enryme Capable of Degrading Cellulose

TITLE OF INVENTION: An Enryme Capable of Degrading Cellulose

TITLE OF INVENTION: An Enryme Capable of Degrading Cellulose

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TITLE OF INVENTION: An Enryme Cellulose

TITLE OF INVENTION: An Enryme Cellulose

TITLE OF INVENTION: An Enryme Cellulose

TITLE OF INVENTION: An Enryme Cellulose

TITLE OF INVENTION AN Enryme

STREET: New York

COMPUTER: New York

STATE: New York

STATE: New York

COMPUTER: Ploppy disk

COMPUTER: STATE OF TOWN 1995

CLASSIFICATION NUMBER: US/08/361,920

FILING DATE: 22-DEC-1994

FILING DATE: 22-DEC-1994

FILING DATE: 22-DEC-1994

FILING DATE: 22-DEC-1994

FILING DATE: DE TOWN 1995

CLASSIFICATION NUMBER: US 09-MAY-1990

PRICE APPLICATION NUMBER: DR 1158/90

FILING DATE: DR 1158/90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFRENCE/DOCKET NUMBER: 3435.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                             CLASSIFICATION: 435

RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0361,920
FILING DATE: 22-DEC-1994
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: PCT/DK91/00124
APPLICATION NUMBER: PCT/DK91/00124
ATTORNEY/AGENT: NOFORMATION:
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MOLECULE TYPE: DNA (genomic)
                   07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-MAY-PRIOR APPLICATION DATA:
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NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REGISTRATION NUMBER: 22000-20544.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
    0; Mismatches
                                                                                               1 CCCTCCTTCTTGTACTCCTCCTGCTC 26
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755 PAGE MILL ROAD
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TELEX: 706141 MRSN FOERSSFO
INPORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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76.9%;
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Best Local Similarity 76.9%
Marches 20; Conservative
         20; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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US-08-324-001-19
                                                                                                                                                                                                                                                                                                                                                    US-08-324-001-19
         Matches
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STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hastrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
                                                                                                                                                                                                                                                                                                                                               63.1%; Score 16.4; DB 1; Length 40; 76.9%; Pred. No. 1.9e+03; ive 0; Mismatches 6; Indels
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FILING DATE: 28-0CT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 5763254
GENERAL INFORMATION:
                                                                             TYPE: nucleic acid
sTRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-483-432-41
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76.9%;
                                    1: 40 base pairs
nucleic acid
EDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                      Query Match 63.1
Best Local Similarity 76.9
Matches 20; Conservative
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: sing
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Best Local Similarity
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US-08-483-432-52/c
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Sequence 20, Application US/08324001
| Patent No. 5624803
| GENERAL INFORMATION:
| APPLICANT: NOONBERG, SARAH B. APPLICANT: HUNT, C. ANTHONY
| TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM TITLE OF SEQUENCES: 25
| NUMBER OF SEQUENCES: 25
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS:
Sequence 19, Application US/08324001
| Patent No. 5624803
| GENERAL INFORMATION |
| APPLICANT: NOONBERG, SARAH B. |
| APPLICANT: HUNT, C. ANTHONY |
| TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING |
| TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM |
| TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM |
| TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM |
| TOTALE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM |
| TOTALE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM |
| TOTALE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM |
| STREET: 755 PAGE MILL ROAD
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Sequence 11, Application US/08324001

Betent No. 5624803

GENERAL INPORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING TITLE OF INVENTION:

MUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSER:

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,001
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REGISTRATION NUMBER: 32000-20544.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.1%; Score 16.4; DB 1; 76.9%; Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                               63.1%; Score 16.4; Dilarity 76.9%; Pred. No. 2e+0 Conservative 0; Mismatches
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US-09-362-842-38/c
; Sequence 38, Application US/09362842
; Patent No. 6511824
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TELEX: 706111 MRSN FORESFO
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                  ; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLGY: linear
US-08-324-001-10
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Best Local Similarity 76.9
Matches 20; Conservative
   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-324-001-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 755 PAGI
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APPLICANT: HUNT, C. ANTHONY
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,001
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REGISTRATION NUMBER: 22000-20544.20
TELERANC (415) 813-5600
TELERAN: (415) 813-5600
TELERAN: (415) 813-5600
TELERAN: (415) 844-0792
TELERA: (415) 494-0792
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COUNTRY: USA
ZID: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/324,001
FILLING DATE: 13-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22000-20544.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCCTCCTTCTTGTACTCCTGCTC 26
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Patent No. 5624803
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : (415) 494-0792
706141 MRSN FOERSSFO
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US-08-324-001-20
                                                                                                 94304-1018
PALO ALTO
                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-324-001-10
                                                                         COUNTRY:
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Matches
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GENERAL INFORMATION:

APPLICANT: Buchman et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK

TITLE OF INVENTION: CHANNELS AND METHODS OF USE

FILE REFERENCE: 7326-104

CURRENT APPLICATION NUMBER: US/09/362,842

CURRENT PELICATION NUMBER: 1999-07-28

PRIOR APPLICATION NUMBER: 09/270,767

PRIOR APPLICATION NUMBER: 09/270,767

NUMBER OF SEQ ID NOS: 70

SOTWARE: Patentin Ver. 2.1

SEQ ID NO 38

LENGTH: 24

TYPE: DNA

VERBER ORGANISM: Drosophila melanogaster

US-09-362-842-38
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Search completed: November 18, 2005, 11:22:02 Job time : 51.5171 secs

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Sequence 60793, A Sequence 204, App Sequence 204, App Sequence 204, App Sequence 204, App Sequence 204, App Sequence 204, App Sequence 204, App

Sequence

4pp 4pp 4pp 4pp

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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Sequence 8, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDWAN, CHRISTINE
; APPLICANT: SRIDWAN, JOHN
; APPLICANT: ROSENWENG, ANTHONY
; TITLE OF INVENTION: A METHON POR DETECTING
; TITLE OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
US-10-843-527-225372
US-11-036-317-60793
                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/469,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  CURRENT APPLICATION DATA:
  Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
  CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-08-469-172-8
Sequence 8, Appli
Sequence 11341, A
Sequence 12431, A
Sequence 224398,
                                                                                  (without alignments)
615.265 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          number of results predicted by chance to have a an or equal to the score of the result being printed, y analysis of the total score distribution.
                                                                     November 18, 2005, 06:36:48; Search time 349.468 Seconds
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:: /cgn2_6/ptodata1/pubpna/US07_PUBCOMB.seq:*

:: /cgn2_6/ptodata1/pubpna/US07_NEW_PUB.seq:*

:: /cgn2_6/ptodata1/pubpna/US06_PUBGOMB.seq:*

:: /cgn2_6/ptodata1/pubpna/US06_PUBGOMB.seq:*

:: /cgn2_6/ptodata1/pubpna/US07_NEW_PUB.seq:*

:: /cgn2_6/ptodata1/pubpna/US08_PUBCOMB.seq:*

:: /cgn2_6/ptodata1/pubpna/US08_PUBCOMB.seq:*

:: /cgn2_6/ptodata1/pubpna/US09_PUBCOMB.seq:*

:: /cgn2_6/ptodata1/pubpna/US10B_PUBCOMB.seq:*

:: /cgn2_6/ptodata1/pubpna/USS0B_PUBCOMB.seq:*

:: /cgn2_6/ptodata1/pubpna/USS0B_PUBCOMB.seq:*

:: /cgn2_6/ptodata1
         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-469-172-8

US-10-788-779-8

I US-10-843-527-11341

I US-10-843-527-22315

I US-10-843-527-224398
                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                     9794790 segs, 4134909567 residues
                                                                                                            US-10-788-779-8
26
1 CCCTCCTTGTACTCCTGCTC 26
                                                                                                                                                                                                                                                                                                        Published Applications NA:*
                                                 nucleic search, using sw model
                                                                                                                                                                                                                                                                                   Listing first 45 summaries
                                                                                                                                                                  Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0% Maximum Match 100%
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Match Length
                                                                                                                                                        IDENTITY NUC
                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 50
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68.5
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68.5
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115.
1198....
1222....
1224....
1226...
1226...
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Pred. No.

26 26 17.8 17.8

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Score

Result Š.

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TYPE: DNA
CORGANISM: SARS Virus
US-10-843-527-11341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-843-527-12315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 11341
LENGTH: 25
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US-10-788-779-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10788779
Publication No. US20040152121A1
GENERAL INFORMATION:
APPLICANT: SEIDWAN, CHRISTINE
SEIDWAN, JOHN
WATKINS, HIGH
ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
DISEASE-ASSOCIATED MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 26; DB 8;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/469,172
FILING DATE: «Unknown»
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.

ZI: 02.109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/788,779
FILING DATE: 27-Feb-2004
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
NFORMATION FOR SEO ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
LENGTH: 26 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CCCTCCTTCTTGTACTCCTGCTC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCTCCTTCTTGTACTCCTCCTGCTC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 26 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: BOSTON
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 227-E
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
US-08-469-172-8
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US-10-788-779-8
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                                                                                                                                               Gaps
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Sequence 12315, Application US/10843527

Publication No. US20050136395A1

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.1

CURRENT APPLICATION NUMBER: US/10/843,527

CURRENT APPLICATION NUMBER: 60/469,545

PRIOR APPLICATION NUMBER: 60/469,545

PRIOR PILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 228196

SOFTWARE MICRAITAY Probe Sequence Listing Generator V 1.1

SEQ ID NO 12315

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Michael Mittmann
APPLICANT: Eric Schell
TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REPERENCE: 3602.1
CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT FILING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 238196
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                           Score 26; DB 20; Length 26; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.5%; Score 17.8; DB 24; 90.5%; Pred. No. 1.4e+03; Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 68.5%; Score 17.8; DB 24; Best Local Similarity 90.5%; Pred. No. 1.4e+03; Matches 19; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                          0; Mismatches
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                    1 CCTCCTTCTTGTACTCCTCCTGCTC 26
                                                                                                                                                                                                                                                                                                                                    US-10-843-527-11341

Sequence 11341, Application US/10843527

; Publication No. US20050136395A1

; GENERAL INFORMATION:
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                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 26; Conservative 0
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Best Local Similarity 90.5'
Matches 19; Conservative
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TYPE: DNA
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APPLICANT:
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APPLICANT:
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Publication No. US20050214823A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
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| Publication No. US2050136395A1
| General Information of US20050136395A1
| General Information of US20050136395A1
| APPLICANT: Michael Mittmann
| APPLICANT: Michael Mittmann
| TILE OF INVENTION: Methods of Genetic Analysis of SARS Virus FILE REFERENCE: 3602.1
| TILE OF INVENTION NUMBER: US/10/843,527
| CURRENT APPLICATION NUMBER: 0044.05-10
| PRIOR APPLICATION NUMBER: 00469,545
| PRIOR FILING DATE: 2003-05-08
| NUMBER OF SEQ ID NOS: 238196
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| SEQ ID NO 225372
               Sequence 224398, Application US/10843527
| Publication No. US20050136395A1
| GENERAL INFORMATION:
| APPLICANT: Michael Mittmann
| APPLICANT: Eric Schell
| TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
| FILE REFRENCE: 3602.1
| CURRENT APPLICATION NUMBER: US/10/843,527
| CURRENT APPLICATION NUMBER: 60/469,545
| PRIOR APPLICATION NUMBER: 60/469,545
| PRIOR PILING DATE: 2004-05-10
| PRIOR PILING DATE: 2003-05-08
| NUMBER OF SEQ ID NOS: 238196
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| SEQ ID NO 224398
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1.4e+03;
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Matches 19; Conservative
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Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-224398
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CORGANISM: SARS Virus
US-10-843-527-225372
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US-10-843-527-225372/c
US-10-843-527-224398/c
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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                                                                                                                                                                                      67.7%; Score 17.6; DB 26; Length 25; larity 83.3%; Pred. No. 1.7e+03; Conservative 0; Miamarat.
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 60793
LENGTH: 25
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CURRENT FILING DATE: 2002-01-04
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Stewart, Timothy A
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Gerritsen, Mary E
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Botstein, David
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Eaton, Dan L.
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US-11-036-317-60793
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Best Local Similarity
Matches 20; Conserv
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Godowski, Paul J.
Grimaldi, Christopher J.
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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APPLICANT: Pan, James
APPLICANT: Panni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: oligonucleotide probe
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 24
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CURRENT APPLICATION NUMBER: US/09/909,088B
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Best Local Similarity
Matches 19; Conserva
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Gaps
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PRIOR PELLING DATE: 1990-07-28

PRIOR PELLING DATE: 1990-07-28

PRIOR PELLING DATE: 1990-07-28

PRIOR PELLING DATE: 1990-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PELLING DATE: 1999-09-08

PRIOR PELLING DATE: 1999-09-13

PRIOR PELLING DATE: 1999-09-15

PRIOR PELLING DATE: 1999-09-15

PRIOR PELLING DATE: 1999-09-15

PRIOR PELLING DATE: 1999-09-15

PRIOR PELLING DATE: 1999-09-15

PRIOR PELLING DATE: 1999-10-05

PRIOR PELLING DATE: 1999-11-29

PRIOR PELLING DATE: 1999-11-29

PRIOR PELLING DATE: 1999-11-20

PRIOR PELLING DATE: 1999-11-30

PRIOR PELLING DATE: 1999-11-30

PRIOR PELLING DATE: 1999-12-02

PRIOR PELLING DATE: 1999-12-02

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ORGANISM: Artificial Sequence
FEATURE:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-08
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PELICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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PRIOR PEDICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/3051
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30911
                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hilavin, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gerritsen, Mary E
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   ilvaroff, Ellen
ong, Sherman
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                                         APPLICANT: Turnas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT PILING DATE: 1006-07-122
PRIOR APPLICATION NUMBER: PCT/0800/04414
PRIOR APPLICATION NUMBER: G 6/143,048
PRIOR APPLICATION NUMBER: G 6/145,698
PRIOR APPLICATION NUMBER: US 6/146,222
PRIOR APPLICATION NUMBER: US 6/146,222
PRIOR APPLICATION NUMBER: PCT/0899/20594
PRIOR APPLICATION NUMBER: PCT/0899/20594
PRIOR APPLICATION NUMBER: PCT/0899/20594
PRIOR APPLICATION NUMBER: PCT/0899/20594
PRIOR PLING DATE: 1999-00-15
PRIOR APPLICATION NUMBER: PCT/0899/2044
PRIOR PLING DATE: 1999-00-15
PRIOR PLING DATE: 1999-00-15
PRIOR PLING DATE: 1999-00-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/0899/2804
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/0899/2806
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/0899/2806
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/0899/2806
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR APPLICATION NUMBER: PCT/US99/30099
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PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR APPLICATION
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Stewart, Timof
Tumas, Daniel
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ö Gaps .; 0 Length 24; 3; Indels ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-902-853-204 Query Match
66.2%; Score 17.2; DB 9;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USO0/00219
PRIOR FILING DATE: 2000-01-05
WUMBER OF SEQ ID NOS: 423
SEQ ID NO 204
LENGTH: 24 ORGANISM: Artificial Sequence FEATURE: TYPE: DNA à

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Gaps

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3; Indels

0; Mismatches

Best Local Similarity 86.4 Matches 19; Conservative

Query Match

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66.2%; Score 17.2; DB 9; Length 24; 86.4%; Pred. No. 2.4e+03;

5 CCTTCTTGTACTCCTCCTGCTC 26

Sequence 204, Application US/09902853
Publication No. US20020192659A1
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bestein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.

RESULT 11 US-09-902-853-204/c

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
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PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: 95/665,350

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR APPLICATION NUMBER: PCT/US99/20944
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OR APPLICATION NUMBER: PCT/US99/21547

OR APPLICATION NUMBER: PCT/US99/21547

OR APPLICATION NUMBER: PCT/US99/23089

OR FILING DATE: 1999-10-05

OR FILING DATE: 1999-11-29

OR APPLICATION NUMBER: PCT/US99/28214

OR APPLICATION NUMBER: PCT/US99/28313

OR APPLICATION NUMBER: PCT/US99/28564

OR FILING DATE: 1999-11-30

OR APPLICATION NUMBER: PCT/US99/28564

OR FILING DATE: 1999-12-02

OR APPLICATION NUMBER: PCT/US99/28565

OR FILING DATE: 1999-12-02

OR APPLICATION NUMBER: PCT/US99/28565

OR FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
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Publication No. US20020197671A1
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Oiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: 10466-14 CURRENT APPLICATION NUMBER: US/09/907,841 CURRENT FILING DATE: 2001-11-20
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                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-824-204
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PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PAPLICATION NUMBER: PC7/28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER 0F SEQ ID NOS: 423
SEQ ID NO 204
LENGTH: 24
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/21547
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Publication No. US20020198366A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Wood, William, I.
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Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerritsen, Mary E
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Best Local Similarity 86.4
Matches 19; Conservative
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Botstein, David
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Eaton, Dan L.
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US-09-907-841-204/c
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Goddard, A.
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US-09-903-640-204/c
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APPLICANT: Kljavin, Ivar.
APPLICANT: Kljavin, Ivar.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
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APPLICANT: Williams, P. Mickey
APPLICANTION NUMBER: US/09/904,011
CURRENT APPLICATION NUMBER: US/065,350
RIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 2000-09-18
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
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PRIOR PILING DATE: 1999-09-15
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                                                   Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 423
SEQ ID NO 204
LENGTH: 24
                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: oligonucleotide probe
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 204, Application US/09904011
Publication No. US20030003530A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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US-09-904-011-204/c
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR PILLING DATE: 1999-10-05
PRIOR FILLING DATE: 1999-10-05
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PRIOR FILLING DATE: 1999-110-29
PRIOR PILLING DATE: 1999-11-29
PRIOR PILLING DATE: 1999-11-30
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PRIOR PILLING DATE: 1999-12-02
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PRIOR PILLING DATE: 1999-12-03
PRIOR PILLING DATE: 1999-12-03
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PRIOR PILLING DATE: 1999-12-20
PRIOR PILLING DATE: 1999-12-20
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PRIOR PILLING DATE: 1999-12-20
PRIOR PILLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 24
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CURRENT APPLICATION NUMBER: US/09/903,640
CURRENT FILING DATE: 2001-07-11
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
FEATURE:
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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Best Local Similarity 86.4
Matches 19; Conservative
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Botstein, David
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Eaton, Dan L.
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APPLICATION NUMBER: PCT/US99/23089
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Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/908,093
CURRENT APPLICATION NUMBER: US/09/098,093
CURRENT APPLICATION NUMBER: US/09/0414
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
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OR FILING DATE: 2000-09-18
OR APPLICATION NUMBER: PCT/USO0/04414
OR FILING DATE: 2000-02-22
OR APPLICATION NUMBER: US 60/143,048
OR FILING DATE: 1999-07-07
OR APPLICATION NUMBER: US 60/146,598
OR FILING DATE: 1999-07-28
OR PLILING DATE: 1999-07-28
OR APPLICATION NUMBER: PCT/US99/20594
OR FILING DATE: 1999-09-08
OR PLILING DATE: 1999-09-08
OR PLILING DATE: 1999-09-13
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: 1999-09-13
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 09/665,350 PRIOR FILING DATE: 2000-09-18 NUMBER OF SEQ ID NOS: 423 SEQ ID NO 204 LENGTH: 24
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Filvaroff, Bilen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
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Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3;
              FRIOR TELLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR PILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/3091

PRIOR PILING DATE: 1999-12-0

PRIOR PILING DATE: 1999-12-16

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PRIOR PILING DATE: 1999-12-20

PRIOR PILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

LENGTH: 24
APPLICATION NUMBER: PCT/US99/28214
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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APPLICANT: Williams, Danlel
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TITLE OF INVENTION Acids Encoding the Same
TITLE OF INVENTION Acids Encoding the Same
TITLE OF INVENTION Acids Encoding the Same
TITLE OF INVENTION Acids Encoding the Same
TITLE OF INVENTION Acids Encoding the Same
TITLE PRESENCE: 10466-1360
RELOR APPLICATION NUMBER: 036/66,350
RELOR APPLICATION NUMBER: 05/66,350
RELOR APPLICATION NUMBER: 05/66,350
RELOR APPLICATION NUMBER: 05/0146,222
RELOR APPLICATION NUMBER: 05/0146,222
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RELOR APPLICATION NUMBER: 05/01899/2094
RELOR FILING DATE: 1999-0-3-18
RELOR APPLICATION NUMBER: PCT/US99/2094
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86.4%; Pred. No. 2.4e+03;
tive 0; Mismatches 3;
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Stewart, Timothy A.
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   Kljavin, Ivar J.
Mather, Jennie P.
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Best Local Similarity 86.4
Matches 19; Conservative
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Tumas, Daniel
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          PRIOR PILLING DATE: 2000-02-22
PRIOR PILLING DATE: 1999-07-07
PRIOR PILLING DATE: 1999-07-07
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PRIOR PILLING DATE: 1999-07-26
PRIOR PILLING DATE: 1999-07-26
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APPLICATION NUMBER: PCT/US00/04414
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Pong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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ORGANISM: Artificial Sequence
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Goddard, A.
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Best Local Similarity 86.4<sup>†</sup>
Matches 19<sup>‡</sup>, Conservative
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Botstein, David
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Eaton, Dan L.
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US-09-906-838-204/c
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Desnoyers, Luc
Eaton, Dan L.
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Gao, Wei-Qiang
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US-09-907-942-204/c
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APPLICANT: Wood, William, I.
FITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
HTLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: DCT/USOO/04414
PRIOR PLING DATE: 2000-02-2
PRIOR PLING DATE: 2000-02-2
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
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CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
                                                                                                                                                                   Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                         Gerritsen, Mary E.
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Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                     Gaps
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     Length 24;
                                                        Indels
Query Match 66.2%; Score 17.2; DB 10; Best Local Similarity 86.4%; Pred. No. 2.4e+03; Matches 19; Conservative 0; Mismatches 3;
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PRIOR APPLICATION NUMBER: PCT/USOU/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
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CURRENT FILING DATE: 2002-01-22
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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                                                                                                                                                                                                                                                                                   Sequence 204, Application US/09907942
Publication No. US20030027146A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
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Hillan, Kenneth, J
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Goddard, A.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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                          PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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PRIOR PLING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: PCT/US99/28113
PRIOR PLING DATE: 1999-11-20
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Publication No. US20030036061A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Wood, William, I.
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Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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US-09-909-204-204/c
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic;
TITLE OF INVENTION: Acide Encoding the Same
FILE REPERBRICE: 10466-14
CURRENT PAPLICATION NUMBER: US/09/904,859
CURRENT FILING DATE: 2001-07-12
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/141,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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                          PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 2044
LENGTH: 24
PRIOR APPLICATION NUMBER: PCT/US99/30911
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APPLICATION NUMBER: PCT/US99/20594
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PRIOR APPLICATION NUMBER: PCT/US99/20944
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Publication No. US20030036060A1
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                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gaps

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APPLICANT: Wood, William, I. 'I'TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3;
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CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US/65,350
PRIOR APPLICATION NUMBER: US/65,350
PRIOR PLINKO DATE: 2000-09-18
PRIOR PLINKO DATE: 2000-09-18
PRIOR PLINKO DATE: 2000-03-22
PRIOR PELING DATE: 1999-07-26
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PRIOR PLING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
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PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28514
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PELING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28056
PRIOR APPLICATION NUMBER: PCT/US99/28056
PRIOR APPLICATION NUMBER: PCT/US99/28056
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28056
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PELING DATE: 1999-12-02
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PRIOR FLILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 204
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Wood, William, I.
                                                                                                                                                                                                                                                            Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                Gurney, Austin L.
Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
Godowski, Paul J.
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          CURRENT PELICATION NUMBER: US/09/909,204
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US/09/909,204
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-26
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; Sequence 204, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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ORGANISM: Artificial Sequence
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Gerritsen, Mary E.
Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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LENGTH: 24
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe
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ilarity 86.4%; Pred. No. 2.4e+03;
Conservative 0; Mismatches 3;
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CURRENT FILING DATE: 2002-01-22
PRIOR FILING DATE: 2000-02-22
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
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PRIOR FILING DATE: 1999-11-30

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PRIOR FILING DATE: 1999-11-02

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PRIOR PILING DATE: 1999-12-20

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PRIOR PILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
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; Publication No. US20030039972A1
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                                                                                                                                              Timothy A
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                                                                              Pan, James
Paoni, Nicholas F.
                                 Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                           Roy, Margaret Ann
                                                                                                                           Stewart, ...
Stewart, ...
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APPLICANT:
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APPLICANT: Williams, P. Mickey
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
ITILE OF INVENTION: Acids Encoding the Same
ITILE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/904,786
CURRENT APPLICATION NUMBER: 12001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2000-09-18
NUMBER: OF SEQ ID NOS: 423
IENGTH: 24
ILENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-786-204
Sequence 204, Application US/09904786
Publication No. US20030039969A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Godowski, Paul J.
Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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ORGANISM: Artificial Sequence
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ilarity 86.4%;
Conservative
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
Eaton, Dan L
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                      Length 24;
                                                                                                                  Indels
                                                      Score 17.2; DB 10;
Pred. No. 2.4e+03;
0; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/09/903,786
CURRENT FILING DATE: 2001-07-11
PRIOR PELICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-22
PRIOR PELICATION NUMBER: DCT/US00/04414
PRIOR PILING DATE: 1999-07-07
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/28565
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o. US20030044793A1
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Grimaldi, Christopher J.
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ilarity 86.4%;
Conservative
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Filvaroff, Ellen
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Hillan, Kenneth, J
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Roy, Margaret Ann
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; Sequence 204, Application US/O
; Publication No. US20030044793A
; GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botsetain, David
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Mather, Jennie P.
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICATION NUMBER:
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US-09-906-700-204
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APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 1099-07-07

PRIOR PLILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR PLILOR DATE: 1999-07-26

PRIOR PLILOR DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-8

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR PLILOR DATE: 1999-09-18

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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Paoni, Nicholas F.
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Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie P.
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                           Genentech, Inc.
Ashkenazi, Avi
Botstein, David
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APPLICANT: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Pred. No. 2.4e+03;
0; Mismatches 3;
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Mather, Jennie P
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Best Local Similarity 86.4
Matches 19; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT:
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APPLICANT: Stewart, Timcthy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,903
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OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-903-786-204
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Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3;
                       PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PRILING DATE: 1999-12-20
PRIOR PRILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 24
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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APPLICATION NUMBER: PCT/US99/20594
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Publication No. US20030044839A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
     PRIOR FILING DATE: 1999-12-02
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                TYPE: DNA
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THIRE REPRENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,119

CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US/09/904,119

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

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PRIOR PILING DATE: 1999-09-13

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PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-02

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                          Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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                                                                                                                                                         Kljavin, Ivar J.
Mather, Jennie P.
Goddard, A.
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APPLICANT:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-903-749A-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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TITLE OF INVENTION: Acids Encoding the Same
                                                                                                       PRIOR PELLING DATE: 2001-07-11
PRIOR PELLING DATE: 2000-02-22
PRIOR PELLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US09/0414
PRIOR FILING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-08
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PRIOR PELLING DATE: 1999-12-06
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PRIOR PELLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR PELLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR PELLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR PELLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR PELLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR PELLING DATE: 1999-10-05
                       FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,749A
CURRENT FILING DATE: 2001-07-11
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Publication No. US20030049621A1
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L
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LENGTH: 24
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APPLICANT: Pann, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timethy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
                                                          ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: oligonucleotide probe US-09-904-956-204
                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                     Length 24;
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                                                                                                                                                                                     Score 17.2; DB 10;
Pred. No. 2.4e+03;
0; Mismatches 3;
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CURRENT FILING DATE: 2001-07-10
PRIOR PLILING DATE: 2001-07-10
PRIOR PLILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR PLILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-28
PRIOR PRILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR FILING DATE: 1999-09-15
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillain, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Publication No. US20030049676A1
GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                     Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative (
ORGANISM: Artificial Sequence FEATURE:
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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PPLICANT: Pan, James
PPLICANT: Roy, Margaret Ann
PPLICANT: Stewart, Timothy A.
PPLICANT: Tumas, Daniel
PPLICANT: Tumas, Daniel
PPLICANT: Wood, Williams, P. Mickey
PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,956

CURRENT PILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: US/09/904,956

CURRENT FILING DATE: 2000-02-22

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

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PRIOR PILING DATE: 1999-09-13

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PRIOR PIL
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                      Sequence 204, Application US/09904956 Publication No. US20030049622A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                              APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Paoni, Nicholas F
Roy, Margaret Ann
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US-09-903-943-204/c
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-902-736-204
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR PAPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PLILNG DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER: PCT/US00/00219
NUMBER: PCT/US00/00219
NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER: PCT/US00/00219
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NUMBER: PCT/US00/00219
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Grimaldi, Christopher J.
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Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Paoni, Nich
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86.4%; Pred. No. 2.4e+03;
tive 0; Mismatches 3;
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US-09-907-794-204
                 PRIOR APPLICATION NUMBER: DS 50/146,222
PRIOR APPLICATION NUMBER: DCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
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APPLICATION NUMBER: US 60/146,222
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Grimaldi, Christopher J.
Gurney, Austin L.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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ORGANISM: Artificial Sequence
PEATURE:
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Gerritsen, Mary E
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Mather, Jennie P.
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Best Local Similarity 86.4<sup>§</sup>
Matches 19, Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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and Transmembrane Polypeptides and Nucleic
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US-09-904-462-204
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86.4%; Pred. No. 2.4e+03;
ive 0; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/09/904,462

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR PLILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR PILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20544

PRIOR PILING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-18

PRIOR PILING DATE: 1999-07-18

PRIOR PILING DATE: 1999-07-18

PRIOR PILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR PILING DATE: 1999-09-13
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FRIOR FILING DATE: 1999-110-05
FRIOR FILING DATE: 1999-11-29
FRIOR FILING DATE: 1999-11-29
FRIOR FILING DATE: 1999-11-29
FRIOR FILING DATE: 1999-11-30
FRIOR FILING DATE: 1999-12-02
FRIOR FILING DATE: 1999-12-02
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FRIOR FILING DATE: 1999-12-02
FRIOR FILING DATE: 1999-12-02
FRIOR PRICATION NUMBER: PCT/US99/30095
FRIOR FILING DATE: 1999-12-16
FRIOR FILING DATE: 1999-12-16
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FRIOR FILING DATE: 1999-12-16
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FRIOR FILING DATE: 1900-12-20
FRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
FRIOR FILING DATE: 2000-01-05
FRIOR FILING DATE: 2000-01-05
FRIOR FILING DATE: 2000-01-05
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Grimaldi, Christopher J.
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Kljavin, Ivar J.
Mather, Jennie P.
Perrara, Napoleone
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                                                                                                             Gao, Wei-Qiang
Gerber, Hanspeter
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                                     llvaroff, Ellen
ong, Sherman
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tewart,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LING DATE:
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                  APPLICANT: Three of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.2%; Score 17.2; DB 10;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 204
LENGTH: 24
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Publication No. US20030054351A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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Stewart, Timothy A.
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ORGANISM: Artificial Sequence
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US-09-904-462-204/c
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic Oligonucleotide Probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR PEDLICATION NUMBER: DCT/USO/04414
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-8
PRIOR PELING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PRIOR DATE: 1999-09-13
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-112-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
SEQ ID NO 204
LENGTH: 24
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APPLICATION NUMBER: PCT/US99/21547
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Publication No. US20030054400A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Wood, William, I.
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Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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US-09-902-692-204/c
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,925

CURRENT APPLICATION NUMBER: US/09/907,925

CURRENT APPLICATION NUMBER: US/09/907,925

CURRENT APPLICATION NUMBER: US/05/65,350

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-15

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PRIOR PILING DATE: 1999-09-15

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PRIOR PILING DATE: 1999-10-15

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PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02
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Publication No. US20030054352A1
                        CCTTCTTGTACTCCTCCTGCTC 26
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Godowski, Paul J.
Grimaldi, Christopher J.
                                                               24 CCTACTACTCCTCCTGCTC 3
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Paoni, Nicholas F.
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Stewart, Timothy
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                    FRIOR FILING DATE: 1999-10-05
PRIOR PELICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR PELICATION NUMBER: PCT/US99/28313
PRIOR PLING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PELICATION NUMBER: PCT/US99/28565
PRIOR PELICATION NUMBER: PCT/US99/30095
PRIOR PELICATION NUMBER: PCT/US99/30091
PRIOR PELICATION NUMBER: PCT/US99/30911
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PRIOR PELICATION NUMBER: PCT/US99/3099
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PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 24
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APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 204, Application US/09903520 Publication No. US20030054401A1
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Grimaldi, Christopher J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Mather, Jennie P.
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Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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Tumas, Daniel
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US-09-903-520-204/c
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              PRIOR FILING DATE: 1999-07-07
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PRIOR PELING DATE: 1999-07-28
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FILING DATE: 2000-02-22
APPLICATION NUMBER: US 60/143,048
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Grimaldi, Christopher J.
Gurney, Austin L.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Botstein, David
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Best Local Similarity 86.4
Matches 19; Conservative
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
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Roy, Margaret Ann
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Gerber, Hanspeter
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Mather, Jennie P.
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
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                                                                                                                             Eaton, Dan L.
                                                                                                Desnoyers,
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APPLICANT:
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                                                                                                                                                                                                                                                                                        APPLICANY: WOOCH, MILLIAM, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File REPERNECE: 10466-14

TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/905,056

CURRENT PLING DATE: 2002-01-25

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PLING DATE: 1999-07-28

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                                                                                                                                                                              Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey Wood, William, I.
                                                                                                                                                 Roy, Margaret Ann
Stewart, Timothy A.
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ORGANISM: Artificial Sequence
                                                                                       Pan, James
Paoni, Nicholas F.
                         Kljavin, Ivar J.
Mather, Jennie P.
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Best Local Similarity
Matches 19; Conserv
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LENGTH: 24
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: oligonucleotide probe
                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Gaps

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Conservative

; Sequence 204, Application US/09909064; Publication No. US20030059772A1; GENERAL INFORMATION:

RESULT 40 US-09-909-064-204/c

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Query Match 66.2%; Score 17.2; DB 10; Length 24; Best Local Similarity 86.4%; Pred. No. 2.4e+03; Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Search completed: November 18, 2005, 15:41:09 Job time : 351.468 secs

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Sequence:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
Unclassified.
I (bases 1 to 25)
Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
Method for detecting hypertrophic cardiomyophathy associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25;
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Mammalian DED-caspase homolog usurpin.
BD217302
BD217302.1 GI:33027072
JP 2002520025-A/17.
Homo sapiens (human)
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/mol_type="unassigned DNA"
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Location/Qualifiers
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5429923.
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AX521320

AX622320

BD005994

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AR401452
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112902.1 GI:910879
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           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                        4708233 segs, 24227607955 residues
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1 CAACTCATCACCACTCTCTTCCATC 25
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PAT 17-JUL-2003

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 41)

1 (Nases 1 to 41)

2 (Nathologo, D.W., Xanthoudakis, S. and Roy, S. Mammalian DED-caspase homolog usurpin)

2 (Datent: JP 2002520025-A 10 09-JUL-2002;

2 (Datent: JP 2002520025-A 10 09-JUL-2002;

3 (Datent: JP 2002520025-A 10 09-JUL-2002;

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Unclassified.
1 (bases 1 to 46)
Abramson,R.D. and Gelfand,D.H.
5' to 3' exonuclease mutations of thermostable DNA polymerases
Patent: US 5795762-A 38 18-AUG-1998;
Location/Qualifiers
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llarity 83.3%; Pred. No. 8.3e+03;
Conservative 0; Mismatches 4;
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llarity 85.7%; Pred. No. 3.2e+04;
Conservative 0; Mismatches 3;
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Sequence 38 from patent US 5466591.
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Sequence 38 from patent US 5795762.
AR023959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens"

    .41
    /organism="Homo sapiens'
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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/organism="unknown"
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Mammalian DED-caspase homolog usurpin.
BD217295.
BD217295.1 GI:33027065
JP 2002520025-A/10.
Homo sapiens (human)
Homo sapiens
Bulancyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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        Nicholson, D.W., Rasper, D.M., Xanthoudakis, S. and Roy, S.
                                                                                                                                                                                                                                                                                                                                                 /organism='Homo sapiens (human)'.
Location/Qualifiers
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Pred. No. 3.1e+03;
0; Mismatches 4; Indels
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                          Mammalian DED-caspase homolog usurpin
Patent: JP 2002520025-A 17 09-JUL-2002;
MERCK FROST CANADA AND CO
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Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR291854 47 bp DNA Sequence 3589 from patent US 6537751.
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/db_xref="taxon:9606"
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/mol_type="genomic DNA"
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AR291854.1 GI:31679138
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PAT 04-DEC-1998
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                                                                                                                                                                                                                                                          Unknown.
Unclassified.
I (bases I to 20)
Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
Gene sequence for spinocerebellar ataxia type I and method for diagnosis
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Orr,H.T., Ranum,L.P.W., Chung,M.-y. and Zoghbi,H.Y.
Gene sequence for spinocerebellar ataxia type 1 and method for
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                  6; Indels
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85.0%; Pred. No. 9.6e+04;
ive 0; Mismatches 3;
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Pred. No. 9.6e+04;
0; Mismatches 3;
 76.0%; Pred. No. 7.7e+04; tive 0; Mismatches 6
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Patent: US 5834183-A 41 10-NOV-1998;
Location/Qualifiers
1. 20
                                                                                                                                                       Sequence 23 from patent US 5741645.
AR002284.1 GI:3963838
                                                                                                                                                                                                                                                                                                                                                     Patent: US 5741645-A 23 21-APR-1998;
Location/Qualifiers
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Seguence 24 from patent US 5962636.
AR078405
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 41 from patent US 5834183.
AR053135.1 GI:5977997
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/wol_type="unassigned DNA"
                                                1 CAACTCATCACCACTCTTCCATC 25
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85.0%;
 Best Local Similarity 76.03
Matches 19; Conservative
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AR053135/c
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AR078405
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KEYWORDS
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             1 (bases 1 to 46)
Abramson, R.D. and Gelfand, D.H.
5' to 3' exonuclease mutations of thermostable DNA polymerases
Patent: US 5465591-A 38 14-NOV-1995;
Location/Qualifiers
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Compositions and methods for the treatment of tumors
Patent: WO 0109189-A 14 08-FEB-2001;
Genentech, Inc. (US)
Location/Qualifiers
                                                                                                                                                                           Query Match 64.8%; Score 16.2; DB 6; Length 46; Best Local Similarity 85.7%; Pred. No. 3.2e+04; Matches 18; Conservative 0; Mismatches 3; Indels
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"
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1 (bases 1 to 25)

1 (kris, M. and Felder, S. High throughput assay system
Patent: US 6759198-A 147 06-JUL-2004;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other sequences; artificial sequences.
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ARS61920.1 GI:53975571
                                                                                                            /organism="unknown"
/mol_type="unassigned DNA"
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Sequence 14 from Patent WO0109189.
AX080737
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/mol_type="genomic DNA"
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synthetic construct
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Unclassified.
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AR561920/c
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TITLE JOURNAL FEATURES

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ORGANISM

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AR078405.1 GI:10005151

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BD061255 21-AUG-2002 A method to identify and breed corn with increased kernel oil concentration.
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Medicaco sativa
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
Medicago.
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Shuji, H. and Shoji, F.
Novel physiologically active substance, process for producing the
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Patent: JP 2001517951-A 72 09-OCT-2001;
EI DU PONT DE NEMOURS & CO
PN JP 2001517951-A/72
PD 09-OCT-2001
PF 19-WAR-1998 UP 1998844487
PR 24-MAR-1997 US 60/041515
PI ROBERT STEFAN REITER
PC C1201/68
CC Strandedness: Single;
CC Strandedness: Single;
FH Key
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                                                                                     Query Match
59.2%; Score 14.8; DB 6;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 2;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial Sequence"

    .21
    /organism="Medicago sativa"
/mol type="genomic DNA"
/db_xref="taxon:3879"

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JP 2001517951-A/72.
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E27249.1 GI:13025266
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// Organism="synthetic construct"
// mol_type="unassigned DNA"
// db_xref="taxon:32630"
// note="Description of Artificial Sequence: Ag4532 Forward"
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                                                                                     1 (bases 1 to 42)
Bachmaier, K., Hessel, A. John., Neu, N. and Penninger, J. Martin. Peptides capable of modulating inflammatory heart disease Patent: US 5962636-A 24 05-071-1999;
Location/Qualifiers
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other sequences; artificial sequences.
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Patent: EP 1386931-A 142 04-FEB-2004;
Genentech, Inc. (US)
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/mol_type="unassigned DNA"
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Location/Qualifiers
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CQ767675.1 GI:45107802
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synthetic construct
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Matches 16; Conservative
                                                                      Inclassified.
                                  Unknown.
                                                      Unknown.
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PAT 07-JAN-2002
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                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                       Keith, T.

Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
Patent: WO 0178894-A 243 25-OCT-2001;
Genome Therapeutics Corp. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
inflammatory bowel disease
Patent: WO 0178894.A 244 25-OCT-2001;
Genome Therapeutics Corp. (US)
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ilarity 75.0%; Pred. No. 1.9e+05;
Conservative 0; Mismatches 6;
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Pred. No. 1.9e+05;
0; Mismatches 6;
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Sequence 1201 from patent US 6537751.
AR289466 1 GI:31676750
                                Sequence 243 from Patent WO0178894. AX327047
                                                                                                                                                                                                                                                                                         1. .41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                            Homo sapiens (human)
Homo sapiens
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Best Local Similarity 75.04
Matches 18; Conservative
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Matches 18; Conserv
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STS of NotI segment E of chromosome 5 in Giardia duodenalis strain
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                                                                                                                         SHUJI HINUMA, SHOJI FUKUZUMI
C12N15/09, A01K67/027, A61K38/00, A61K38/00, C07K14/47, C07K16/18,
                                                                                                                                                                                                                                     A61K37/02, A61K37/02, C12N5/00, (C12N15/00, C12R1:91), (C12N5/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.

1 (Dases 1 to 50)
Upcroft, J.A., Chen, N. and Upcroft, P.
Mapping variation in chromosome homologues of different Giardia strains
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97077435
8920002
                                                                                                                                                                                                                                                                                                                                 /organism='Unidentified'
Location/Qualifiers
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:5741"
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
Bame and utilization thereof
Patent: JP 1999009286-A 40 19-JAN-1999;
TAKEDA CHEM IND LTD
OS Unidentified
PN JP 1999009286-A/40
PD 19-JAN-1999
PP 27-APR-1999 JP 1998117189
                                                                                                                                                                                                                                                                                                                                                                   1. .31
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Giardia intestinalis
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nes 17; Conservative
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PAT 07-OCT-1996

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Mezes, P.S., Rastelli, L., Herrmann, J.L., Macdougall, J.R., Zhong, H., Casman, S.J., Boldog, F., Shimkets, R.A., Gorman, L., Crasta, O.R., Wayore, K.K., Folkerts, O., Martin, G.B., Eisen, A., Spaderna, S.K., Vernet, C.A., Bergh, C., Spytek, K.A., Dipippo, V.A., Zerhusen, B.D., Peyman, J.A., Ellerman, K., Stone, D.J., Grosse, W.M., Alsobrook, J.P., Lepley, D.M., Rieger, D.K., Burgess, C.B. and Edinger, S. Proteins and nucleic acids encoding same Parent: WO 02055705-A 255 18-JUL-2002; Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified.

1 (bases 1 to 24)

Prockop, D.J., Ala-Kokko, L. and Ritvaniemi, P.

Primers and methods for detecting mutations in the procollagen II gene that indicate a genetic predisposition for osteoarthritis patent: US 5558988-A 208 24-SEP-1996;
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                                                                                                                       Score 14.2; DB 6;
Pred. No. 2.5e+05;
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Pred. No. 2.5e+05;
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/db_xref="taxon:32630"
/note="oligonucleotide primer"
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synthetic construct
other sequences; artificial sequences.
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Sequence 208 from patent US 5558988.
126516
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Sequence 265 from Patent WO02055705.
AX511858
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/mol_type="unassigned DNA"
                                                 /mol_type="unassigned DNA"
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                       /organism="unknown"
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84.2%;
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                                                                                                                       56.8%;
84.2%;
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Best Local Similarity
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Prockop, D. G., Ala-Kokko, L., Williams, C. G., Ritvaniemi, P.,
Baldwin, C., Hopkinson, I. and Ahmad, N. Nina.
Primers and methods for detecting mutations in the procollagen II
gene (COL2A1) that indicate a genetic predisposition for a
COL2A1-associated disease
Patent: US 5948611-A 208 07-SEP-1999;
Location/Qualifiers
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                                                                 1 (bases 1 to 47)
Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 1201 25-WAR-2003;
Location/Qualifiers
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Crf 2? ligands in combination therapy
Crf 2? ligands in combination therapy
Patent: WO 0205749-A 3 24-JAN-2002;
Bristol-Myers Squibb Pharma Company (US)
Location/Qualifiers
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Sequence 3 from Patent WO0205749.
AX496861
                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
                                                                                                                                                                                                                                               organism="unknown"
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An optimal procedure for isolation of mutant mitochondrial alleles.
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11-SED-2001
27-FEB-1998 UP 1998537738
28-FEB-1997 US 08/810599
WILLIAM DAVIS PARKER, CORINNA HERRNSTADT, SOUMITRA GHOSH, EOIN D
                                                                                                                                          1 (bases 1 to 22)
Hernstade, C., Ghosh,S., Fahy,E.D. and Davis,R.E.
An optimal procedure for isolation of mutant mitochondrial alleles
Patent: JP 2001500020-A 2 09-JAN-2001;
                                                                                                                                                                                                                                                          CORINNA HERRNSTADT, SOUMITRA GHOSH, EOIN D FAHY, ROBERT E DAVIS CO7H21/04, C12Q1/68, C12P19/34 Strandedness: Double; Topology: Linear; Key
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Parker, W.D., Herrnstadt, C., Ghosh, S. and Fahy, E.D.
Methods for detecting mitochondrial mutations diagnostic for
Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid
Patent: JP 2001514500-A 22 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methods for detecting mitochonarial mutations diagnostic for Alzheimer's disease and methods for determining heteroplasmy of mitochondrial nucleic acid.
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Methods for detecting mitochondrial mutations diagnostic
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Pred. No. 3.1e+05;
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    .22
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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JP 2001500200-A/2
09-JAN-2001
26-NOV-1997 JP 1998524745
27-NOV-1996 US 08/757438
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BD070465.1 GI:22616068
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 22)
Parker, W.Davis., Herrnstadt, C., Ghosh, S. and Fahy, E.D.
Methods for detecting mitochondrial mutations diagnostic for
Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid
mitochondrial pacle 2 02-NOV-1999;
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Detection of genetic polymorphisms
Patent: WO 02052044-A 7518 04-JUL-2002;
Riken (JP)
        No. 2.5e+05;
smatches 3;
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Pred. No. 2.4e+05;
0; Mismatches 3;
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Seguence 7518 from Patent WO02052044.
AX521320
                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        1. .41
/organism="Homo sapiens"
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Sequence 22 from patent US 5976798.
AR082996.
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                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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          Pred.
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                                                        1 CAACTCATCACCACTCTCT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ACTCATCACCACTCTTTC 21
                                                                            22 CAACTAATCACCATGCTCT 4
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      84.2%;
                                                                                                                                                                                                                                                         Homo sapiens (human)
        Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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RESULT 25 AR082996/c LOCUS

DEFINITION

ACCESSION VERSION

KEYWORDS

SOURCE

ORGANISM

AUTHORS TITLE

JOURNAL

ORIGIN

REFERENCE

RESULT 26 BD005994/c

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FEATURES

ORIGIN

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PAT 28-SEP-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                 56.0%; Score 14; DB 6; Length 25; llarity 77.3%; Pred. No. 3.1e+05; Conservative 0; Mismatches 5; Indels
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Human single nuclocide polymorphisms
Patent: WO 0166800-A 1285 13-SEP-2001;
WHITEHRAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Cargill, M., Ireland, J.S. and Lander, E.S.
Human single nucleotide polymorphisms
Patent: WO 0166800-A 295 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 56.0%; Score 14; DB 6; Best Local Similarity 87.5%; Pred. No. 3e+05; Matches 14; Conservative 1; Mismatches
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Sequence 295 from Patent WO0166800.
AX248216

    .31
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/db_xref="taxon:9606"
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    .31
    /organism="Homo sapiens"

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Homo sapiens
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Matches 17; Conserv
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Homo sapiens
Eukarycis, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Polynucleotides for use as tags and tag complements, manufacture and use thereof
Pand use thereof
Patent: WO 02059355-A 1055 01-AUG-2002;
TM BIOSCIENCE CORP (CA)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/mol_txpe="taxon:32630"
/note="Artificially Synthesized DNA Sequence"
                                                                                                                                                                                                Score 14; DB 6; Lews-Pred. No. 3.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.0%; Score 14; DB 6; Length 24; 77.3%; Pred. No. 3.1e+05; rive 0; Mismatches 5; Indels
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                                                                 'organism='Unidentified'.
                             Location/Qualifiers
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Patent: WO 02072882-A 1702 19-SEP-2002;
OGHAM GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                            24 bp DNA Sequence 1055 from Patent W002059355. AX494081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other sequences; artificial sequences
                                                                                                                                                                                                       Query Match 56.0%; Score 14; DB Best Local Similarity 77.3%; Pred. No. 3.1e Matches 17; Conservative 0; Mismatches
                                                                             1. .25
/organism="Homo sapiens"
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mitochondrial nucleic
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AX494081/c DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 28

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TITLE

REFERENCE

JOURNAL

FEATURES

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RESULT 29 AX610677/c

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Gaps

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PAT 11-MAY-2001

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synthetic construct
other sequences; artificial sequences.

In (bases 1 to 29)
Beavo, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
RIBOZYME PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002509721-A/213
PD 02-APR-2002
PP 20-APR-2002
PP 20-APR-1999 JP 2000541291
PR 27-MAR-1999 JP 2000541291
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PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use thereof
                             Length 20;
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Pred. No. 3.7e+05;
0; Mismatches 2;
                          55.2%; Score 13.8; DB 6; 88.2%; Pred. No. 3.8e+05; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Picoult-Newburg, L. and Pohl, M. Genotyping reagents, kits and methods of Patent: W0 0129262-A 3199 26-APR-2001; Orchid BioSciences, Inc. (US) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Primer"
                                                                                                                                                                                                                                                                                                                  DNA
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                                                                                                                                                                                                                                                                                                       Sequence 3199 from Patent WO0129262. AX118076
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88.2%;
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AX118076/c
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BD197187/c
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I (bases 1 to 20)

Mistubashi,T. and Okumura,N.

Method for differentiating varieties of pig by DNA sequence
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/mol_type="unassigned DNA"
/db_xref="taxon:32610"
/note="Artificially synthesized primer sequence for RT-PCR"
                                                                                                                                                                                                                                                                                                                                                                                                           Method of diagnosing colon and gastric cancers
Patent: WO 2004021010-A 43 11-MAR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the president of the university of Tokyo (JP)
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                   CQ786866 32 bp DNA
Sequence 43 from Patent WO2004021010.
                                                                                                                                                                                                                                                                                                                                     other sequences; artificial sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AACTCATCACCACTCTTCCA 23
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                          30 CACCACACTCTTCCRT 15
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synthetic construct
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polymorphism.
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Matches 17; Conserv
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CQ786866
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E59389/c
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Bahr,G., Cocude,C. and Capron,A.
Rhile polypeptides and its fragments and polynucleotides encoding
said polypeptides and therapeutic uses
Patent: WO 0185955-A 15-NOV-2001;
Istac (FR); INSTITUT PASTEUR DE LILLE (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bahr,G., Cocude,C. and Capron,A.
Rhile polypeptides and its fragments and polynucleotides encoding said polypeptides and therapeutic uses
Batent:WO 0185955-A 8 15-NOV-2001;
Istac (FR) ; INSTITUT PASTEUR DE LILLE (FR)
Location/Qualifiers
                                                                                                                                                                                                                                  Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Targeted alphavirus and alphaviral vectors. BD235713
BD235713.1 GI:33045483
JP 2002523053-A/16.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                               Sequence 4 from Patent WO0185955.
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                                                                                                                               AX300835.1 GI:17382113
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Best Local Similarity 88.2
Matches 15, Conservative
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     RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BD252384 29 bp RNA linear PAT 17-JUL-2003 Regulation of repressor genes using nucleic acid molecules. BD252384 BD252384. GI:33062154 JP 2002541795-A/177.
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Synthesized Hammerhead Ribozyme
The letter 'n' stands for any base or bases forming a loop or
stem-loop
that may contain multiple nucleic acid analogues or 2'- CC
deoxynucleotides.
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PN JP 2002541795-A/177

PD 10-DEC-2002

PF 11-APR-1999 US 60/129390

PI LARRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN IS C12D15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12D5/10, PC C12P21/02,
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1 (bases 1 to 29)

Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.

Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 177 10-DEC-2002;

RIBOZYME PHARMACEUTICALS INC
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PAT 17-JUL-2003

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PN JP 2002523053-A/16

PD 30-JUL-1999 JP 2000566453

PR 30-JUL-1999 JP 2000566453

PR 30-JUL-1999 JP 2000566453

PR 30-JUL-1999 JP 2000566453

PR 30-JUL-1999 JP 2000566453

PR 30-JUL-1999 JP 2000566453

PR 30-JUL-1999 JP 2000566453

PR 50-JUL-1999 JP 2000566453

PR GOIN33/48/(C12N7/00,A61K48/00,A61P35/00,C12N7/00,PC

C12Q1/02,A61K35/76,A61K38/00,A61K48/00,A61P35/00,C12N15/00,PC

C12Q1/02,GC GOIN33/48/(C12N7/00,C12R1:92),(C12Q1/02,C12R1:92),C12N15/00,PC

CC Description of Artificial Sequence: primer

FH Key 1. 31

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                                                                                                                       Dropulic, B., Dropulic, L. and Hardwick, M.J. Targeted alphavirus and alphaviral vectors Patent: JP 2002523053-A 16 30-JUL-2002; JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
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|db_xref="taxon:32630"

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other sequences; artificial sequences.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

RESULT 1

Myosin, heavy chain, non-invasive, hypertrophic cardiomyopathy, diagnosis, primer; mutation, detection, 88. Beta-cardiac myosin heavy chain PCR primer B9.1F. (HARD) HARVARD COLLEGE. (BGHM) BRIGHAM & WOMENS HOSPITAL. (GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA. AAQ91129 standard; cDNA; 25 BP. 92US-00989160. 92US-00989160. 19-FEB-1996 (first entry) 11-DEC-1992; 11-DEC-1992; 04-JUL-1995. US5429923-A. Synthetic. AAQ91129; AAQ91129

Non-invasive method for diagnosis of hypertrophic cardio-myopathy useful for testing asymptomatic individual(s). WPI; 1995-245715/32.

Watkins H, Rosenzweig A;

Seidman J, Seidman C,

Example 1; Col 10; 22pp; English

AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hyperrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (sporadic or familial, SHC and FHC) comprises detecting a mutation associated with hypertrophic cardiomyopathy in an amplified product of a beta cardiac myosin heavy chain DNA. The mutations associated with SHC/FHC are detected in the myosin gene isolated from blood, by detecting mis-matched areas in RNA-DNA hybrid double strands (RNA from the normal gene, DNA from the suspect ample). FHC associated point mutation can be classified and used to determine life expectancy in affected individuals e.g. using a Kaplan-Meier curve for the classified type of FHC causing point mutation. Also included are an RNA probe comprising ribonucleotides arranged in a sequence which is complementary to at least a portion of beta-cardiac myosin heavy-chain DNA and a set of DNA oligonucleotide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two
asymptomatic individuals suspected of having the disease. The method has a broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B, buchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease and phenylketonuria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC; familial hypertrophic cardiomyopathy; SHC; Gaucher's disease; sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia; buchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease; phenylketonuria; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a presence or absence of a mutation associated with hypertrophic cardiomypachy, useful for diagnosing cystic fibrosis or hemophilia, by detecting a mutation in an amplified product of a beta cardiac myosin heavy-chain DNA.
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(SEID/) SEIDMAN J.
(WATK/) WATKINS H.
(ROSE/) ROSENZWEIG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                         ACA63119;
                                                                                                                                                                                                                                                                                                                              RESULT 2
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             DNA. The method is useful for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. This method is usepecially useful for diagnosing SMC and PHC, as well as for determining the estimated the life expectancy of a person with familial hypertrophic cardiomyopathy. In particular, the method is useful for determining individual's genetic information, and diagnosing e.g. Gaucher's disease, haemophilla, Duchenne's muscular dystrophy, sickle cell ansemia, Tay-Sachs disease, phenylketonuria or cystic fibrosis. The present sequence is a PCR primer used to amplify a region of the beta cardiac myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (familial or sporadic, FHC, SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy, comprising amplifying beta-cardiac myosin heavy-chain DNA forming an associated product, and detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy in the amplified product, thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also included are a set of DNA oligonucleotide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting mutations associated with hypertrophic cardiomyopathy to diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac myosin heavy-chain DNA and detecting the mutation in the amplified product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human beta cardiac myosin heavy chain mutation detection primer B9.1F.
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, beta cardiac myosin, heavy chain, PCR; primer, ss, FHC, SHC, familial hypertrophic cardiomyopathy, sporadic hypertrophic cardiomyopathy.
                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                         Score 25; DB 9; Length 25; Pred. No. 0.55;
                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                       Sequence 25 BP; 6 A; 12 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watkins H, Rosenzweig A;
                                                                                                                                                                                    chain gene containing an FHC-associated mutation
                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; SEQ ID NO 9; 22pp; English.
                                                                                                                                                                                                                                                                                                                                 1 CAACTCATCACCACTCTCTTCCATC
                                                                                                                                                                                                                                                                                                                                                   1 CAACTCATCACCACTCTTCCATC
                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-00989160.
95US-00469172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-2004; 2004US-00788779
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR05305 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                             25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seidman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROSE/) ROSENZWEIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-592586/57.
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SEID/) SEIDMAN C. (SEID/) SEIDMAN J. (WATK/) WATKINS H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004152121-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-AUG-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR05305;
                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
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us-10-788-779-9.rng

which amplify beta-cardiac myosin heavy-chain DNA (the set of oligonucleotide primers being useful for facilitating the diagnosis of hypertrophic cardiomyopathy by being capable of detecting a hypertrophic cardiomyopathy associated mutation) and a kit for facilitating the diagnosis of hypertrophic cardiomyopathy (comprising a first container of cardiomyopathy-associated mutation, a second container of hypertrophic cardiomyopathy-associated mutation, a second container of hypertrophic cardiomyopathy-associated mutation, a second container of hypertrophic cardiomyopathy-associated mutation a second container or absence of a hypertrophic cardiomyopathy-associated mutation in cardiomyopathy associated mutation in a second container or absence of a hypertrophic cardiomyopathy associated with cardiomyopathy for facilitating the diagnosis of the hypertrophic cardiomyopathy for facilitating the diagnosis of the hypertrophic cardiomyopathy relies on the presence of the explained ventricular cardiomyopathy relies on the presence of the hypertrophic cardiomyopathy relies on the presence of the hypertrophy cardiomyopathy relies on the presence of the hypertrophy of the present invention is non-invasive and based, at least in cardial symptoms and the demonstration of unexplained ventricular cardiomyopathy is caused by point mutations in the beta cardiac myosin heavy-chain gene. Prior art creveals that there are ne extensive studies involving a large number of families which established that this particular disease or disorder was careed by point mutations in the beta cardiac myosin heavy-chain gene cardiac myosin heavy chain sene and cardiac myosin heavy chain gene. cardiac myosin heavy chain having a disease-related point mutation. Sequence 25 BP; 6 A; 12 C; 0 G; 7 T; 0 U; 0 Other;

Score 25; DB 13; Length 25; Pred. No. 0.55; ; Mismatches 0; Indels 100.0%; Scortion. No. v.. 0; Mismatches 1 CAACTCATCACCACTCTTCCATC 25 Query Match
Best Local Similarity 100.0
....hes 25; Conservative

CAACTCATCACCACTCTTCCATC 25

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0; Gaps

AAZ57003/c ID AAZ57003 standard; DNA; 41 AAZ57003; RESULT 4

ВP

Forward amplimer for generating usurpin constructs. 12-MAY-2000 (first entry)

Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta; usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive; caspase; cytostatic; antiParkinsonian; antidiabetic; PCR primer; ss.

Homo sapiens

WO200003023-A1

20-JAN-2000.

99WO-CA000615 07-JUL-1999; (MERI) MERCK FROSST CANADA INC

98US-0092005P.

08-JUL-1998;

Nicholson DW, Rasper DM, Xanthoudakis S,

ŝ Roy

WPI; 2000-160929/14.

Novel recombinant DNA molecules and polypeptides for treating apoptosis mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's disease,

Example 7; Page 33; 69pp; English.

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The invention provides recombinant nucleic acid molecules encoding usurpin-alpha (lacking the first death effector domain (DED) or its prodomain, usurpin-beta or usurpin-gamma. Usurpin polypeptides are useful for in vitro and in vivo identification of usurpin-procaspase interaction inhibitor. Usurpin is useful as modulator of the sensitivity of cells to CD95[Res/Apo-1] mediated approcise; Modulation of appptosis is useful for treating disease like autoimmune diabetes, cancer and parkinson's disease. Activators and inhibitors of usurpin-procaspase interaction are also useful for treating various diseases mediated by apoptosis. Usurpin provides an attractive model for modulating caspase activation. Sensitivity of cells bearing CD95(Res/Apo-1) receptor can be regulated at several levels in the presence of usurpin, conferring resistance to Fas-ligand cell death. The present sequence represents a forward amplimer for generating usurpin-alpha, delDED-A usurpin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome, biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel biallelic markers used to construct a high density disequilibrium map of the human genome.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                             Length 41;
                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                           Sequence 41 BP; 9 A; 5 C; 16 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human map-related biallelic marker SEQ ID NO:3589.
                                                                                                                                                                                                                                                                                                                             Score 18.6; DB 3;
Pred. No. 2.8e+02;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                    25
                                                                                                                                                                                                                                                                                                                                                                                                                                       41 CAAATCCTCACCAATCTCTGCCATC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers replace (24, A)
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                                                                                                                                                                                                                                                                                                                                                                                                    1 CAACTCATCACCACTCTTCCATC
                                                                                                                                                                                                                                                                                                                               74.48;
84.08;
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98US-0109732P.
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ID AAZ69233 standard; DNA; 47
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-013267/01.
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ69233;
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                                                                                                                                                                                                                                                                                                                                                                  Matches
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The invention provides recombinant nucleic acid molecules encoding usurpin-alpha (lacking the first death effector domain (DED) or its prodomain, usurpin-beta or usurpin-agama. Usurpin polypeptides are useful for in vitro and in vivo identification of usurpin-procapase-8 interaction inhibitor. Usurpin is useful as modulation of apoptosis of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis is useful for treating diseases like autoimmune diabetes, cancer and Parkinson's disease. Activators and inhibitors of usurpin-procapase-8 interaction are also useful for treating various diseases mediated by apoptosis. Usurpin provides an attractive model for modulating caspase activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be resistance to Fas-ligand cell death. The presence of usurpin, conferring resistance to Fas-ligand cell death. The present sequence represents a forward amplimer for generating delDED-A usurpin constructs
                                                                                                                                                                                                                                                                                                                                                ö
have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2813, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta; usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive; caspase; cytostatic; antiParkinsonian; antidiabetic; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel recombinant DNA molecules and polypeptides for treating apoptosis mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                               ch 74.4%; Score 18.6; DB 3; Length 47; 1 Similarity 84.0%; Pred. No. 2.9e+02; 21; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Forward amplimer for generating delDED-A usurpin construct.
                                                                                                                                                                                                                                                          Sequence 47 BP; 15 A; 9 C; 14 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicholson DW, Rasper DM, Xanthoudakis S,
                                                                                                                                                                                                                                                                                                                                                                                        1 CAACTCATCACCACTCTTCCATC 25
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AAZ56996 standard; DNA; 41 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-CA000615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                  present invention
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Best Local &
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ID AAZ5
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                                                                                                                                                                                                                                                                                                             Tag polymerase; mutant; thermostable; DNA polymerase; exonuclease; PCR; amplification; reverse primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA polymerases with altered 5'-3' exo nuclease activity having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
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0
                                    70.4%; Score 17.6; DB 3; Length 41; 83.3%; Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.8%; Score 16.2; DB 2; Length 46; 85.7%; Pred. No. 2.9e+03;
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                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46 BP; 12 A; 17 C; 2 G; 15 T; 0 U; 0 Other;
           Sequence 41 BP; 9 A; 7 C; 15 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 10; Page 102; 185pp; English.
                                                                                              24
                                                                                                             CAPATCCTCACCAATCTCTGCCAT 17
                                                                                              1 CAACTCATCACCACTCTCTTCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-00590213.
90US-00590466.
90US-00590490.
                                                                                                                                                                                                                                                                                 Oligonuleotide primer TAFR01.
                                                                                                                                                                                                                                                                                                                                                                                                                                           91WO-US007035.
                                                                                                                                                                                              AAQ24360 standard; DNA; 46
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                                                                                                                                                                                                                                                       (first entry)
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                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gelfand DH, Abramson
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les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CETU ) CETUS CORP.
                                                   Local Similarity
Les 20; Conserv
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28-SEP-1990;
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                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                       Query Match
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ID AAF3
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                                                                                                                                                                                AAQ24360
                                                                                                                                                                  RESULT
X S
                                                                                                                                                                                                            셤
                                                                                                8
                                                                                                                    셤
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AAF30389;

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New polypeptide-human lysyl oxidase 46.31 for treating malignant tumor, hemopathy, human immunodeficiency virus infection, immunological disease and various inflammations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide-human lysyl oxidase 46.31 for treating malignant tumor, hemopathy, human immunodeficiency virus infection, immunological disease
                                                                                                                                                                                                                                                                                                                                                                                                                        described is a process for producing (1) using DNA recombination technology. (1) can be used in the treatment of several diseases, such amalignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological disease and various inflammations. The present sequence represents a PCR primer for (1), which is used in an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, lysyl oxidase 46.31; enzyme; malignant tumour; haemopathy; human immunodeficiency virus infection; HIV infection; inflammation; immunological disease; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes human lysyl oxidase 46.31 (I). Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.4%; Score 15.6; DB 6; Length 3
81.8%; Pred. No. 5e+03;
ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33 BP; 12 A; 4 C; 11 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 17 (Disclosure); 33pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lysyl oxidase 46.31 probe 1 SEQ ID NO:8.
                                                                                                                                              (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CTCATCACCACTCTCTTCCATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTATTCCACTCTCTTCCATC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                           26-SEP-2000; 2000CN-00125428.
                                                                                                      26-SEP-2000; 2000CN-00125428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-2000; 2000CN-00125428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2000; 2000CN-00125428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABQ83619 standard; DNA; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                                                                                                                                                                                WPI; 2002-539343/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-539343/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                        Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN1345944-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-2002.
                   24-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ83619;
                                                                                                                                                                                      Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
ABQ83619/
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of forward PCR primer ST239ABMF, which was used with reverse primer ST239ABTCR (see AAF30390) for the PCR undplication of human full-length ADAMB DDNA (see AAF30377). The forward primer includes an NsII restriction site toward the 5' end followed by the sequence at the beginning of the mature sequence of ADAMB. The PCR product was used in the construction of plasmid pST239.ADAMBmat for expression of mature ADAMB protein (see AAB20251) in Bscherichia coli strain 58F3 cells. The ADAMB gene is amplified in the genome of certain tumour cells. Such gene amplification is associated with overexpression of ADAMB protein and contributes to tumourigenesis. ADAMB is therefore a useful target for the diagnosis and/or treatment of certain cancers. Therapeutic agents may take the form of anteagonists of ADAMB, such as anti-ADAMB antibodies, or may be ADAMB antisense constructs
                                                                                                                                         ADAM8; human; tumour; cancer; therapy; diagnosis; antitumour; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies against ADAM8 polypeptides, useful e.g. for diagnosis and treatment of tumors and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lysyl oxidase 46.31; enzyme; malignant tumour; haemopathy;
human immunodeficiency virus infection; HIV infection; inflammation;
immunological disease; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 4; Length 42;
Pred. No. 3.5e+03;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 42 BP; 12 A; 16 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lysyl oxidase 46.31 PCR primer 3 SEQ ID NO:5.
                                                                                               Human ADAM8 cDNA forward primer ST239A8MF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AACTCATCACCACTCTTCCATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 75; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AATGCATCAAGACTCTCTGCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ83617/c
ID ABQ83617 standard; DNA; 33 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.0%;
                                                                                                                                                                                                                                                                                                                                      27-JUL-2000; 2000WO-US020731.
                                                                                                                                                                                                                                                                                                                                                                                99US-0146217P.
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bodary SC, Fisher KL;
                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-182943/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                  WQ200109189-A2
                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1999;
                                                       14-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-2003
                                                                                                                                                                                                                                                                                            08-FEB-2001
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Example 6; Page 19 (Disclosure); 33pp; Chinese

and various inflammations.

Homo sapiens

ABQ83617;

RESULT 9

Query Match Matches

ð 셤 CN1345944-A

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Gaps

; 0

DB 6; Length 33;

as

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           The present invention describes human lysyl oxidase 46.31 (I). Also described is a process for producing (I) using DNA recombination technology. (I) can be used in the treatment of several diseases, such as malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological disease and various inflammations. The present sequence represents a probe for (I), which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting nucleic acid target in sample by using combination comprising multiple regions each of which has two different loci of anchors in association with a bifunctional linker that has portion specific for
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                              High throughput assay system; nucleic acid detection; anchor; target;
                                                                                                                                                                 ö
                                                                                                                                     Score 15.6; DB 6; Length 41;
Pred. No. 5.1e+03;
); Mismatches 4; Indels
                                                                                                            Sequence 41 BP; 15 A; 7 C; 13 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                      Attenuation factor oligonucleotide SEQ ID NO:147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HIGH-) HIGH THROUGHPUT GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 30; Page 114; 129pp; English.
                                                                                                                                                                                        4 CTCATCACCACTCTTCCATC 25
                                                                                                                                                                                                      CICIATICCACTCTTCCATC 2
                                                                                                                                                               ;
                                                                                                                                                                                                                                                                              BP,
                                                                                                                                       ch 62.4%; l Similarity 81.8%; 18; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001; 2001US-00888413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-2002; 2002WO-US020039
                                                                                                                                                                                                                                                                            ABZ72744 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-201508/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kris RM, Felder S;
                                                                                                                                     Query Match
Best Local Similarity
                                                                                       present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003002750-A2
                                                                                                                                                                                                                                                                                                                               09-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                             linker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting
                                                                                                                                                                                                                                                                                                       ABZ72744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anchor.
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                     RESULT 11
ABZ72744/c
¥888888888
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The present invention describes a method for detecting a nucleic acid target (T) in a sample (S). The method involves: (a) contacting (S) which may comprise the target(S) with a nuclease protection fragment(S) (I) specific for and which binds to the target(S), exposing the (S) to a nuclease effective to digest remaining single stranded nucleic acid, and then contacting the resultant (S) with a combination (II) which comprises, before addition of (S), a surface comprising multiple spatially discrete regions at least two of which are substantially discrete regions at least two of which are substantially the anchors at each locus, each in association with a bifunctional linker which has a first portion that is specific for the anchor, and a second portion that comprises a probe which is specific for the combination, where two or more of the anchors located at a first locus of a region are in association with different bifunctional linkers, having different target specificities, and (b) detecting the bound protection fragment (S), and where the regions are tubes, and the loci of anchors are arranged in a

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linear array in the tubes. Such an assay can be termed a multi array plate screen (MAPS) method or assay. When the probes are oligonucleotides, the MAPS can be used for diagnosing the presence of genetic variations or defects e.g. polymorphisms or specific mutations associated with disease such as cystic fibrosis or pathogenic organisms. When the probes are antigen binding molecules, the assays can be used for screening variant proteins or protein expression patterns. The assay can also be used for mapping expressed sequence tags (ESTs). ABZ7259 to ABZ72762, and ABPS6911, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR; primer; ss; actin; 21.34; zinc finger; PHD structural domain; int tumour; haemopathy; HIV; immunological disease; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide-human actin 21.34 contained zinc finger and PHD finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises the amino acid and coding sequence of the human actin 21.34 protein (which contains a zinc finger and a PHD structural domain). The 21.34 DNA and protein sequences are useful for treating: malignant tumour; haemopathy; HIV; immunological disease; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malignant tumour; haemopathy; HIV; immunological disease; and inflammations. The present DNA sequence represents a PCR primer for the human actin 21.34 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structural domain and its encoding polynucleotide useful for treating
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                           ;
0
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0
                                                                                                                                                                                                                                      61.6%; Score 15.4; DB 8; Length 25; 76.0%; Pred. No. 5.9e+03; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.6%; Score 15.4; DB 6; Length 33; 76.0%; Pred. No. 6.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                     Sequence 25 BP; 4 A; 1 C; 12 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33 BP; 8 A; 7 C; 13 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                              1 CAACTCATCACCACTCTTCCATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAACTCATCACCACTCTTCCATC 25
                                                                                                                                                                                                                                                                                                                                          CACCICATAAGCACTCICAACCACC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 20; 33pp; Chinese.
                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human actin 21-34 PCR primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-2000; 2000CN-00125360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-SEP-2000; 2000CN-00125360
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL50996 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-548937/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g., HIV infection.
                                                                                                                                                                                                                                                        Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CN1345794-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL50996;
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   AAL50996/
         8838888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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Spinocerebellar ataxia type 1; SCA 1; presymptomatic diagnosis;

LR40A PCR primer; ss

WO9501437-A2

Synthetic.

12-JAN-1995

Spinocerebellar ataxia type 1 LR40A PCR primer.

(revised)
(first entry)

25-MAR-2003 28-SEP-1995

AAQ95137;

AAQ95137 standard; DNA; 20 BP.

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The invention describes isolated tor-1, tor-2 polypeptides (I). A vector comprising a polynucleotide (II) encoding (I) is useful for making a corsin polypeptide which involves culturing the vector for a duration of time under conditions suitable for expression of the torsin polypeptide of a polynucleotide that is 70-90% or more identical to (II) is useful for detecting a polynucleotide encoding a polypeptide having 70% or more for more protein a polynucleotides and polypeptide having torsin activity. The polynucleotides and polypeptides of the invention are useful for treating symptoms or treating one or more protein-aggregation-associated disease or which involves administering the polynucleotides or polypeptides to a human being or an animal in need. The one or more protein-aggregation-associated disease, tasopath is a closen from Alzheimer's disease, Parkinson's disease, dystonia, and familial amyotrophic lateral sclerosis. (I) is useful for controlling expression of one or more isolated polypeptides having amino acid sequence identical to (I) in an organism. This sequence represents a reverse transcriptuse, PCR primer used in the isolation of
                                                                                                                                                                                                             nootropic; neuroprotective; antiparkinsonian; anticonvulsant; protein aggregates formation supressor; gene therapy; tor-1; tor-2; torsin; protein-aggregation-associated disease; Alzheimer's disease; Parkinson's disease; prion disease; tauopathy; Huntington's disease; polyglutamine disease; dystonia; familial amyotrophic lateral sclerosis; worm; tor-2; reverse transcriptase PCR; primer; ss; torsin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated tor-1, tor-2 polypeptides, useful for treating protein-aggregation-associated diseases e.g. Alzheimer's disease, Parkinson's disease, prion disease, tauopathy and Huntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.6%; Score 15.4; DB 12; Length 36; 76.0%; Pred. No. 6.1e+03; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36 BP; 10 A; 11 C; 3 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                     Worm torsin-2 RT-PCR primer segid 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; SEQ ID NO 12; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding worm torsin-2 (tor-2).
                                          ADL23552 standard; DNA; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-2002; 2002US-00177104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-2002; 2002US-00177104
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 76.0
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caldwell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYAL-) UNIV ALABAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-070571/07.
                                                                                                                                                                                                                                                                                                                                                                                                             US2003235823-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caldwell GA,
                                                                                                                             20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-DEC-2003
                                                                                  ADL23552
RESULT 13
                      ADL23552
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Human alpha myosin heavy chain-derived peptide M7A-alpha homologue DNA.
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Heart disease; inflammatory; autoimmune; cardiomyopathy; myosin;
Chlamydia; induction; vaccine; ds.
                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                          Query Match 60.8%; Score 15.2; DB 2; Length 20; Best Local Similarity 85.0%; Pred. No. 6.9e+03; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                              Sequence 20 BP; 5 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                      1 CAACTCATCACCACTCTT 20
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                               20 CAACTCATGACCCCTCTCCT 1
                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00133774.
                                                                                                                                                                                                                                                                                                                                                                      AAZ28187 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5962636-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                    AAZ28187;
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                         RESULT 15
AAZ28187
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Gaps

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1 CAACTCATCACCACTCTTCCATC 25 caacrcarcarraaacrcrrrcrrc 35

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11

RESULT 14 AAQ95137/c

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AAQ85137 and AAQ95138 are a pair of primers for the PCR amplification of AAQ84793, a new autosomal dominant spinocerebellar ataxia type 1 (SCA 1) nucleic acid. The nucleic acid and its protein product (AAR71111) can be used to develop products, for the presymptomatic detection of a SCA 1 disorder. (Updated on 25-MAR-2003 to correct PN field.)

New autosomal dominant spinocerebellar ataxia type 1 nucleic acid - used to develop prods. for detection or presymptomatic diagnosis of a SCA1

93US-00084365.

29-JUN-1993; 28-JUN-1994; 29-JUN-1994;

94WO-US007336

Chung M, Zoghbi HY;

Orr HT,

WPI; 1995-061001/08.

(MINU) UNIV MINNESOTA.

Example I; Page 39; 111pp; English.

disorder.

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WPI; 2002-539343/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                             This sequence represents DNA encoding the human homologue of the murine alpha myosin heavy chain-derived peptide, M7A-alpha (AAY4723). Like M7A-alpha anyosin heavy chain-derived peptide, M7A-alpha (AAY4723). Like M7A-alpha, the human homologue inflammatory cardiomyopathy (ICM) via an autoimmune response in mice immunised with it. It contains an amino acid sequence motif MAXXXS (AAY42722) which appears to be required for the induction of this disease. The motif was originally identified in M7A-alpha when it was compared with a peptide derived from a homologues can did not cause the disease. Several peptide fragments containing the motif were identified from a database and were found to be fragments of Chlamydia. These peptides also induced ICM, indicating that infection with Chlamydia may be involved in the development of ICM. Inflammatory cardiomyopathy peptides are used to determine the risk of ICM by incubation with a subject's T cells and measuring the degree of proliferation (an increased degree being indicative of risk) or to raise specific antibodies which can be used therapeutically and for the detection of Chlamydia. Such can be used measuring an adjuvant and an excipient in a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cardiant; murine alpha myosin heavy chain; inflammatory myocarditis; autoimmune inflammatory cardiomyopathy; Chlamydia; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                   Peptides that induce or suppress inflammatory cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.8%; Score 15.2; DB 2; Length 42; Best Local Similarity 85.0%; Pred. No. 7.6e+03; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42 BP; 7 A; 19 C; 4 G; 12 T; 0 U; 0 Other;
                                                          Neu N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bachmaier K, Hessel AJ;
                                                          Penninger JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human peptide M7A-alpha coding sequence.
                                                                                                                                         Example 1; Col 20; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AACTCATCACCACTCTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AGCICAIGGCCACICITC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ99170 standard; DNA; 42 BP.
           98US-00133774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00303862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN CANADA INC.
                                 (AMGE-) AMGEN CANADA INC
                                                         Hessel AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hybridization probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penninger JM,
                                                                                 WPI; 1999-589735/50
                                                                                                                                                                                                                                                                                                                                                                                      for decreasing ICM
                                                                                           P-PSDB; AAY42731
                                                         Bachmaier K,
          12-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6034230-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ99170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nen N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 16
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This sequence represents the cooling sequence or the numan nomologue of the murine many halpha peptide (Y83811) derived from the murine alpha myosin heavy chain polypeptide. The peptide was used to evaluate its ability to induce autoimmune inflammatory cardiomyopathy. A similar experiment was carried out using the peptide WAA-beta (Y8381). The invention relates to the isolation of sequences coding for peptide experiments are searched based on the sequence cardiomyopathy. The peptide sequences are searched based on the sequence of the MTA peptides derived from the murine alpha myosin heavy chain polypeptide. The consensus sequence of the murine MTA-alpha/beta peptides of the MTA peptides derived from the murine of the murine of the sequence of the murine solar and viral sequences able to cause inflammatory cardiomyopathy. The screen isolated the peptides valsals and their corresponding coding and viral sequences able to cause inflammatory cardiomyopathy. The screen isolated the peptides with other therapeutics, for inducing or inhibiting or inflammatory cardiomyopathy in vivo, where the cardiomyopathy is autoimmune inflammatory cardiomyopathy. The peptides may also be used for increasing inflammatory cardiomyopathy. The peptides may also be used for increasing the mammal. The peptides may also be used in vaccines. Nucleic acids encoding the peptides may also be used in vaccines.

Nucleic acids encoding the peptides may be used as hybridization probes, con in diagnostic assays to test for the presence of Chlamydia DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                       DNA molecules encoding novel myocardial peptides used for inhibiting and inducing inflammatory cardiomyopathy in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, lysyl oxidase 46.31; enzyme; malignant tumour; haemopathy;
human immunodeficiency virus infection; HIV infection; inflammation;
immunological disease; probe; ss.
                                                                                                                                                                                                                                                                                                                                               sequence represents the coding sequence of the human homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 42 BP; 7 A; 19 C; 4 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lysyl oxidase 46.31 probe 2 SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AACTCATCACCACTCTTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTCATGGCCACTCTTTC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SHAN-) SHANGHAI BIOWINDOW GENE
                                                                                                                                                                                                                                                           Claim 1; Col 19; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ83620 standard; DNA; 41 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2000; 2000CN-00125428.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.83
Best Local Similarity 85.03
Matches 17; Conservative
WPI; 2000-255712/22.
                                                P-PSDB; AAY83820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mao Y, Xie Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CN1345944-A.
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treatment in an individual. The diseases include cardiac allograft

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                                                                                                                The present invention describes human lysyl oxidase 46.31 (I). Also described is a process for producing (I) using DNA recombination technology. (I) can be used in the treatment of several diseases, such as malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological disease and various inflammations. The present sequence represents a probe for (I), which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for adagnosing a disease, monitoring (rate of) propression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response
                 otide-human lysyl oxidase 46.31 for treating malignant tumor, human immunodeficiency virus infection, immunological disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * system for leukocyte expression profiling, diagnosing a disease, or nitoring (the rate of) progression of a disease, e.g. atherosclerosis congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phillips J;
                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leukocyte gene expression profiling probe SEQ ID NO 6966.
                                                                                                                                                                                                                                                                                         6; Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prentice J,
                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                       Sequence 41 BP; 15 A; 8 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                         Score 15; DB 6; Le
Pred. No. 9.2e+03;
                                                                                 Example 6; Page 19 (Disclosure); 33pp; Chinese
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Johnson
                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 9.2
tive 0; Mismatches
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Woodward R, Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 553; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0241994P.
2001US-0296764P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-2001; 2001WO-US047856
                 polypeptide-human lysyl
                                                                                                                                                                                                                                                                                         60.08;
                                                                                                                                                                                                                                                                                                                                                             11 CCACTCTCTTCCATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABZ06975 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                             ccacrererrecare 2
                                                 and various inflammations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                         15; Conservative
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                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-636525/68
                                                                                                                                                                                                                         present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2000;
08-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-2003
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                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 18
                   New
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                    lupus erythematosus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prentice J, Phillips J;
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                   rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
              rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte gene expression profiling probe SEQ ID NO 6576.
                                                                                                      , DB 6; Leus.
.. 9.4e+03;
5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15; DB 6; Length 50;
Pred. No. 9.4e+03;
0; Mismatches 5; Indels
                                                                                  Sequence 50 BP; 10 A; 23 C; 1 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50 BP; 16 A; 1 C; 23 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Altman P, P; Johnson F;
                                                                                                                                                       0; Mismatches
                                                                                                                    Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fry K, Matcuk G, A]
I R, Quertermous T,
                                                                                                                                                                                          2 AACTCATCACCACTCTCTTCCAT 24
                                                                                                                                                                                                                           24 AACTCATCTCGAATCTCTCAT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 542; Opp; English.
                                                                                                                                                                                                                                                                                                                  뮵.
                                                                                                                    60.0%;
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                                                                                                               Query Match
Best Local Similarity 78.3°
Matches 18; Conservative
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Best Local Similarity 78.3
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-636525/68.
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                                                                                                                cardiovascular, infectious; neurodegenerative; immune; haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic; antiinflammatory; neuroprotective; antilipaemic; anabolic; cardiant; neurogenesis; wound healing; anglogenesis; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; primer; human.
                                                                                                          ss; NOVX; metabolic disorder; diabetes; anorexia; cancer;
                                                                                            Forward PCR primer used to amplify human NOVX DNA SegID1372.
     24
               27 AACTCATCTCGAATCTCTCAT 5
    AACTCATCACCACTCTCTTCCAT
                                                                                                                                                                                                                                                                                                                                                                                2001US-0278652P.
2001US-0278775P.
2001US-0278778P.
2001US-0279882P.
                                                   ADI17836 standard; DNA; 22 BP
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267823P.
268974P.
271664P.
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2001US-0276397P.
2001US-0276768P.
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2001US-0272788P.
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2001US-0275950P.
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2001US-0276448P.
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2001US-0285133P.
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                                                                              (first entry)
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                                                                                                                                                                       WO200268649-A2.
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19-JUN-2001; 2
13-AUG-2001; 2
                                                                                                                                                                                                                                                                    08-FEB-2001;
                                                                                                                                                          Homo sapiens.
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                                                                              15-APR-2004
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This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism.

Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic assays and furthermore in the treatment of cliverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids.

The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating metabolic disorders, diabetes, and haematopoietic diseases as well as various dyslipidaemias.

Accordingly, these molecules have many activities including anorectic, virucide, nootropic, antiinflammatory, neuroprotective, antilipaemic, anabolic and cardiant. Purthermore, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome amapping, tissue typing, preventive medicine and pharmacogenomics. This oligonucleotide is a PCR primer used to amplify human NOVX DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burgess CE;
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primer; RTQ PCR; real time quantitative PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zerhusen BD, Patturajan M, Shimkets RA;
garu M, Anderson DW, Rastelli L, Miller CE;
Gusev VY, Colman SD, Wolenc AR, Pena CEA;
sobrook JP, Lepley DM, Rieger DK, Burgess Cl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 BP; 4 A; 11 C; 0 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 1372; 1498pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               nev VT, Spytek KA, Zeline, Gangolli EA, Padigaru M, Andele, VI, Taupier RJ, Gusev VY, Col. VI, Taupier RJ, Bobrook JP, L)
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                                                          2001US-0315470P.
2001US-0316447P.
2001US-031811BP.
2001US-0318118P.
2001US-0318740P.
2001US-0323379P.
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2001US-0312908P.
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nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerlach VL, Taupier F
Furtak K, Grosse WM,
                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
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19-SEP-2001;
                                                                                                                               07-SEP-2001;
07-SEP-2001;
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                                  21-AUG-2001;
                                                                 28-AUG-2001;
                                                                                                   31-AUG-2001;
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The invention relates isolated 162 NOVX polypeptides (NOV1-NOV99, including splice variants) and the nucleic acids (NA) that encode them. Also included are the mature NOVX proteins (and their encoding polynucleotides), a vector comprising NOVX NA, a cell comprising the presence or amount of NOVX in a sample, determining the presence or amount of NOVX in a sample, determining the presence or amount of NOVX in a sample, determining the presence or amount of NOVX in a sample, determining the presence of alsoader, determining the presence of or predisposition to a disease associated with altered levels of NOVX and treating a pathological state in a mammal comprising administering a polypeptide which is at least 95% in a mammal comprising administering a polypeptide which is at least 95% in a mammal comprising administering a polypeptide which is at least 95% in appropriate expression and activity of NOVX (e.g. cancer, diabetes, prevention, treatment and diagnosis of diseases associated with cardionyopathy and/or atherocelerosis). The anti-NOVX antibodies and cardiomyopathy and not a samples (e.g. by enzyme linked a manual comprises may also be used to down regulate expression and activity of NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples (e.g. by enzyme linked immunosorbant assay (ELISA). The agents and methods may be used in this way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy now the presence of NOVX in samples is a real time quantitative and not cancer, diabetes, cardiomyopathy now the presence of NOVX in sequence is a real time quantitative and not cancer.
                                                                                                                                                                                                                                                                                                                                                  Burgess CE
                                                                                                                                                                                                                                                                                        Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
Li L, Gangolli BA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
Gerlach V, Taupier RJ, Guev VY, Colman SD, Wolenc AR, Pena CEA;
Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RTQ PCR) primer for tissue specific expression studies for a NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated NOVX polypeptides and polynucleotides, useful for preventing diagnosing and/or treating cancer, diabetes, cardiomyopathy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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nes 16; Conservative
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Gerlach V, Taupier RJ
Furtak K, Grosse WM,
                                  GERLACH V.
TAUPIER R J.
GUSEV V Y.
COLMAN S D.
WOLENC A R.
FENRA C E A.
FURTAK K.
GROSSE W M.
ALSOBROOK J F.
                                                                                                                                                                                                                              RIEGER D K.
BURGESS C E.
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RASTELLI L.
MILLER C E.
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RIEGER D K.
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(MILL/)
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(FURI/)
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(RIEG/)
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(WOLE/)
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2001US - 0265514P
2001US - 0265517P
2001US - 0266406P
2001US - 0266767P
2001US - 026675P
2001US - 0267459P
2001US - 0267459P
2001US - 0267459P
2001US - 0267459P
2001US - 0267459P
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2001US-0279884P.
2001US-0280147P.
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001US-0272788P.
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2001US-0278652P.
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ZERHUSEN B D.
PATTURAJAN M.
SHIMKETS R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GANGOLLI E A.
PADIGARU M.
ANDERSON D W.
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                                                      US2004033493-A1.
                  Homo sapiens.
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09-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2001;
21-AUG-2001;
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(SHIM/)
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(GANG/)
(PADI/)
(ANDE/)
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Human, PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                                                                                                   98US-0077450P

98US-0077641P

98US-0077641P

98US-0077641P

98US-0077641P

98US-007804P

98US-007804P

98US-007804P

98US-0078936P

98US-0078936P

98US-0078936P

98US-0078936P

98US-0078936P

98US-0078936P

98US-007963P

98US-0081033P

98US-0081033P

98US-0081033P

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98US-0081033P

98US-0081033P

98US-008123P

98US-0081252P

98US-008123P

98US-008123P

98US-0081252P

98US-008133P

98US-008133P

98US-008133P

98US-008133P

98US-0081876P

98US-008332P

98US-008332P

98US-008334P

98US-008334P

98US-008334P

98US-008334P

98US-008334P

98US-008334P

98US-00834P

98US-008358P

98US-008358P

98US-008358P

98US-008358P

98US-008358P

98US-008358P

98US-008358P

98US-008358P
                                                                                     99WO-US005028
                               Synthetic.
Homo sapiens.
                                                       WO9946281-A2
                                                                                                                                                                                                                                                                                                                                    08-APR-1998;
08-APR-1998;
09-APR-1998;
09-APR-1998;
                                                                                    08-MAR-1999;
                                                                     16-SEP-1999
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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted and transmembrane polypeptides and their polynucleotides ful for treating blood coagulation disorders, cancers and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;
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; Mismatches
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          98US-0084600P

98US-0084637P

98US-0084640P

98US-00846418P

98US-00846418P

98US-0085338P

98US-0085573P

98US-0085573P

98US-0085573P

98US-008560P

98US-008560P

98US-008560P

98US-008560P

98US-0085697P

98US-0085700P

98US-0086430P

98US-0086430P

98US-0086430P

98US-0086430P

98US-0086430P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 88.9
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                       Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-551358/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adhesion disorders.
                                                                                                  13-MAY-1998;
13-MAY-1998;
15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
                                                07-MAY-1998;
07-MAY-1998;
07-MAY-1998;
13-MAY-1998;
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15-MAY-1998;
15-MAY-1998;
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22-MAY-1998;
22-MAY-1998;
22-MAY-1998;
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28-MAY-1998
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AAC78692/c
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Matches
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Human; secreted and transmembrane protein; PRO; antiinflammatory; antiartosclerotic; cardiant; anti-infertiilty; anti-HTV; cytostatic; antidiabetic; gene therapy; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing; PCR; primer; ss.
                                                             Novel human secreted and transmembrane protein related primer #71.
                                                                                                                                                                                                                                                                                                                                    970S-0064250P
970S-006449P
970S-006449P
980S-0077450P
980S-0077641P
980S-0077641P
980S-0077641P
980S-0077641P
980S-0077641P
980S-0078910P
980S-0078936P
980S-0078938P
980S-0079656P
980S-0079638P
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980S-0079638P
980S-0079638P
980S-0079638P
980S-0079638P
980S-0079638P
980S-0080338P
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980S-0081079P
980S-0081079P
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                               16-JUN-2003 (first entry)
                                                                                                                                                                                                                                           US2002192706-A1.
                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                         24-OCT-2001;
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11-MAR-1998;
12-MAR-1998;
13-MAR-1998;
17-MAR-1998;
20-MAR-1998;
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26-MAR-1998;
27-MAR-1998;
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27-MAR-1998;
27-MAR-1998;
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30-MAR-1998;
31-MAR-1998;
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31-MAR-1998;
31-MAR-1998;
01-APR-1998;
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15-APR-1998;
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    ACA63579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC78458 to AAC78599 represent polynuclectide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polyneptides. The PRO polynuclectides and polypeptides have eytostatic activity. The polynuclectides and polypeptides have eytostatic activity. The polynuclectides and polypeptides can be used for detecting the presence of PRO polypeptides is samples, for linking biological activities of feels using the polypeptides and for modulating biological activities of calls for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78897 represent PCP primers and probes used in the isolation of the PRO polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ', Gerber H, Gerritsen ME;
Gurney AL, Hillan KJ;
Paoni NF, Roy MA, Shelton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities.
Human; secreted protein, transmembrane protein; PRO; EST; cytostatic; expressed sequence tag; detection; cancer; PCR primer; probe; ss.
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Gerritsen ME;
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Pred. No. 1e+04;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashkenazi AJ, Baker KP, Botstein D, Desnoye
Ferrara N, Filvaroff E, Fong S, Gao W, Ges
Goddard A, Godowski PJ, Grimaldi CJ, Gurney
Klavin IJ, Kuo SS, Napier MA, Pan J, Paor
Stewart TA, Tumas D, Williams PM, Wood WI;
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                                                                                                                                                                            990S-0123957P
990S-0126733P
990S-0130232P
990S-0131245P
990S-0145698P
990S-0145698P
990S-0145698P
990O-07802813
                                                                                                                                                                                                                                                                                                                                    99WO-US028565.
99WO-US030095.
99WO-US031243.
                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
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88.9%;
                                                                                                                                    2000WO-US004341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
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Best Local Similarity
                                                                        WO200053756-A2.
                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                  02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
                                                                                                                                    18-FEB-2000;
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29-OCT-1999;
                                                                                                                                                                                                                                                                                                                    02-DEC-1999;
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23-JUN-1999;
                                                                                                                                                                                                                                                                                                        30-NOV-1999;
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29-MAR-1999
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98US-0082804P. 98US-0082796P. 98WO-US021141.

23-APR-1998; 07-OCT-1998;

ACA63579 standard; DNA; 24 BP

ACA63579/c ID ACA6: XX

Best Loc Matches

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Gaps

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Indels

5:

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Human; ds; thrombolytic agent; interferon; interleukin; cytokine; erythropoietin; colony stimulating factor; cancer; colorectal carcinoma; appprosis related condition; AIDS; amyotrophic lateral scaterois; inflammatory disease; asthma; atherosclerosis; neurodegenerative disease; gastrointestinal disorder; Alzheimer's disease; Parkinson's disease; hypertension; myocardial ischaemia; kidney disease; carcinogenesis; glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia; bronchial asthma; gastric ulcer; renal failure; cardiovascular disease; inflammatory bowel disease; reproductive disorder; premature labour.
                                                                                                                                                                                                                                                     Human PRO polypeptide associated oligonucleotide SEQ ID NO 142.
Mismatches
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                               21
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98US-0079658P.
98US-0079664P.
98US-0079664P.
98US-0079788P.
98US-007978P.
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98US-0077632P.
98US-0077641P.
98US-0077649P.
98US-0077791P.
98US-0077791P.
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98US-0079923P.
98US-00105413.
98US-00168978.
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97US-0065311P.
97US-0066364P.
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98US-0078910P.
98US-0078936P.
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98US-00184216.
98US-00187368.
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98US-00218517
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                               CTCATCACCACTCTCTTC
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                                                                                                                                        .743/c
ACA71743 standard; DNA; 24
                                                                                                                                                                                                                     (first entry)
 16; Conservative
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-MAR-1998;
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30-MAR-1998;
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07-DEC-1998
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21-NOV-1997
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                                                                                                                                                                                      ACA71743;
                                 4
Matches
                                                                                                                       RESULT 25
                                                                                                                                     ACA71743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated nucleic acid (I) comprising, or which is at least 80 % sequence identity to, or the full-length coding sequence off, any of 118 300-2100 nucleotide sequences, which encodes its corresponding PRO polypeptide selected from 118 100-700 amino acid sequences, all given in the specification. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaccuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This sequence represents a novel human secreted and transmembrane PRO polypeptide associated primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Baton DL;
Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
Stewart TA, Tumas D, Williams PM. Wood WT.
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                                                                                                                                                                                                                                                                                     2000WO-US005004.
2000WO-US005841.
2000WO-US006319.
2000WO-US007532.
                                                                                                                                                                                                                                                                                                                                                     2000WO-US008439.
2000WO-US013705.
2000WO-US014042.
                                                                                              99WO-US028313.
99WO-US028551.
99WO-US028565.
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20-DEC-2000; 2000WO-US034956.
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25-MAY-2001; 2001WO-US017092
01-UTUN-2001; 2001WO-US0176900.
20-UTUN-2001; 2001WO-US0196920.
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05-JAN-2000;
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99US-00265686 99US-00267213

10-MAR-1999 10-MAR-1999

Score 14.8; DB 8; Length 24; Pred. No. 1e+04;

59.2%;

Query Match Best Local Similarity

Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;

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polypeptide is also useful as a thrombolytic agent, interferon, interfleukin, erythropoletin, colony stimulating factor and other cytokines. The PRO polypeptide is useful for treating disease such as cancer e.g. colorectal carcinoma; useful for treating disease such as cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS, amyotrophic lateral sclerosis; inflammatory disease e.g. asthma, catherosclerosis; neurodegenerative disease e.g. Alzheimer's disease, Parkinson's disease; cardiovascular disease e.g. Alzheimer's disease, Parkinson's disease; lung disease e.g. pulmonary hypertension and myocardial ischaemia; kidney disease e.g. renal failure and asthma; gastrointestinal disorders e.g. pulmonary hypertension, bronchial asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory bowel disease; reproductive disorders e.g. premature labour and present associated oligonucleotide of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this paten
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Pred. No. 1e+04;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PRO polypeptide; secreted and transmembrane protein;
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                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;
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98US-0078004P.
98US-00040220.
98US-0078886P.
98US-0078936P.
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88.9%;
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26-MAR-1998;
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Jao W, Gerber H, Gerritsen ..
Arney AL, Hillan KJ;
'NF, Roy MA, Shelton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated secreted and transmembrane polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful in PRO polypeptide detection methods. The PRO polypeptide is useful for linking a bioactive melecule to a cell. The PRO polypeptide or an antibody against it is useful for modulating a biological activity of a cell. The PRO polypeptide is useful in industrial applications including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying modulators of receptor-ligand interactions.
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Filvarcff E, Fong S, Gao W, Ger
Godowski PJ, Grimaldi JC, Gurney
GNOS, Napier MA, Pan J, Paor
Tumas D, Williams PM, Wood WI;
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   99US-00284291.
99US-00311832.
99WO-US010733.
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99US-00380138.
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25-MAY-2001;
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Stewart TA,
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20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WG-US034956.
22-MAR-2001; 2001WG-US006520.
22-MAR-2001; 2001US-00816744.
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22-MAR-2001; 2001US-00816920.
10-MAY-2001; 2001US-00854208.
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01-JUN-2001; 2001US-00872035.
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(GETH) GENENTECH INC.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for modulating bloactive molacules to cells expressing PRO polypeptides, for modulating bloactive molacules to calls expressing PRO polypeptides, and for for chordifying agonists or antagonists. The bloactive molecule maybe a coxin, radiolabel or antibody, and causes apoptosis or death of the cell. The PRO polypeptides are useful for treating immune disorders, diabetes or hyper-or hypo-insulinaemia, cardiac insufficiency, nervous system disorders, kidney disorders, bone and cartilage disorders or arthritis, tumours, and wound healing. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the presartion of PRO polypeptides, for generating transgenic animals or knockout animals, for the generation of antisense RNA and DNA, in the presartion of PRO polypeptides of the present sequence represents a PCR primer used in the examples of the present invention. Note: The sequence data for this at seqdata.uspto.gov/psipsDDEntry.html I, Baker KP, Botstein D, Desnoyers L, Eaton D;
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Kuo SS, Napier MA, Pan J, Pooni NF, Roy MA, Shelton DL;
Tumas D, Williams PM, Wood WI; Human; ss; PCR; secreted protein; transmembrane protein; PRO; primer; malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma; leuksemia; lymphoma; inflammatory disease; necrosis; atherosclerosis; infertility; premature agina; psoriasis; inflammatory disease; renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis; hepatitis; multiple sclerosis; gene therapy. Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies. 59.2%; Score 14.8; DB 8; Length 24; 88.9%; Pred. No. 1e+04; Live 0; Mismatches 2; Indels Human secreted/transmembrane protein PRO352 PCR primer #5. Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other; Example 23; Page 138; 459pp; English. ACA66124 standard; DNA; 24 BP 97US-0062250P. 97US-0064249P. 15-OCT-2001; 2001US-00978189. 24-JUN-2003 (first entry) Best Local Similarity 88.9 Matches 16; Conservative WPI; 2003-288163/28. US2003004102-A1. Ashkenazi A, Ferrara N, F Goddard A, G Kljavin IJ, Stewart TA, 17-OCT-1997; 03-NOV-1997; Homo sapiens 02-JAN-2003 ACA66124; 23 Query Match RESULT 27 ACA66124/ 8 원

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97US-006531IP.
91US-0065364P.
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01-MAR-2000;
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06-JAN-2000;
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08-MAR-1999;
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12-MAR-19
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02-JUN-19
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14-UN-2001; 2001US-00882636. 19-UN-2001; 2001US-00886342. 20-UN-2001; 2001WO-US019692. 29-UUN-2001; 2001WO-US021066. 09-UL-2001; 2001US-00918585. 2001WO-US009552. 2001WS-00854208. 2001WS-00854280. 2001WS-0854280. 2001WS-0854280. 2001WS-0872035. 2001US-00874503 (GETH) GENENTECH INC 22-MAR-2001; 22-MAR-2001; 10-MAY-2001; 25-MAY-2001; 25-MAY-2001; 01-JUN-2001; 01-JUN-2001; 14-JUN-2001;

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL; Stewart TA, Tumas D, Williams PM, Wood WI;

WPI; 2003-341189/32.

New genes and secreted and transmembrane polypeptides (e.g. PRO337 or PRO1559), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple sclerosis in mammals.

Example 23; Page 135; 460pp; English.

The invention relates to a new isolated nucleic acid molecule comprises a sequence with at least 80% identity to: (a) a nucleotide encoding any of 94 ROY polypeptides whose sequences are fully defined in the specification; or (b) any of 94 mucleotide sequences fully defined in the specification; or the full length coding sequence fully defined in the corring at least 80% positives when compared to any of the PRO polypeptide corring at least 80% amino acid sequence identity to: (a) an amino acid sequence identity to: (a) an amino acid sequence identity to: (a) an amino acid sequence identity to: (b) the PRO polypeptide having at least 80% amino acid sequence identity to: (a) an amino acid sequence identity to: (b) the PRO polypeptide, lacking its associated signal peptide, a vector comprising the wettor (and producing a PRO polypeptide), a chimaeric molecule comprising the PRO polypeptide, with or lacking its associated signal peptide), a vector (and producing a PRO polypeptide), a chimaeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence and an anti-PRO antibody. The PRO polypeptides or polymorelocides are useful as pharmacenticials, color-cetal cancer, asrcoma, lenkaemia or lampional, inflammatory disease, nearly disease, necrosis, atherosclerosis, infertility, premature aging, psoriasis, inflammatory disease, renal disease, arthritis, immune-mediated alopecia, stroke, encephalitis, hepatitis, or multiple solerosis in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases. The PRO polypeptides are useful as molecular weight markers, or for chromosome content to the presence of these diseases. The PRO genes are useful as bob used in gene therapy, particularly for replacing a defective and the procure of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective cDNA encoding a PRO polypeptide

Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;

Gaps ö DB 8; Length 24; 2; Indels Match 59.2%; Score 14.8; DB 8 Local Similarity 88.9%; Pred. No. 1e+04; les 16; Conservative 0; Mismatches Query Match Best Loca Matches

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98US-0083322P
98US-00833254P
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      Human; secreted and transmembrane protein; PRO; tissue typing; chromosome identification; vaccine; cancer; retinal disorder; poptre-related joint disorder; osteoarthritis; rheumatoid arthritis; wound healing; obesity; diabetes; hearing loss; cardiac insufficiency disorder; kidney disorder; nervous system disorder; haemoglobin associated disorder; PCR; primer; ss.
                                                                                                                                                                                    Secreted and transmembrane PRO protein associated primer #73.
                                                                                          ADA24681 standard; DNA; 24 BP
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CACATCACCACCTCTTC
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03-NOV-1997;
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ACD29725;
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E. Fong S, Gao W, Gerber H, Gerritsen ME;
PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated PRO polypeptides for example extracellular, secreted and membrane bound proteins, useful for modulating the biological activities of cells and for treating, for example diabetes, cancer, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated secreted and transmembrane (PRO) polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993 polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is useful for detecting PRO559, PRO700 and PRO739 in a sample. PRO4993 is useful for linking a bioactive molecule to a cell expressing a PRO493 polypeptide, and PRO337 is useful for linking a bioactive molecule to cell expressing a PRO493 polypeptide. PRO1559 is useful for linking a bioactive molecule to a cell expressing a PRO493 polypeptide. PRO700 and PRO739 polypeptide, and PRO735, PRO700 and PRO739
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2000MO-US007532
2000MO-US013705.
2000MO-US013705.
2000MO-US014042.
2000MO-US016441.
           99WO-US028551.
99WO-US028565.
99WO-US030095.
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2000WO-US032678.
2000WO-US034956.
2001WO-US006520.
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2000WO-US005004.
                                                                                                   2000WO-US000277.
2000WO-US000376.
2000WO-US003565.
                                                                        99WO-US031274,
2000WO-US000219.
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Ferrara N, Filvaroff E, Fo
Goddard A, Godowski PJ, Gr
Kljavin IJ, Kuo SS, Napier
Stewart TA, Tumas D, Willi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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         02-DEC-1999;
16-DEC-1999;
16-DEC-1999;
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05-JAN-2000;
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17-MAY-2000; 2
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peripheral neuropathy; diabetic peripheral neuropathy;
AIDS-associated neuropathy; Charcot-Marie-Tooth disease;
Refusum's disease; Abetalipoproteinaemia; Tangier disease;
Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;
Dejerine-Sottas syndrome; chromosome mapping; gene therapy;
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                                                                                                                                                                                                 16-OCT-2001; 2001US-00978403
                         08-SEP-2003 (first entry)
                                                                                                                                                           US2003050240-A1.
                                                                                                                        PCR; primer; ss.
                                                                                                                                          Homo sapiens.
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Gaps

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23

Matches

ઠે 셤 ACD29725/c ID ACD29725 standard; DNA; 24 BP.

RESULT 29

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98US-0083495P

98US-0083545P

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98US-0083545P

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99WO-US028551
28-APR-1998;
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06-MAY-1998;
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The invention describes an isolated, secreted and transmembrane polypeptide, termed PRO polypeptide (1). (1) is useful for detecting PRO4993, PRO373, PRO185, PRO785, PRO789 polypeptide, and for linking a bioactive molecule to a cell expressing the above polypeptides. The bioactive molecule is a toxin, radiolabel or an antibody and causes cell death. (1) is useful as therapeutic agent, in medical and industrial applications e.g. for treating neuropathy, especially peripheral neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy, charcot-Marie-Tooth disease, Refusum's disease, Abetalipoproteinaemia, Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's
                                                                                                                                                                                                                                                                                                                                                                                                                         Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Grimalaldi JC, Gurney AL, Hillan KJ; Klo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL; Stewart TA, Tumas D, Williams PM, Wood WL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
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                                                        2000MO-US004341.
2000MO-US00504.
2000MO-US005811.
2000MO-US005312.
2000MO-US01532.
2000MO-US013705.
2000MO-US014042.
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2000WO-US023328.
2000WO-US032678.
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09-JUL-2001; 2001WO-US021735.
30-JUL-2001; 2001US-00918585.
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2001WO-US019692
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ID ADA12342 standard; DNA; 24
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hes 16; Conservative
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24-FEB-2000;
10-MAR-2000;
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31-MAR-2000;
11-MAY-2000;
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Human secreted/transmembrane polypeptide PRO352 primer #5.

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98US-0083742P.
98US-0084441P.
98US-0084441P.
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   primer; ss; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cancer; diabetic complication; tissue typing; human; PCR.
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970S-006224P.
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970S-006424P.
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diabetic peripheral neuropathy; autonomic neuropathy; reduced motility of the gastrointestinal tract; atony of the unimary bladder; post polio syndrome; Krabbe's disease; Charcot-Marie-Tooth disease; Pabry's disease; Tangier disease; Refsum's disease; PCR; primer; ss.
    cardiac - insufficiency disorder; peripheral neuropathy;
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97US-0064249P
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Fong S, Gao W, Gerber H, Gerritsen
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2000WO-US000219.
2000WO-US000376.
2000WO-US003565.
2000WO-US004341.
2000WO-US005064.
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2000WO-US006319.
2000WO-US007532.
2000WO-US008439.
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2000WO-US020710.
2000WO-US023328.
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2000WO-US034956.
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2001WO-US017800.
2001US-00874503.
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2001US-00816920.
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99WO-US031243
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2000WO-US032678.
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2001US-00886342.
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88.9%;
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nes 16; Conservative
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Ferrara N, Filvaroff E,
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16-DEC-1999;
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PR 22-DEC-1999; 98US-0013023P.
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PR 22-DEC-1999; 98US-0013013P.
PR 23-DEC-1999; 98US-0013013P.
PR 23-DEC-19
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Gaps
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Pred. No. 1e+04
0; Mismatches
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XX
AC ADB73648;
XX
C ADB73648;
XX
C 4-DEC-2003 (first entry)
XX
C Human PRO DNA PCR primer #71.
XX
W Human; PRO polypeptide; secreted
XW
Cell death; neuropathy; neuropat
XW
Charcot-Marie-Tooth disorder; Re
XM
Charcot-Marie-Tooth disorder; Re
XM
Charcot-Marie-Tooth disorder; Re
XM
Antibacterial; immunosuppressive
XX
CS
Homo sapiens.
XX
YX
PD
OG-MAR-2003.
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PF
16-OCT-2001; 2001US-00978608.
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        99WO-US028313
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les 16; Conservative
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11-FEB-2000;
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06-MAY-1998;
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07-MAY-1998;
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15-MAY-1998;
15-MAY-1998;
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07-MAY-1998;
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Pred. No. 1e+04;
0; Mismatches 2; Indels
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Best Local Similarity 88.9%;
Matches 16; Conservative
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25-MAY-2001; 2001WO-US017092
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29-MAR-1999;
21-APR-1999;
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Gerritsen ME; Eaton DL;

Botstein D, Desnoyers L, Fong S, Gao W, Gerber H,

Ashkenazi AJ, Baker KP, Ferrara N, Filvaroff E,

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                                                                                                                                                                                      The present invention relates to the isolation of novel human PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for inking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The bioactive molecule maybe a toxin, radiolabel or antibody, and cause cell death. The PRO polypeptides are useful for treating neuropathy and neuropathy related diseases such as Charcot-Marie-Tooth disorder, Refeum's disease, and Krabbe's disease. The polymucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for
                                                                                              New PRO polypeptides useful for treating peripheral neuropathy, neuropathies associated with systemic disease such as post-polio syndrome
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                  Shelton DL;
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 Hillan KJ;
Roy MA,
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PJ, Grimaldi JC, Gurney AL, B
Napier MA, Pan J, Paoni NF,
Williams PM, Wood WI;
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                                                                                                                              or AIDS-associated syndrome.
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 Godowski PJ,
Kuo SS, Na
                               Tumas D,
                                                               WPI; 2003-755118/71.
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Goddard A, G
Kljavin IJ,
Stewart TA,
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13-MAR-1998;
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22-MAY-1998; 28-MAY-1998; 28-MAY-1998; 26-UW-1998; 26-UW-1998; 26-UW-1998; 26-UW-1998; 26-UW-1998; 26-UW-1998; 20-WW-1998; 20-WW-1998; 20-WW-1999; 22-DEC-1999; 22-DEC-1999; 22-DEC-1999; 22-MAR-1999; 22-MAR-2000; 24-PEB-2000; 2	

98US-0079294P. 98US-0079294P. 98US-0079294P. 98US-0079294P. 98US-0079268P. 98US-007968P. 98US-007928P. 98US-007928P. 98US-0079928P. 98US-0080107P. 98US-0080107P. 98US-0080137P. 98US-0080134P. 98US-0080132P. 98US-008132P. 98US-0081392P.	98US-00853338P 98US-0085338P 98US-0085339P 98US-0085580P 98US-0085580P 98US-0085682P 98US-008560P 98US-0085704P 98US-0085704P 98US-0085704P 98US-0086733P
20-MAR-1998; 25-MAR-1998; 26-MAR-1998; 27-MAR-1998; 27-MAR-1998; 27-MAR-1998; 27-MAR-1998; 27-MAR-1998; 31-MAR-1998; 32-APR-1998; 33-APR-1998; 33-AP	, o o o o o o o o o o o o o o o o o o o
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98US-0079786P

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18-MAY-1998;
22-MAY-1998;
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22-MAR-2001; 2001US-00816744.
22-MAR-2001; 2001WG-US009552.
10-MAY-2001; 2001WG-US009552.
10-MAY-2001; 2001WG-00854208.
10-MAY-2001; 2001WG-00854208.
25-MAY-2001; 2001WG-00854208.
01-JUN-2001; 2001WG-00817092.
01-JUN-2001; 2001WG-00817092.
19-JUN-2001; 2001WG-00818263.
19-JUN-2001; 2001WG-00819692.
29-JUN-2001; 2001WG-US0119692.
29-JUN-2001; 2001WG-US011735.
30-JUL-2001; 2001WG-US011735.
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ADC61550 standard; DNA; 24 BP.
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20-DEC-2000; 2000W0-US034956.
28-FEB-2001; 2001W0-US006520.
22-MAR-2001; 2001W0-US006520.
22-MAR-2001; 2001W0-US009552.
10-MAY-2001; 2001WS-00816920.
98US-0100038P
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98US-001689216
98US-00184216
98US-0109304P
98US-010202654
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99WO-US031243.
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06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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21-WAR-2000;
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                                                                                                                 Length 24;
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                                                                                               Desnoyers L,
                                                                                                                59.2%; Score 14.8; DB 10; 88.9%; Pred. No. 1e+04;
                                                                                                                         le+04;
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05-JUN-2001; 2001US-00874503.
14-JUN-2001; 2001US-00882636.
19-JUN-2001; 2001US-00886342.
20-JUN-2001; 2001WO-US019692.
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ADC63514 standard; DNA; 24 BP
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                                                                                             Ashkenazi AJ, Baker KP,
                                                                                                                         Local Similarity 88.9
les 16; Conservative
                                                                           (GETH ) GENENTECH INC
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Example 23; SEQ ID NO 142; 472pp; English.
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98US-00202054.
98US-00218517.
30-JUL-2001; 2001US-00918585.
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Matches 16; Conservative
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           (GETH ) GENENTECH INC.
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Shelton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Baker KP, Botstein D, Desnoyers L, Eaton DL; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Sodowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Kuo SS, Napier MA, Pao J, Paoni NF, Roy MA, Shelto Tumas D, Williams PM, Wood WI;
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2001US-00816744
2001US-00816920
2001WS-008552
2001US-00854208
2001US-00854280
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99WO-US005028.
99WO-US005190.
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99WO-US012252.
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2000WO-US023328.
2000US-00709238.
2000US-00723749.
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2000WO-US014941.
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2000WO-US000277.
2000WO-US000376.
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2000WO-US005841
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2001WO-US019692.
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Ferrara N, Filvaroff B, Fr
Goddard A, Godowski PJ, G;
Kljavin IJ, Kuo SS, Napien
Stewart TA, Tumas D, Will:
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The Invention Observines an isolated secreted and transmembrane known the Invention Observines an isolated such as PR0213, PR0700, PR0320 or PR0615 is useful in biotechnological and medical research, as well as in various industrial applications. PR0 polypeptide such as PR0310, PR0320, PR0323, PR0320, PR0321, PR0351, PR0351, PR0313, PR0615, PR0712, PR0853, PR0320, PR0860 or PR0846 is useful for therapeutic purposes. PR0361 is useful to the reatment of wound healing, tissue growth and therapeutically in vivo for lessening the effects of viral infection. PR0300 is useful for the treatment of wound healing, tissue growth and muscle generation and regeneration. PR0317 is useful for treating contraction and regeneration. PR0317 is useful for treating contraction. PR0317 is useful for generating transgenic animals or knockout animals which are useful for generating transgenic animals or knockout animals which are useful for generating transgenic animals or knockout animals which are useful for generating sequences, and to construct hybridisation probes for reagents, as probes for generating a pool of sequences for identifying reagent with genetic disorders, for recombinantly expressing (1) and for chromosome identification. (1) is useful as molecular marker for for chromosome identification. (1) is useful as molecular marker for contracting lectrophoresis purposes, and as therapeutic agents. (1) is also cuseful for screening compounds to identify those that mimic the PRO polypeptide (aniquists) or prevent the effect of the PR0 polypeptide (aniquists) or prevent the effect of the PR0 polypeptide care useful for immunohistochemical staining and/or assay of sample conferenting its expression in specific cells, tissue typing. PR0 antibodies are useful in diagnostic assay of sample conferenting its expression in specific cells, tissues or serum, and for altimity purification of PR0 from recombinant cell culture or natural conferences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, ss; PCR; secreted protein; transmembrane protein, PRO; cytostatic; ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnerary; auditory; tumour growth, retinal disorder; sports-related joint problem; articular cartilage defects; osteoarthritis; rheumatoid arthritis; wound healing; hearing loss; primer.
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The invention describes an isolated secereted and transmembrane PRO
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97US-0065311P.
98US-0077450P.
98US-0077632P.
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98US-0077641P.
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PR 13-MAR-1998; 98US-0078004P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079224P.
PR 25-MAR-1998; 98US-007924P.
PR 27-MAR-1998; 98US-0079264P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079268P.
PR 31-MAR-1998; 98US-0079328P.
PR 31-MAR-1998; 98US-0079328P.
PR 31-MAR-1998; 98US-0079328P.
PR 31-MAR-1998; 98US-0081332P.
PR 31-MAR-1998; 98US-0081239P.
PR 31-MAR-1998; 98US-0081332P.
PR 31-MAR-1998; 98US-0081332P.
PR 31-MAR-1998; 98US-0081332P.
PR 32-ARR-1998; 98US-008135SP.
PR 32-ARR-1998; 98US-00813SP.
PR 32-ARR-1998; 98U
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98US-0085704P

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98US-0086414P

98US-0086416P

98US-0086416P

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98US-0087106P

98US-0017010P

98US-0017010P

98US-00181141

98US-001821141

98US-0018216P

98US-00182116

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2000WO-US00277.
2000WO-US003565.
2000WO-US003565.
2000WO-US005841.
2000WO-US005841.
2000WO-US005841.
2000WO-US005841.
2000WO-US008439.
2000WO-US008439.
2000WO-US013705.
2000WO-US014941.
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99WO-US030095.
99WO-US031243.
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08-NOV-2000; 2000US-00709238
27-NOV-2000; 2000US-00723749
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06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
24-FEB-2000;
15-MAY-1998,
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28-MAY-1998,
28-MAY-1998,
28-MAY-1998,
26-JUN-1998,
26-JUN-1998,
10-JUL-1998,
11-SEP-1998,
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14-MAY-1999;
14-MAY-1999;
02-JUN-1999;
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29-OCT-1999;
30-NOV-1999;
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30-DEC-1999;
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23-JUN-1999
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25-AUG-1999
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Human, 88; PCR; secreted protein, transmembrane protein, PRO; cytostatic, ophthalmological, antiarthritic; osteopathic; antirheumatic; vulnerary; auditory; tumour growth, retinal disorder; sports-related joint problem, articular cartilage defects; osteoarthritis; rheumatoid arthritis; wound healing; hearing loss; primer.
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Pred. No. 1e+04;
); Mismatches
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                     20000S-00747259.
2001W0-US014956.
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2001US-00816920.
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2001US-00854280.
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98US-007891P.
98US-0078910P.
98US-0078936P.
98US-0078936P.
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88.9%;
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les 16; Conservative
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01-DEC-2000;
20-DEC-2000;
28-FEB-2001;
28-FEB-2001;
22-MAR-2001;
22-MAR-2001;
10-MAY-2001;
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10-JUN-2001;
25-MAY-2001;
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10-MAR-1998;
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12-MAR-1998;
20-MAR-1998;
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JUN-1998; 98US-0090863P.

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-OCT-1998; 98US-009155P.

-NOV-1998; 98US-010302141.

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NOV-1998; 98US-010302141.

-DEC-1998; 98US-0113296P.

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J-DEC-1999; 99US-0131679P.

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J-DEC-1999; 99US-01319.

J-DEC-1999; 99US-013189.

J-DEC-1999; 99US-013189.

J-DEC-1999; 99US-013189.

J-DEC-1000; 2000WO-US015264.

J-DEC-2000; 2000WO-US01526.

J-DEC-2000; 2000WO-US01526.

J-DEC-2000; 2000WO-US01526.

J-DEC-2000; 2000WO-US01526.

J-DEC-2000; 2000WO-US01526.

J-DEC-2000; 2000WO-US0159.

J-DEC-2000; 2000WO-US01569.

J-DEC-2000; 2000WO-US0169.

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### (GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL; Stewart TA, Tumas D, Williams PM, Wood WI;

### WPI; 2003-695924/66.

New isolated secreted and transmembrane PRO polypeptides, useful in the preparation of a medicament for treating a condition responsive to the polypeptide, and as therapeutic agents e.g. vaccines.

## Example 23; SEQ ID NO 142; 467pp; English.

The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity

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20-NOV-1998;
 in the specification (including PRO lacking its associated signal processes of the specification (including PRO lacking its associated signal peptide). A PRO extractallular domain with or without its associated signal peptide). Also included are mucleic acids encoding the PRO proteins mentioned above, a vector comprising a PRO nucleic acid), a host cell comprising the vector and producing PRO, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence, and an anti-PRO artibody. PRO337 polypeptide is useful for detecting a PRO4993 polypeptide is useful for detecting PRO337 polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting PRO355. PRO700 or PRO739 polypeptide is useful for detecting PRO355. PRO700 or PRO739 polypeptide is useful for detecting PRO355. PRO700 or PRO739 polypeptide is useful for detecting PRO355. PRO700 or PRO739 polypeptide is useful for detecting PRO355. PRO700 or PRO739 polypeptide is useful for linking a bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive molecule is the toxin, radiolabel, or an antibody. The bioactive molecule causes death of the cell. PRO337 polypeptide is useful for linking a
 Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytostatic; ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnerary; auditory; tumour growth; retinal disorder; sports-related joint problem; articular cartilage defects; osteoarthritis; rheumatoid arthritis; wound healing; hearing loss; primer.
 Gaps
 ;
 y Match 59.2%; Score 14.8; DB 10; Length 24; Local Similarity 88.9%; Pred. No. 1e+04; nes 16; Conservative 0; Mismatches 2; Indels C
 4 CTCATCACCACTCTTC 21
 97US-0064249P.
97US-0065311P.
97US-0065344P.
98US-0077632P.
98US-0077643P.
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 18-DEC-2003 (first entry)
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28-FEB-2001; 2000WO-US034956.
28-FEB-2001; 2001WO-US006520.
22-MAR-2001; 2001WO-US009552.
25-MAY-2001; 2001WO-US009552.
 2000WO-US00376.
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20-JUN-2001; 2001WO-US019692.
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21-MAR-2000; 2
30-MAR-2000; 2
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 02-JUN-2000;
 16-JUN-1999
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## (GETH ) GENENTECH INC

KP, Botstein D, Desnoyers L, Eaton DL;
E, Fong S, Gao W, Gerber H, Gerritsen ME;
PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
Williams PM, Wood WI; Ferrara N, Filvaroff E, Fr Goddard A, Godowski PJ, Gr Kljavin IJ, Kuo SS, Napier Stewart TA, Tumas n

## WPI; 2003-657582/62.

Novel secreted and transmembrane polypeptides, designated PRO polypeptides, and polynucleotides encoding them useful for treating kidney diseases, bone, cartilage and retinal disorders.

## Example 23; SEQ ID NO 142; 468pp; English.

The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity on amino acid sequence chosen from 9% fully defined sequences as given in the specification (including PRO lacking its associated signal peptide, a PRO extracellular domain with or without its associated signal

ö peptide). Also included are nucleic acids encoding the PRO proteins mentioned above, a vector comprising a PRO nucleic acid), a host cell comprising the vector and producing PRO, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence, and an anti-PRO antibody. PRO337 polypeptide is useful for detecting a PRO4993 polypeptide in a sample suspected of containing PRO4993 polypeptide. Similarly, PRO4993 polypeptide is useful for detecting PRO327 polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting Gaps . 0 Length 24; Indels 59.2%; Score 14.8; DB 10; 88.9%; Pred. No. 1e+04; iive 0; Mismatches 2; 4 CTCATCACCACTCTTC 21 9 CACATCACCACCCTCTTC Query Match Best Local Similarity 88.9 Matches 16; Conservative 8888888888 ઠે 셤

Search completed: November 18, 2005, 11:52:35 Job time : 174.148 secs

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Embryophyta; Tracheophyta;               | opsida; Poales;<br>Zea.<br>g engineered Res<br>94304, USA<br>s cut by single<br>sequence from s                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Location/Qualifiers 148 148 148 148 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 248 24                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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| AV833578<br>CL528695<br>AI4103975<br>AI41968<br>TA221E12Q<br>BH9009685<br>AI186273<br>BH903343<br>TA110A12Q<br>AJ595714<br>BZ381485<br>CF920754<br>BZ381485<br>CF920754<br>BZ381802<br>BH903344<br>BH861884<br>BH861884<br>BH861886<br>AA717367<br>BH813018<br>AA717367<br>BH813018<br>AU103251<br>CG695865                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ALIGNMENTS 48 bp 1007 - Rescuemu 40702                                                                                                                  | Spermatophyta; Magnollophyta; Lill. Clade; Panicoldeae; Andropogoneae; I (bases 1 to 48) Walbot, V. Walze genomic sequences found usin. Walze genomic sequences found usin. Unpublished (2001) Contact: Walbot V Department of Biological Sciences Stanford University P Tel: 650 723 227 Tel: 650 723 227 Email: Walbotostanford.edu Very probable ligation site of end Reverse complemented post-ligation Class: transposon-taqqed.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | "Zea mays" "genomic DNA" mixed backgr taxon:4577" pe="leaf" "Bling" "DIIO" "DIIO" "Backbone); t backbone); t backbone); t backbone); t backbone); t backbone); t ner; t pactate: "Grid H wae ted from leaf                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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Magn<br>licoldeae;<br>mic seque<br>d (2001)<br>albot v<br>of Biolo<br>niversity<br>rnia Ave,<br>23 2227<br>25 8211<br>bocostanf<br>mplemente<br>mplemente<br>7071 col                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Location/Qualifier 148 /organism="Zea may /mol_type="genomic /cultivar="mixed b. /db_xref="taxon:45 /fisue type="leaf /lab_host=ge="allt" /lab_host=ge="allt" /lab_host=ge="allt" /lab_host=ge="allt" /lab_host=ge="allt" /lab_host=ge="allon" /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf /note="organ: leaf |
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                                               | RESULT 1 BH627451 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM                                                                           | REFERENCE<br>AUTHORS<br>AUTHORS<br>JOURNAL<br>COMMENT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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CD531219 DME546976 AA179783

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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Balos; Lo 32)

E. (base; Lo 32)

B. (base; Lo 32)

S. Jann, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacce, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
 ö
 Ē
 AZ641286

32 bp DNA linear GSS 14-DEC-200
1M0503C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0503C14 R, genomic survey sequence.
 /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
 Gaps
 ö
 4; Indels
 Score 15.6; DB 8; Length Pred. No. 3.2e+04; 0; Mismatches 4; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0503 row: C column: 14
Seg primer: CACACAGGAAACAGCTATGACC
 organism="Mus musculus"
 /mol_type="genomic DNA"
/strain="C57BL/6J"
 Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
 db_xref="taxon:10090"
 clone="UUGC1M0503C14"
 4 CTCATCACCACTCTCTTCCATC 25
 2 CTCCTCTCCCTCTTCCACC 23
 Mus musculus (house mouse)
 AZ641286.1 GI:11765116
 62.4%;
81.8%;
 /sex="Male"
 18; Conservative
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
 Best Local Similarity
 Mus musculus
 AZ641286
 Query Match
 source
 VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 REFERENCE
AUTHORS
 Matches
 ACCESSION
 RESULT 2
AZ641286
 JOURNAL
 FEATURES
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TITLE

COMMENT

```
CONN Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 ö
 CTCGAGTTTTTTTTTTTTT 3' Average insert size: 0.9 kb."
 ö
adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 48) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 AA576280

mm60g01.s1 NCI CGAP Br3 Homo sapiens cDNA clone IMAGE:1072656 3' similar to gb:X63563 DNA-DIRECTED RNA POLYMERASE II 140 KD
 /tissue trype="breast tumor"
/lab_host="SOLR (kanamycin resistant)"
/clone lib="NCI CGAP Br3"
/note="Organ: breast; Vector: Bluescript SK-; Site_1:
/note="Organ: breast; Vector: Bluescript SK-; Site_1:
/note="Organ: breast tumor. 5' adaptor sequence: 5'
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
 Gaps
 Gaps
 æ
 .
0
 ö
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
 Query Match 58.4%; Score 14.6; DB 1; Length 48; Best Local Similarity 81.0%; Pred. No. 8.6e+04; Matches 17; Conservative 0; Mismatches 4; Indels
 5; Indels
 Length
 Score 15; DB 8; I
Pred. No. 5.4e+04;
 Trace considered overall poor quality Insert Length: 1214 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
 0; Mismatches
 Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:1072656"
 3 ACTCATCACCACTCTCTTCCATC 25
 7 Acrearcacecerecraciae 29
 ACACATCACGACTCTCTACAA 27
 3 ACTCATCACCACTCTTCCA 23
 AA576280.1 GI:2350795
 /sex="female"
 60.0%;
 Homo sapiens (human)
Homo sapiens
 Tumor Gene Index
Unpublished (1997)
 Conservative
```

```
Musucatura Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. E. (bases 1 to 44)

E. (bases 1 to 44)

Dumn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diamid inserts

Dumplished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 AZ983982
2M0265013F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0265013 F, genomic survey sequence.
 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Insert Length: 983 Std Error: 0.00
Seq primer: mob.REGA+ET
 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
 Length 34;
 Score 14; DB 7; Length 34;
Pred. No. 1.5e+05;
0; Mismatches 5; Indels
 1. .34
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/mol_type="mRNA"
/db_xref="GDB:1269213"
/db_xref="taxon:9606"
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Location/Qualifiers
 25
 25 CTCAACACCAGTCTCCACAATC 4
 Mus musculus (house mouse)
 4 CTCATCACCACTCTTCCATC
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 AZ983982.1 GI:13855209
 similarity 77.3%;
 Query Match
Best Local Similarity 77,000
To Conservative
 rel: 801 585 5606
 Mus musculus
 GSS.
 source
 DEFINITION
 AZ983982/c
 ORGANISM
 REFERENCE
AUTHORS
 JOURNAL
 ACCESSION
 FEATURES
 KEYWORDS
 RESULT 6
 VERSION
 TITLE
 ORIGIN
 셤
 ઠે
 Lyberc Contract Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and hil@sanger.ac.uk and hil@sanger.ac.uk and hil@sanger.ac.uk and Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H and venter, JC. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell. Oxford University Press, 1999).
 TA133D12P 29 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 133d12, forward sequence,
 34 bp mRNA linear EST 16-OCT-1996 zd47g08.81 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:343838 3' similar to PIR:S24168 S24168 hypothetical protein - W69493
 ö
 Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primatee; Catarrhini, Hominidae, Homo.

1 (Dases 1 to 34)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulran,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Gaps
 Trypanosoma.
1 (bases 1 to 29)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
 Trypanosoma brucei
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
 ö
 56.8%; Score 14.2; DB 9; Length 29; 84.2%; Pred. No. 1.2e+05; ive 0; Mismatches 3; Indels
 l. .29
/organism="Trypanosoma brucei"
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/clone="133d12"
 ocation/Qualifiers
 The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
 genomic survey sequence.
 CTTCACCCTCCCTTCCAT 10
 6 CATCACCACTCTCTTCCAT 24
 AL465919.1 GI:11835041 GSS.
 W69493.1 GI:1378774
 Homo sapiens (human)
 Trypanosoma brucei
 Best Local Similarity 84.2
Matches 16; Conservative
 Homo sapiens
 Wilson, R.
 Query Match
RESULT 4
TA133D12P/c
 VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 5
W69493/c
LOCUS
DEFINITION
 DEFINITION
 ACCESSION
VERSION
KEYWORDS
 ORGANISM
 TITLE
JOURNAL
 REFERENCE
AUTHORS
 ACCESSION
 REFERENCE
 AUTHORS
 JOURNAL
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Gaps .. 5

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Fax: 801 585 7177
 GSS.
 source
 RESULT 8
AG188152/c
 DEFINITION
 ORGANISM
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 AUTHORS
 JOURNAL
 JOURNAL
 AUTHORS
 REFERENCE
 FEATURES
 TITLE
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 DRIGIN
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 /lab hose="B." coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Wouse 10kb plasmid UUGC2M library"
/clone_lib="Wouse 10kb plasmid UUGC2M library"
/note="Weetor: PWD42nt, Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares). The DNA
was blut cand-repaired by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent B. coli Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Contact: Robert B. Weiss University of Utah Genome Center Rule Genome Center Sty of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 AZ340483 44 bp DNA linear GSS 29-SEP-2000 1M0072N19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0072N19 F, genomic survey sequence.
 ö
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 44)
Bunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Menen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Gaps
 ;
0
 Query Match 56.0%; Score 14; DB 8; Length 44; Best Local Similarity 77.3%; Pred. No. 1.5e+05; Matches 17; Conservative 0; Mismatches 5; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0265 row: O column: 13
 Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 44.
Location/Qualifiers
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/clone="UUGC2M0265013"
 4 CTCATCACCACTCTTCCATC 25
 42 CTCCTTTACCCTCTTCCATC 21
 Mus musculus (house mouse)
Mus musculus
 AZ340483.1 GI:10415782
 sex="Female"
 rel: 801 585 5606
 AZ340483
 DEFINITION
 ORGANISM
 ACCESSION
 REFERENCE
 AUTHORS
 JOURNAL
 VERSION
KEYWORDS
 RESULT 7
AZ340483
 FEATURES
 TITLE
 COMMENT
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ORIGIN

SOURCE

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Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 Submitted (07-378-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)
 AG188152 33 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-061L05.T7, genomic survey
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIN library"
/note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
 Gaps
 2 (bases 1 to 33)
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Bun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43
 .
0
 55.2%; Score 13.8; DB 8; Length 44; 88.2%; Pred. No. 1.9e+05; ive 0; Mismatches 2; Indels
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: N column: 19
 plate: 0072 row: N column: 19
Seq primer: CGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 44.
Location/Qualifiers
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/strain="C57BL/6J"
 /db_xref="taxon:10090"
/clone="UUGC1M0072N19"
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 1 CAACTCATCACCACTCT 17
 23 CAACAGATCACCACTCT 39
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 Query Match
Best Local Similarity 88.23
Matches 15; Conservative
 Pan troglodytes
 Unpublished
 AG188152
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us-10-788-779-9.rst

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http://signal.salk.edu/tdna_protocols.html"
 Turs.
At1959520.
Class: TDNA tagged.
Location/Qualifiers
 1 CAACTCATCACCACTCTT 20
 16 cracrarcrecacrarerr 35
 11 CATCTGCGCTCTTTCTATC 30
 6 CATCACCACTCTTCCATC 25
 ..
 BH866288.1 GI:22102186
 found at
 Conservative
 Conservative
 Query Match
Best Local Similarity
 Similarity
 Query Match
Best Local Simi
Matches 16;
 16;
 source
 RESULT 11
AI201105
LOCUS
DEFINITION
 SOURCE
ORGANISM
 DEFINITION
 Matches
 JOURNAL
COMMENT
 ACCESSION
 VERSION
KEYWORDS
 AUTHORS
 REFERENCE
 BH866288
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 TITLE
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Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
 BZ377820 46 bp DNA linear GSS 26-NOV-2002 SALK_106264.42.05.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_106264.42.05.x, genomic
 ö
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Simmerman,J. and Bcker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
 /clone_SALK 106264.42.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
 Arabidopsis thaliana (thale crees)
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
 This is single pass sequence recovered from the left border of {	t TDNA}.
 Gaps
 ö
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone_trype="lymphocytes"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
 54.4%; Score 13.6; DB 9; Length 33; 80.0%; Pred. No. 2.2e+05; ive 0; Mismatches 4; Indels
 1. 46
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/ecoEype="Col-0"
 db xref="taxon:3702"
 Location/Qualifiers
 Class: TDNA tagged.
Location/Qualifiers
 : pBACe3.6
: EcoRI
 2 AACTCATCACCACTCTTC 21
 28 ACCTCATCACCACCATCCTC 9
 BZ377820.1 GI:25467955
 : ECORI
 Sequencing: T7
 16; Conservative
 (bases 1 to 46)
 survey sequence.
BZ377820
 R.Site 1
R.Site 2
 Query Match
Best Local Similarity
 Vector
 BZ377820
 LIBRARY
 Source
 VERSION
KEYWORDS
SOURCE
ORGANISM
 Source
 DEFINITION
 Matches
 RESULT 9
BZ377820
 ACCESSION
 REFERENCE
 AUTHORS
 JOURNAL
 FEATURES
 FEATURES
 COMMENT
 TITLE
 COMMENT
 ORIGIN
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8 요

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AI201105
49 bp mRNA linear EST 14-OCT-1998 qf69g04.xl Soares testis NHT Homo sapiens cDNA clone IMAGE:1755318 3' similar to gb:X68285 ĞLYCEROL KINASE (HUMAN);, mRNA sequence.
 ö
 /db xref="taxon:3702"
/clone="SALK 101113"
/clone="SALK 101113"
/clone="Taxon:3702"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the atte of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.

(pases 1 to 48)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
 BH866288 110113 Arabidopsis thaliana TDNA linear GSS 05-AUG-200 SALK_101113 Arabidopsis thaliana genomic clone SALK_101113, genomic survey sequence.
 Gaps
 Gaps
 This is single pass sequence recovered from the left border TDNA. This sequence lies within 300 bases of the 5' end of
 ö
 .;
0
 46;
 54.4%; Score 13.6; DB 8; Length 48; 80.0%; Pred. No. 2.38+05; ive 0; Mismatches 4; Indels
 Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 630 879
Email: ecker@salk.edu
 4; Indels
 Length
54.4%; Score 13.6; DB 8;
80.0%; Pred. No. 2.3e+05;
ive 0; Mismatches 4;
 1.48
/organism="Arabidopsis thaliana"
/mol type="Genomic DNA"
/ecorype="Col"
 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
```

us-10-788-779-9.rst

```
Mus musculus (house mouse)
 AZ635993.1 GI:11758183
 Tel: 801 585 5606
Fax: 801 585 7177
 plasmid inserts
 Local Similarity
nes 17; Conserv
 USA
 AZ635993
 84112,
 Query Match
 LOCUS
 AZ635993/c
 ORGANISM
 JOURNAL
 Matches
 ACCESSION
 RESULT 13
 VERSION
KEYWORDS
 REFERENCE
 AUTHORS
 FEATURES
 TITLE
 ORIGIN
 SOURCE
 ð
 /clone lib="Soares testis NHT"
/clone lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
 Bonaldo, Ph.D. CDN Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CRP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
 AZS90062 1000 1000 1000 1000 1000 1000 10000 10000 10000 10000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 100
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 42)
Dunn,D., Aoyagi, Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Patima Bonaldo."
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Gaps
 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 ö
 Score 13.6; DB 1; Length 49;
Pred. No. 2.3e+05;
0; Mismatches 4; Indels
 4; Indels
 Trace considered overall poor quality
Seq primer: -400P from Gibco
High quality sequence srop: 1.
Location/Qualifiers
 . .49
organism="Homo sapiens"
 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1755318"
 /sex="male"
/lab_host="DH10B"
 Mus musculus (house mouse)
 5 TCATCACCACTCTTCCAT 24
 rcarracrecrrrcrrccar 35
 AZ590062.1 GI:11712252
 GI:3753711
 54.4%;
 Homo sapiens (human)
 Tumor Gene Index
Unpublished (1997)
 Query Match
Best Local Similarity 80.0
Matches 16; Conservative
 Homo sapiens
 musculus
 AI201105
AI201105.1
 AZ590062
 GSS.
 SOURCE
ORGANISM
ACCESSION
VERSION
KEYWORDS
SOURCE
 ORGANISM
 AZ590062/c
 DEFINITION
 REFERENCE
AUTHORS
TITLE
 JOURNAL
 ACCESSION
 REFERENCE
 AUTHORS
 KEYWORDS
 FEATURES
 VERSION
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwb12 (gil #132114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
 5
 AZ635993 25 bp DNA linear GSS 13-DEC-2000 1M0493E20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0493E20 R, genomic survey sequence.
 ö
 Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
 Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/64 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
Mouse whole genome scaffolding with paired end reads from 10kb
 Gaps
 ö
 53.6%; Score 13.4; DB 8; Length 42; ilarity 73.9%; Pred. No. 2.8e+05; Conservative 0; Mismatches 6; Indels
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0399 row: M column: 23
Seq primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
 organism="Mus musculus"
 /mol_type="genomic DNA"
/strain="C57BL/63"
 /db_xref="taxon:10090"
/clone="UUGC1M0399M23"
 High quality sequence stop: 42.
 Location/Qualifiers
 3 ACTCATCACCACTCTCTTCCATC 25
 40 AATCATTATAACACTCTTCCTTC 18
```

```
j. .39
 Homo sapiens
 AI192173
LOCUS
DEFINITION
 VERSION
KEYWORDS
SOURCE
ORGANISM
 source
 source
 REFERENCE
AUTHORS
 ACCESSION
 RESULT 15
 JOURNAL
 FEATURES
 FEATURES
 TITLE
 COMMENT
 COMMENT
 ORIGIN
 셤
 ð
 /Bab. mais.
/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ clone_lib="Mouse 10kb plasmid UUGCIM library"
/ clone_lib="Wouse 10kb plasmid UUGCIM library"
/ note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
 39 bp DNA linear GSS 06-DEC-2000 sapiens genetrap T47D Human Breast Carcinoma Library Homo AZ576137 Genomic 5', genomic survey sequence.
AZ576137.1 GI:11562448
 5
 ö
 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 39)
Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M.,
Exon-trap tags from a T47D GenomeScreen(TM) Library
Unpublished (2000)
 E., SLC,
Mouse whole genome scaffolding with paired end reads from 10kb
 Gaps
 ö
 S. 2030
 52.8%; Score 13.2; DB 8; Length 25; 83.3%; Pred. No. 3.1e+05; ive 0; Mismatches 3; Indels
 plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0493 row: E column: 20
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
 /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
 clone="UUGC1M0493E20"
 4 CTCATCACCACTCTTC 21
 20 CTCCTCTCTCTCTTC 3
 Homo sapiens (human)
Homo sapiens
 /sex="Male"
 Query Match 52.8°
Best Local Similarity 83.3°
Matches 15; Conservative
 LOCUS
 RESULT 14
A2576137/c
 ORGANISM
 JOURNAL
COMMENT
 TITLE
JOURNAL
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 AUTHORS
 FEATURES
 TITLE
 ORIGIN
 8
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Tel: 854404836

Fax: 8584046719

Email: henkelgoaurorabio.com

Pools of cells ware isolated from a GenomeScreen(TM) library. The library of cells ware isolated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase proceeded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAmp-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.

Location/Qualifiers
 /clone lib="Genetrap T47D Human Breast Carcinoma Library" hote="Organ: Breast; Vector: pAmp-1; 3' RACE of total RNA from genetrap posts; shotgun clone in pAmp-1 and used to transform DHS-alpha competent bacteria."
 EST 28-OCT-1998
 ö
 qc96b07.x1 Soares pregnant_uterus NbHPU Homo sapiens cDNA clone IMAGE:1722037 3' similar to SW:IMAZ_MOUSE P52293 IMPORTIN ALPHA-2 SUBUNIT; mRNA sequence.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 43) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Ontract: Robert Strausberg, Ph.D.

Contact: Rober Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

This Consortium (lift@elmage.llnl.gov) for further information.

Trace considered overall poor quality

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers
 Gaps
 ö
 Query Match 52.8%; Score 13.2; DB 8; Length 39; Best Local Similarity 83.3%; Pred. No. 3.3e+05; Matches 15; Conservative 0; Mismatches 3; Indels
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
 /tissue_type="Carcinoma"
/cell_type="Epithelial"
/cell_line="T47D"
 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="IMAGE:1722037"
 20
 35 ACTCTTTACCTCTCTTT 18
 AI192173.1 GI:3743382
 3 ACTCATCACCACTCTTT
 Homo sapiens (human)
 Tumor Gene Index
Unpublished (1997)
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ORIGIN

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13-MAR-2003
lines
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 04-SEP-2002
 ó,
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Bcker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
The Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
 can
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 /clone="SALK_102585.22.30.x"
/clone="SALK_102585.22.30.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
 BZ766487 13.60.x Arabidopsis thaliana TDNA inear GSS 13-MAR-2 SALK 137474.23.60.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_137474.23.60.x, genomic
 SALK 102585.22.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_102585.22.30.x, genomic
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g23970 Class: TDNA tagged.
 Gaps
 Gaps
 GSS
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 ;
0
 Length 47;
 Length 43;
 linear
 Indels
 Indels
 Score 13.2; DB 1;
Pred. No. 3.4e+05;
0; Mismatches 3;
 Ouery Match
52.8%; Score 13.2; DB 8;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 3;
 /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
 DNA
 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
 47 bp
 Location/Qualifiers
 10
 8 TCACCACTCTTTCCATC 25
 BH903423.1 GI:22714608
 18
 N
 52.8%;
83.3%;
 ecker@salk.edu
 reaceacrereraceare
 1 CAACTCATCACCACTCTC
 CAACTCTTCATCAGTCTC
 Query Match 52.8
Best Local Similarity 83.3
Matches 15; Conservative
 (bases 1 to 47)
 survey sequence.
 survey sequence.
 BH903423
 Email:
 GSS.
 RESULT 17
BH903423/c
 source
 ORGANISM
 DEFINITION
 DEFINITION
 ACCESSION
VERSION
KEYWORDS
SOURCE
 RESULT 18
B2766487
 REFERENCE
AUTHORS
 JOURNAL
 FEATURES
 TITLE
 COMMENT
 ORIGIN
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 8
 셤
 /dlone="INMAGE:897317"
//dlone="INMAGE:897317"
//dlone="pooled (6)"
//dlone lib="Gessler Wilms tumor"
//dlone lib="Gessler Wilms tumor"
//dlone lib="Gessler Wilms tumor"
//dlone lib="Gessler Wilms tumor"
//dlone lib="Gessler Wilms tumor"
//dlone lib="Gessler Wilms tumor"
//dlone lib="Gessler Wilms tumor"
//dlone lib="Gessler Wilms tumor RNAs
was prepared by acid-phenol, followed by one round of
oligo dT selection. cDNA library preparation was with
the BRL/Life Tech. Superscript Plasmid system. An
oligo-dT NotI primer for first strand synthesis generated
gcggccgccc(t)n at the 3' end of the clones. A 5' Sall
adaptor was used with sequence 5'-grgacccacgcgccg-3'.
Resulting cDNAs were size selected (average size 2 kb),
NotI digested, and ligated into NotI/Sall-cut pSPORTI.
Library was constructed by Dr. Manfred Gessler."
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library
 AA488318 43 bp mRNA linear EST 05-MAR-1998 ae30d03.rl Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897317 5' similar to TR:G1216387 G1216387 SPKAP115. ;, mRNA sequence.
 ö
 Eukaryota; Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
Hillar, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Morce, B., Schellenberg, K., Steptce, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washington University School of Medicine
Washington University School of Medicine
 /dev_stage="adult"
/lab_host="DH10B"
/clone lib="Soares_pregnant_uterus_NDHPU"
/fnote="Organ: uterus, Vector: pT7T3-Pac; Site_1: Not I;
/icte_2: Eco RI; 1st_strand cDNA was primed with a Not I
 Faxi.i est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 779 Std Error: 0.00
 Gaps
 ô
 52.8%; Score 13.2; DB 1; Length 43; llarity 83.3%; Pred. No. 3.4e+05; Conservative 0; Mismatches 3; Indels
 constructed by M. Fatima Bonaldo."
 organism="Homo sapiens"
 'db xref="taxon:9606"
 Insert Length: 779 Std Brror
High quality sequence stop: 1.
Location/Qualifiers
 type="mRNA"
 25
 29
 AA488318.1 GI:2215749
sex="female"
 8 TCACCACTCTCTTCCATC
 12 rccrcacacrcrrccarc
 Homo sapiens (human)
 Tel: 314 286 1800
Fax: 314 286 1810
 Į
 Query Match
Best Local Similarity
Matches 15; Conserv
 Homo sapiens
 AA488318
 source
 RESULT 16
AA488318/c
 DEFINITION
 ORGANISM
 TITLE
 ACCESSION
 REFERENCE
 AUTHORS
 KEYWORDS
 FEATURES
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COMMENT

5

us-10-788-779-9.rst

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwMD42 (gil#732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis
 /lab host="B. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 Gaps
 BX534557 33 bp DNA linear GSS 04-API
Arabidopsis thaliana T-DNA flanking sequence GK-510D07-019532,
 ..
 52.0%; Score 13; DB 8; Length 33; 76.2%; Pred. No. 3.9e+05; ive 0; Mismatches 5; Indels
 Bioinformatics 19 (11), 1441-1442 (2003)
22755829
12874060
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: N column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
 Laboratory Mouse DNA Resource
 /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
 /db_xref="taxon:10090"
/clone="UUGC1M0011N24"
 1 CAACTCATCACCACTCTTC 21
 CATCTCCTCATCACCCTCATC 24
 genomic survey sequence.
 BX534557.1 GI:31411687
 /sex="Male"
 University of Utah
 Tel: 801 585 5606
Fax: 801 585 7177
 16; Conservative
 Query Match
Best Local Similarity
Matches 16; Conserv
 Rm. 308, B
 thaliana
 GSS
 Bource
 SOURCE
ORGANISM
 DEFINITION
 AUTHORS
TITLE
 PUBMED
REFERENCE
 ACCESSION
 REFERENCE
 JOURNAL
 MEDLINE
 KEYWORDS
 FEATURES
 BX534557
 VERSION
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 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
L Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
 AZ308699 33 bp DNA linear GSS 29-SEP-2000
1M0011N24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids, eurosids, Erassicales, Brassicaceae, Arabidopsis.
 directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bass 1 to 33)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Nese,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 /db xref="txxxon:3702"
/db xref="txxon:3702"
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/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At1920210 and 300 bases of the 5' end of At1920210. Class: TDNA tagged.
 Gaps
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 52.8%; Score 13.2; DB 8; Length 47; 83.3%; Pred. No. 3.4e+05; ive 0; Mismatches 3; Indels
 clone UUGCIM0011N24 R, genomic survey sequence. AZ308699
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 Arabidopsis thaliana (thale cress)
 /mol_type="genomic DNA"
/ecotype="Col-0"
 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
 Location/Qualifiers
 Mus musculus (house mouse)
Mus musculus
 BZ766487
BZ766487.1 GI:28939040
 5 TCATCACCACTCTTTCC 22
 22 TCATCATCACTITCTCCC 39
 AZ308699.1 GI:10348959
 15; Conservative
 Best Local Similarity
 Query Match
ACCESSION
VERSION
KEYWORDS
 ORGANISM
 DEFINITION
 ORGANISM
 REFERENCE
 JOURNAL
 Matches
 ACCESSION
 REFERENCE
 AUTHORS
 AZ308699
LOCUS
 JOURNAL
 KEYWORDS
 FEATURES
 TITLE
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 COMMENT
 ORIGIN
 VERSION
 COMMENT
 SOURCE
```

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Contact: Susheng Gan
Department of Horticulture
 Unpublished (2000)
 Best Local Similarity 76.2
Matches 16; Conservative
 Tel: 801 585 5606
Fax: 801 585 7177
 USA
 Rm. 308,
84112, US
 3', mRNA
CD531219
 Query Match
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KEYWORDS
SOURCE
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 source
 DEFINITION
 TITLE
JOURNAL
COMMENT
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CD531219
 REFERENCE
AUTHORS
 ACCESSION
 FEATURES
 COMMENT
 ORIGIN
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 Direct Submission

Loughtted (11-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (11-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (11-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Subchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
IT 19G15. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for Flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 /ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana |
/note="PCR was performed on DNA from the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion.
 ô
 A2938244 36 bp DNA linear GSS 26-APR-2001
2M0196E11R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0196E13 R, genomic survey sequence.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 /db_xref="taxon:3702"
/clone="GK-510D07-019532"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
 Gaps
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
 ..
0
Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 52.0%; Score 13; DB 9; Length 33; 76.2%; Pred. No. 3.9e+05; ive 0; Mismatches 5; Indels
 T-DNA derived sequences were removed."
 (bases 1 to 33)
sso,M.G., Strizhov,N., Li,Y. and Weisshaar,B.
 /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
 5 TCATCACCACTCTTCCATC 25
 1 rcarcacacartriccic 21
 Mus musculus (house mouse)
 AZ938244.1 GI:13797754
 Conservative
 Mus musculus
 Weisshaar, B.
 Local Similarity
hes 16; Conserv
 14682050
 14756321
 AZ938244
 Query Match
 source
 Best Loca
Matches
 ORGANISM
 DEFINITION
 REFERENCE
AUTHORS
 TITLE
JOURNAL
 AUTHORS
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 AUTHORS
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 JOURNAL
 PUBMED
 RESULT 21
 FEATURES
 AZ938244
 TITLE
 TITLE
 COMMENT
 TITLE
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/lab host="E" coli strain XL10-Gold, T1-resistant, F-"
/lab host="E" coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42Dv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically shaared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored vector DNA, and transformed into
chemically-competent E. coli Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
 09P20 Arabidopsis Leaf Senescence Library Arabidopsis thaliana CDNA 3', mRNA sequence.
 5
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 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 Gaps
 ö
 52.0%; Score 13; DB 8; Length 36; 76.2%; Pred. No. 4e+05; tive 0; Mismatches 5; Indels
 (bases 1 to 43)
Guo, Y., Cai, Z. and Gan, S.
Transcriptome of Arabidopsis leaf senescence
Plant Cell Environ. 27 (5), 521-549 (2004)
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
 Plate: 0196 row: E column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
 organism="Mus musculus"
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
 /mol_type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
 /db xref="taxon:10090"
/clone="UUGC2M0196E13"
/sex="Female"
 High quality sequence stop: 36.
 Location/Qualifiers
 4 CTCATCACCACTCTTCCAT 24
 11 cccaccccacccrcrrcar 31
 CD531219.1 GI:40451231
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Gaps

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46 bp mRNA linear EST 10-MAR-1998 INGO ST 10-MAR-1998 IMAGE:612899 5' similar to SW:R27A_HUMAN P14798 40S RIBOSOMAL AA179783
 /gex="female"
/dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="STratzagene HeLa cell s3 937216"
/note="Vector: pBluescript SK-; Site_1: BcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases I to 40.

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Morte,Y., White,Y., White,Y., Wyle,Y., Waterston,R., Tan,P., MashU-NCI, human EST Project

 .44
/note="P element insertion in the 3' to 5' orientation"

 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7e1: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 528 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
 Length 44;
 52.0%; Score 13; DB 1; Length 46; 69.6%; Pred. No. 4.2e+05; ive 0; Mismatches 7; Indels
 Length 46;
 Indels
 52.0%; Score 13; DB 9; Le 100.0%; Pred. No. 4.1e+05;
 Mismatches
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 organism="Homo sapiens"
 /mol_type="mRNA"
/db_xref="GDB:4644738"
/db_xref="taxon:9606"
/clone="IMAGE:612899"
 /clone_lib="P{RS3}"
/note="read=5' end"
 Location/Qualifiers
 1 CAACTCATCACCACTCTTCCA 23
 ö
 AA179783.1 GI:1761049
 Homo sapiens (human)
 Contact: Wilson RK
 11 CCACTCTCTTCCA 23
 ccacrcrcrrcca 16
 Query Match 52.0
Best Local Similarity 69.6
Matches 16; Conservative
 Conservative
 Unpublished (1997
 Homo sapiens
 Similarity
 misc_feature
 Best_Local Sim
Matches 13;
 Query Match
 DEFINITION
 ORGANISM
 TITLE
JOURNAL
 24
 ACCESSION
 REFERENCE
 AUTHORS
 VERSION
KEYWORDS
 AA179783
 FEATURES
 COMMENT
 RESULT
 SOURCE
 ORIGIN
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 GSS 24-FEB-2003
element insertion
 ö
 /tissue_type="Leaf"
/dev stage="Yellow Leaf With Greenish Base Area"
/lab_host="E. coli"
/clone lib="Arebidopsis Leaf Senescence Library"
/note="Organ: Rosette Leaf; Vector: pBluscript SKII+;
Site 1: EcoRI, Site 2: EcoRI; Senescent rosette leaves #5
and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly
yellow excepted for the leaf base areas that were still
 Cornell University, Ithaca, NY 14853-5904, USA
 Mapping of RS P element insertions in Drosophila melanogaster for
the DrosDel second generation deficiency kit
Unpublished
 University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM The insertion point of the P element is before base 1 of the sequence. Further information about this P element insertion line can be found at http://www.flyseq.org.uk and http://www.drosdel.org.uk.
 DMES46976 44 bp DNA linear GSS 24-FEB-
Drosophila melanogaster flanking sequence of RS P element inser
P{RG3}CB-5509-3, clone library P{RS3}, genomic survey sequence.
 coulson, D. Dickson, B., Drummond, J., Blows, F., Bucheton, A., Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N., Hafen, B., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P., Mechler, B., O'Kane, C., Pflugfelder, G., Rasmuson-Lestander, A., Reuter, G., Roote, J., Szidonya, J., Wang, S., Webster, J. and
 Gaps
 AJ546976.1 GI:28555186
GSS; genome survey sequence.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Direct Submission Syder B.J., Department of Genetics, Submitted (17-FEB-2003) Ryder B.J., Department of Genetics,
 ö
 Score 13; DB 6; Length 43; Pred. No. 4.1e+05; Mismatches 5; Indels
 /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
 organism="Arabidopsis thaliana"
Cornell University
119 Plant Science, Cornell University,
Tel: 607 254 5418
Fax: 607 255 0599
Email: 89288@cornell.edu
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POLYA=No.
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/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
 Location/Qualifiers
 Location/Qualifiers
 1 CAACTCATCACCACTCTTC 21
 8 cárcicriráctrorcirc 28
 /chromosome="3L"
 Query Match
Best Local Similarity 76.2%;
Matches 16; Conservative
 (bases 1 to 44)
 .43
 Ryder, E.J
 source
 LOCUS
 ORGANISM
 RESULT 23
DME546976
 REFERENCE
AUTHORS
TITLE
 ACCESSION
 REFERENCE
 AUTHORS
 JOURNAL
 KEYWORDS
SOURCE
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Homo sapiens (human)
 Local Similarity
ses 16; Conserv
 11375929
 Query Match
 source
 ORGANISM
 DEFINITION
 REFERENCE
AUTHORS
 MEDLINE
PUBMED
 Matches
 ACCESSION
 RESULT 27
 VERSION
KEYWORDS
 JOURNAL
 FEATURES
 AU103975
 FEATURES
 TITLE
 COMMENT
 ORIGIN
 ORIGIN
 SOURCE
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 EST 22-JUN-2001
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 CL528695 48 bp DNA linear GSS 17-MAY-2004
ASV3D06.fwd ASLV-vector integration sites in human 293T-TVA cells
 Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooldeae, Triticeae, Hordeum.
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 48)
Mitchell, R. S., Beitzel, B. F., Schroder, A. R. W., Shinn, P., Chen, H., Berry, C.C., Ecker, J. R. and Bushman, F.
Retroviral DNA integration: ASLV, HIV and MLV Show Distinct Target Site Preferences
 AVB33578 K. Sato unpublished cDNA linear EST 22-JUN-200
AVB33578 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
clone bags15m02, mRNA sequence.
 Homo sapiens genomic clone ASV3D06.fwd, genomic survey sequence.
CL528695
 /dev_stāgē="germination"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare shoots germination"
 Gaps
 Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct
 ö
 database:http://www.shigen.nig.ac.jp/barley/Barley.html
 Location/Qualifiers
 Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2001)
 organism="Hordeum vulgare subsp. vulgare"
 52.0%; Score 13; DB 1; Length 46; 76.2%; Pred. No. 4.2e+05;
 5; Indels
 Contact: Karuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Emall: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp,
 0; Mismatches
 /db_xref="taxon:112509"
/clone="bags15m02"
 /mol_type="mRNA"
/cultivar="Haruna Nijo"
 /sub_species="vulgare"
 tissue_type="shoots"
CTCAAAATCAATCTTTTCCAT 25
 4 CICATCACCACTCTTCCAT 24
 Contact: Frederic Bushman
 AV833578.1 GI:14525667
 CL528695.1 GI:47421906
 Homo sapiens (human)
 (bases 1 to 46)
 Unpublished (2004)
 16; Conservative
 Homo sapiens
 Similarity
 AV833578
 Query Match
 Best Local
 source
 AV833578/c
 DEFINITION
 ORGANISM
 DEFINITION
 ORGANISM
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VERSION
KEYWORDS
SOURCE
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AUTHORS
 TITLE
JOURNAL
 Matches
 RESULT 26
CL528695
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 JOURNAL
 REFERENCE
 AUTHORS
 FEATURES
 TITLE
 COMMENT
 RESULT
 ORIGIN
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fortering 293T cells expressing the subgroup A avain retrovirus receptor (293T-TVA) were infected with an ASLV-based vector. DNA was isolated and cleaved with restriction enzymes, linkers were ligated onto the cleaved DNA and DNAs and DNAs and one that bound to the ASLV cDNA. Junctions between integrated ASLV proviruses and cellular
 Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Basil: ysuzuki@ima.u-cokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 AU103975 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP10657, mRNA sequence.
 ö
 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
 Gaps
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/db_xref="taxon:9606"
/db_cone="ASV3D06.fwd"
/clone=lASV3D06.fwd"
/clone_lib="ASSV-vector integration sites in human 293T-TVA cells"
 ;
0
 Salk Institute Infectious Disease Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1630
Fax: 858 554 0341
Email: bushman@salk.edu
 Length 48;
 Indels
 52.0%; Score 13; DB 9; Le:
ilarity 76.2%; Pred. No. 4.2e+05;
Conservative 0; Mismatches 5;
 NNA were cloned and sequenced."
 1. .50
/organism="Homo sapiens"

 .48
 /organism="Homo sapiens"

 Class: PCR with specific primers.
Location/Qualifiers
 Location/Qualifiers
 21
 17 cágcrcárcccrcrcaccrc 37
 1 CAACTCATCACCACTCTTC
 AU103975.1 GI:13553496
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Gaps

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all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Gibcobbl Life Technologies' CDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with EcoRI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n=15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: paul.keim@nau.edu,
 GSS 13-DEC-2000
 Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
innert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
 TA221E12Q 32 bp DNA linear GSS 13-DE T. brucei sheared genomic DNA clone 221e12, reverse sequence,
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 ;
0
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 .
0
 Length 32;
 Query Match 51.2%; Score 12.8; DB 1; Length 3
Best Local Similarity 87.5%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels
 Indels
 Query Match 51.2%; Score 12.8; DB 9; Best Local Similarity 70.8%; Pred. No. 4.8e+05; Matches 17; Conservative 0; Mismatches 7;
 /organism="Trypanosoma brucei"
 type="genomic DNA"
 /db_xref="taxon:5691"
/clone="221e12"
 Location/Qualifiers
 genomic survey sequence.
 AL480383.1 GI:11846152
 10 ACCACTCTCTTCCATC 25
 12 ACCACTCTCCACC 27
 Trypanosoma brucei
Trypanosoma brucei
 (bases 1 to 32)
 Trypanosoma.
 AL480383
 GSS.
 TA221E12Q/c
 source
 DEFINITION
 SOURCE
ORGANISM
 ACCESSION
 JOURNAL
 REFERENCE
 RESULT 29
 AUTHORS
 KEYWORDS
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 Fax: 314 286 1800
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 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theishing, B., Allen, M.,
Schurk, R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Waterston, R. and Wilson, T., Jackson, Y., Cardenas, M.,
Unpublished (1999)
 /clone_lib="Gm-cl004"
/note="Wector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize the
cDNA. First- strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is hemimethylated.
 A1441968 31 bp mRNA linear EST 23-JUL-2004 sa83d11.yl Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1004-5902 5' similar to TR:024099 024099 MTN12 ;, mRNA
 ö
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Strategene's first-strand synthesis primer was used [GAGAGAGAGAGAGAGACTAGTCTCGAG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI;
 Gaps
 Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 ..
0
 'db xref="taxon:3847"
'clone="GENOME SYSTEMS CLONE ID: Gm-c1004-5902"
 4.2e+05;
 52.0%; Score 13; DB 1; Length 50; 76.2%; Pred. No. 4.2e+05; ive 0; Mismatches 5; Indels
 Contact: Shoemaker R/Public Soybean EST Project
 /organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
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 23
 3 CTGACCACCCTCTTTCTAT
 AI441968.1 GI:4292882
 Glycine max (soybean)
 16; Conservative
 (bases 1 to 31)
 Local Similarity
 Glycine max
 seguence.
 POLYA=No.
 AI441968
 Query Match
 Source
 DEFINITION
 Best Loc
Matches
 ACCESSION
VERSION
KEYWORDS
SOURCE
 ORGANISM
 TITLE
JOURNAL
COMMENT
 REFERENCE
 AUTHORS
 AI441968
 FEATURES
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Gaps

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04-SEP-2002
 Arabidopsis thaliana subaryophyta; Embryophyta; Tracheophyta; Spermatophyta; Spermatophyta; eudicotyledons; core eudicots; roside; euroside II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 39)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 BH903343 1.50.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_102465.31.50.x, genomic
 Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1920 Std Brror: 0.00
Seq primer: -40UP from Gibco
 This is single pass sequence recovered from the left border of
 Gaps
 .
0
 Query Match 51.2%; Score 12.8; DB 1; Length 37; Best Local Similarity 87.5%; Pred. No. 4.9e+05; Matches 14; Conservative 0; Mismatches 2; Indels
 Arabidosis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
TH: 858 453 4100 x1752
Fax: 858 6379
 Arabidopsis thaliana (thale cress)
 1. .37
/organism="Homo sapiens"
 Contact: Robert Strausberg, Ph.D.
 High quality sequence stop: 1.
Location/Qualifiers
 BH903343.1 GI:22714519
 21
 CAACACCAGTCTCTTC 30
 Email: ecker@salk.edu
 6 CATCACCACTCTTC
 Tumor Gene Index
Unpublished (1997)
 survey sequence.
 BH903343
 GSS.
 15
 source
 RESULT 32
BH903343/c
 LOCUS
 ORGANISM
 JOURNAL
 AUTHORS
TITLE
 JOURNAL
COMMENT
 ACCESSION
 REFERENCE
 REFERENCE
 AUTHORS
 KEYWORDS
 FEATURES
 TITLE
 VERSION
 ORIGIN
 SOURCE
 à
 원
 BH909685 34.05.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 055402.24.05.x, genomic
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 EST 28-OCT-1998
 /db xrefe="cxxon:3702"
/clone="SALK 055402.24.05.x"
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 36)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Squence,A., Karnes,M., Kim,C.J., Parker,H., Frednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the
 qd11g10.x1 Soares placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA
clone IMAGE:1723458 3' similar to TR:042204 042204 PUTATIVE
TRANSMEMBRANE PROTEIN E3-16. ;, mRNA sequence.
 Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 This is single pass sequence recovered from the left border of
 Gaps
 ö
 51.2%; Score 12.8; DB 8; Length 36; 87.5%; Pred. No. 4.9e+05; ive 0; Mismatches 2; Indels
 Arabidopsis Genome
Unpublished (2001)
Upublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
Intollo N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
 linear
 organism="Arabidopsis thaliana"
 mRNA
 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
 'mol_type="genomic DNA"
'ecotype="Col-0"
 37 bp
 24
 25 CAATACATCATCGCTTTCAT 2
 Class: TDNA tagged.
Location/Qualifiers
 BH909685.1 GI:22722618
 AI188273
AI188273.1 GI:3739482
 ecker@salk.edu
 CTCAACTCTCTTCCAT 33
 9 CACCACTCTTTCCAT 24
 14; Conservative
 survey sequence.
BH909685
 Similarity
 AI188273
 Email:
 Query Match
 Local
 source
 ORGANISM
 DEFINITION
 ORGANISM
 DEFINITION
 JOURNAL
COMMENT
 ACCESSION
VERSION
 Matches
 ACCESSION
 RESULT 30
 REFERENCE
 AUTHORS
 VERSION
KEYWORDS
 RESULT 31
 A1188273
LOCUS
 KEYWORDS
 BH909685
 FEATURES
 TITLE
 ORIGIN
 SOURCE
 SOURCE
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8

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EMBO Rep. 3 (12), 1152-1157 (2002)
 422E10, genomic survey sequence. AJ595714
24
 36 CACGTCAGCATCACTCTGTCGCAT 13
 survey sequence.
BZ381485
BZ381485.1 GI:25475482
 of pre-insertion sites
 51.2%;
87.5%;
 32 ACTCGTCACCACTCAC 17
 3 ACTCATCACCACTCTC
 2 (bases 1 to 40)
Balzergue, S.
 14; Conservative
 Query Match
Best Local Similarity
 12446565
 misc_feature
 SOURCE
ORGANISM
 DEFINITION
 Matches
 BZ381485/c
 DEFINITION
 AJ595714/c
 REFERENCE
AUTHORS
 TITLE
JOURNAL
 ACCESSION
 VERSION
KEYWORDS
 AUTHORS
 ACCESSION
 REFERENCE
 RESULT 35
 RESULT 34
 JOURNAL
 PUBMED
 FEATURES
 TITLE
 VERSION
 COMMENT
 ORIGIN
 a
 ð
 셤
 8
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and nhi@sanger.ac.uk Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 T. brucel sheared genomic DNA clone 110a12, reverse sequence, AL461772
 ö
 ö
 /clone="SALK_102465.31.50.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
 Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
 Gaps
 Gaps
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
 Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 ö
 ..
0
 51.2%; Score 12.8; DB 8; Length 39; 70.8%; Pred. No. 4.9e+05; ive 0; Mismatches 7; Indel8
 51.2%; Score 12.8; DB 9; Length 39; 70.8%; Pred. No. 4.9e+05; ive 0; Mismatches 7; Indels
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/mol_type="genomic DNA"
/ecotype="Col-0"
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
/strain="TREU927"
 'db_xref="taxon:3702"
 xref="taxon:5691"
 39 AATTCTACACTCTAACCCATC 16
 2 AACTCATCACCACTCTTCCATC 25
 Class: TDNA tagged.
Location/Qualifiers
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 AL461772.1 GI:11832134
 Query Match
Best Local Similarity 70.89
Marches 17; Conservative
 rypanosoma.
(bases 1 to 39)
 Query Match 51.2
Best Local Similarity 70.8
Matches 17; Conservative
TDNA
 RESULT 33
TA110A12Q/c
 DEFINITION
 ORGANISM
 TITLE
JOURNAL
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 AUTHORS
 FEATURES
 FEATURES
 COMMENT
 ORIGIN
 à
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Direct Submission

Submitted (23-OCT-2003) Balzergue S., UWRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Evy cedex, FRANCE
Gaston Cremieux, 91057 Evy cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence floanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtp://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program Genoplante (http://www.genoplante.com and http://genoplante-info.infopiogen.fr).

Location/Qualifiers
 BZ381485 SALK 116783.20.40.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_116783.20.40.x, genomic
 ö
AJ595714 15-JAN-2004 Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Alavin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Pred. No. 5e+05;
0; Mismatches 2; Indels
 AJ595714.1 GI:37945342
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
 organism="Arabidopsis thaliana"
 /note="T-DNA flanking sequence
left border"
 /mol type="genomic_DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="422E10"
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/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones generated from soybean root hair tissue treated with Bradyrhizobium japonicum for 3 hours."
 (http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
 GSS 20-FEB-2001
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L (base 1 to 42).

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nederlly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 AZ828302 20-FEB-200 2M015011F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0105011 F, genomic survey sequence.
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UUGCNH library"
/note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 /mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/db_tresue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
gmrhRww3"
 Gaps
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 Score 12.8; DB 7; Length 42;
Pred. No. 5e+05;
0; Mismatches 7; Indels
 Laboratory Mouse DNA Resource
 Std Error: 0.00
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Plate: 0105 row: O column: 11
Seg primer: CGTTGTAAAACGACGGCCAGT
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 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0105011"
 /organism="Glycine max"
 High quality sequence stop: 42.
Location/Qualifiers
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
 1 CAAGACCTCGTCATTCTCTTCAAT 24
 1 CAACTCATCACCACTCTTCCAT 24
 Location/Qualifiers
 Mus musculus (house mouse)
Mus musculus
 AZ828302.1 GI:12998210
 Query Match 51.2%;
Best Local Similarity 70.8%;
Matches 17; Conservative (
 Single pass sequence
 Class: plasmid ends
 /sex="Male
 1, .42
 plasmid inserts
 Seg primer: T7
 84112, USA
 GSS.
 Source
 source
 AZ828302/c
 DEFINITION
 ORGANISM
 REFERENCE
AUTHORS
 ACCESSION
 RESULT 37
 VERSION
KEYWORDS
 JOURNAL
 FEATURES
 FEATURES
 TITLE
 COMMENT
 ORIGIN
 SOURCE
 LOCUS
 g
 ਨੇ
 CF920754 42 bp mRNA linear EST 05-NOV-2003 gmrhRww3-01_C02_1_012 Soybean root hair subtracted cDNA library gmrhRww3 Glycine max cDNA, mRNA sequence.
 ö
 /clone="SALK 116783.20.40.x"
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 41)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 1 (bases 1 to 42)
Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
Expressed sequence tags from soybean root hair subtractive CDNA
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeeke, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
 Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 A.752
Exx: 858 558 6379
This sequence recovered from the left border of This is single pass sequence recovered from the left border of Thom.
 Gaps
 ö
 51.2%; Score 12.8; DB 8; Length 41; llarity 70.8%; Pred. No. 5e+05; Conservative 0; Mismatches 7; Indels
 'organism="Arabidopsis thaliana"
 Contact: Gary Stacey
University of Missouri
University of Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
 /mol_type="genomic_DNA"
/ecotype="Col-0"
 db xref="taxon:3702"
 2 AACTCATCACCACTCTTTCCATC 25
 41 AATTCCACACTACTCTAACCCATC 18
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Location/Qualifiers
 Email: staceyg@missouri.edu
 CF920754.1 GI:38191548
 Glycine max (soybean)
 Unpublished (2003)
 Best Local Similarity
Matches 17; Conserva
 Glycine max
 Glycine.
 Query Match
 SOURCE
ORGANISM
 source
 SOURCE
ORGANISM
 DEFINITION
 ACCESSION
 REFERENCE
 AUTHORS
 JOURNAL
 RESULT 36
 VERSION
KEYWORDS
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 AUTHORS
 JOURNAL
KEYWORDS
 CF920754
 FEATURES
 TITLE
 TITLE
 COMMENT
 COMMENT
 ORIGIN
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BH861884.1 GI:22097210
 Email: ecker@salk.edu
 Similarity 70.8%;
17; Conservative
 At3g62020.
Class: TDNA tagged
 Conservative
 1. .44
 Best_Local Similarity
Matches 17; Conserv
 GSS
 Best Local S
Matches 17
 Query Match
 source
 DEFINITION
 ORGANISM
 DEFINITION
 ACCESSION
VERSION
 RESULT 39
 REFERENCE
 AUTHORS
 JOURNAL
 RESULT 40
 KEYWORDS
 BH861884
 FEATURES
 BH901162
 TITLE
 SOURCE
 ORIGIN
 Locus
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophorasis. Vector DNA was prepared from a derivative of pwM22 (gi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adappored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BH903344 102466.48.25.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_102466.48.25.x, genomic
 ö
 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 43)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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/clone="lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
 This is single pass sequence recovered from the left border of IDNA.
 Gaps
 ;
0
 51.2%; Score 12.8; DB 8; Length 42; 70.8%; Pred. No. 5e+05; Lindels 0; Mismatches 7; Indels
 Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Bcker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 658 6379
 'organism="Arabidopsis thaliana"
 /mol_type="genomic_DNA"
/ecotype="Col-0"
 2 AACTCATCACCACTCTTCCATC 25
 Class: TDNA tagged.
Location/Qualifiers
 BH903344.1 GI:22714520
 ecker@salk.edu
 Conservative
 survey sequence.
BH903344
 Query Match
Best Local Similarity
 Email:
 17;
 BH903344/c
 LOCUS
 ACCESSION
VERSION
KEYWORDS
 SOURCE
ORGANISM
 Matches
 JOURNAL
 RESULT 38
 REFERENCE
 AUTHORS
 FEATURES
 TITLE
 COMMENT
 ORIGIN
 ORIGIN
```

ð g 51.2%; Score 12.8; DB 8; Length 43;

Query Match

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ö
 BH861884 155-AUG-2002 SALK 088239 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 088239, genomic survey sequence.
 04-SEP-2002
 ö
 Frabidopsis thaliana Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacea; Arabidopsis.

1 (bases 1 to 44)
Alonso,J.W., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Shinn,P., Zimmerman,J. and Ecker,J.R.
Asquence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
 BH901162 46.x Arabidopsis thaliana TDNA inear GSS 04-SEP-2 SALK 073346.39.40.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_073346.39.40.x, genomic
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
 Gaps
 Gaps
 .;
0
 ö
 51.2%; Score 12.8; DB 8; Length 44; 70.8%; Pred. No. 5e+05;
 Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA 11: 858 453 4100 x1752
 Indels
 Indels
 7;
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/mol_type="genomic DNA"
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0; Mismatches
Pred. No. 5e+05;
0; Mismatches
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 2 AACTCATCACCACTCTTCCATC 25
 43 AATTCTACACTACTCTAACCCATC 20
 12 ACCACATCACATCTTTCCTCCAAC 35
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 Location/Qualifiers
 BH901162.1 GI:22712043
 survey sequence.
BH901162
 ACCESSION
VERSION
KEYWORDS
```

us-10-788-779-9.rst

```
Arabidopsis thaliana (Liate Cress)

Rabidopsis thaliana (Liate Cress)

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 45)

Alonso,J.W., Leisse,T.J., Barajas,P., Chen,H., Chenk,R., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)

Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
 /db_xref="taxon:3702"

/clone="SALK 073346.39.40.x"

/clone=lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"
 Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At1g76170.
Class: TDNA tagged.
Location/Qualifiers
 51.2%; Score 12.8; DB 8; Length 45; llarity 70.8%; Pred. No. 5.1e+05; Conservative 0; Mismatches 7; Indels
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Arabidopsis thaliana (thale cress)
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Gaps

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Sequence

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Run on:

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Result

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APPLICANT: SEIDMAN, JOHN
APPLICANT: WATKINS, HUGH
APPLICANT: ROSENZWEIG, ANTHONY
APPLICANT: ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
 ALIGNMENTS
 ATTORNEY/AGENT INPORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFRENCS/DOCKET NUMBER: GML-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-7400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
 CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
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 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
CLASSIFICATION: 435
 1 CAACTCATCACCACTCTCTTCCATC
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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 TYPE: nucleic acid
STRANDEDNESS: single
 Massachusetts
 ; MOLECULE TYPE: cDNA
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 linear
 U.S.A.
 BOSTON
 02109
 COUNTRY:
 US-07-989-160-9
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114.2
11.2
11.2
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Gaps

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Fatent No. 5795762
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: S. TO 3' EXONUCLEASE MUTATIONS OF TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSES: Hoffmann-la Roche Inc.
STREET: 340 Kingsland Street
 NAME: Luann Cserr
REGISTRATION UNMBER: 31,822
REFERRUCALOCKET NUMBER: Case No. 5466591 8753
TELECOMMUNICATION INPORMATION:
 PRIOR AFFLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
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PRIOR APPLICATION NUMBER: US 455,611
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 APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
 US 143,441
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85.7%;
 FILING DATE: 15-MAY-1990
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APPLICATION NUMBER: US 14
FILING DATE: 12-JAN-1988
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 TYPE: nucleic acid
STRANDEDNESS: single
 STREET: 340 Kings
CITY: Nutley
STATE: New Jersey
 US-07-977-434-38
 US-08-458-819-38
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 ð
 GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REPERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422, 978
CURRENT FILING DATE: 1999-10-20
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER PILING DATE: 1999-04-21
MUMBER OF SEQ ID NOS: 11796
SEQ ID NO 3589
 Gaps
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 APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingeland Street
CITY: Nutley
STATE: New Jersey
ZIP: O'110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7
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 SOFTWARE: WordPerfect 2.1
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APPLICATION NUMBER: US/07/977,434
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CLASSIFICATION: 435
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APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
 Sequence 3589, Application US/09422978 Patent No. 6537751
 32 caccicaryagcacigicirceric
 Sequence 38, Application US/07977434 Patent No. 5466591 GENERAL INFORMATION:
 28-SEP-1990
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 FILING DATE: 28-SEP-
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ORGANISM: Homo Sapiens
 Query Match
Best Local Similarity
Matches 20; Conserv
 NAME/KEY: allele
 US-09-422-978-3589/c
 US-07-977-434-38
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Gaps

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Score 16.2; DB 1; Length 46; Pred. No. 5.2e+02; 0; Mismatches 3; Indels

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FILING DATE: 28-SEP-1990
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FILING DATE: 12-JAN-1980
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FILING DATE: 17-JUN-1987
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FILING DATE: 15-AUG-1996
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FILING DATE: 12-DEC-1990
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FILING DATE: 20-NOV-1990
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FILING DATE: 20-NOV-1990
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 PCT-US91-07035-38
 RESULT 5
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COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macinicosh
OPERATING SYSTEM: 7
SOFTWARE: Wordberfeet 2.1
SURRENT APPLICATION NUMBER: Ug/08/458,819
FILING DATE: 02-UN-1955
CLASSITCATION NUMBER: Ug/977,434
FILING DATE: 2-FEB-1993
RIGH APPLICATION NUMBER: US 590,490
FILING DATE: 2-FEB-1990
RIGH APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
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FILING DATE: A1-DIC
 TOPOLOGY: linear
MOLECULE TYPE: DNA primer TAFR01
HYPOTHETICAL: NO
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
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Best Local Similarity 85.73
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STRANDEDNESS:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Bougueleret, Lydie

APPLICANT: Chumakov, Ilya

APPLICANT: Chumakov, Ilya

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

TITLE OF INVENTION OWBER: US 09/641,638

PRIOR FILING DATE: 2000-08-16

PRIOR PILING DATE: 2000-02-11

PRIOR FILING DATE: 1099-02-07

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 1304

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 Length 47;
 Indels
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 ; LOCATION: 24
; OTHER INFORMATION: 10-507-364 : polymorphic base C or
US-09-641-638-1288
 Query Match
61.6%; Score 15.4; DB 3;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 1; Mismatches 2;
 US-10-170-097-1288
Sequence 1288, Application US/10170097
Patent No. 6794143
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 Query Match 61.6
Best Local Similarity 84.2
Matches 16; Conservative
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 TYPE: DNA
ORGANISM: Homo Sapiens
 NAME/KEY: allele
 NAME/KEY: allele
 LOCATION: 24
 TYPE: DNA
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 à
 Sequence 1281, Application US/09641638

Sequence 1281, Application US/09641638

Batent No. 642648

GENERAL INFORMATION:
APPLICANT: Blumenfield, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
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APPLICANT: Chumakov, Ilya
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APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
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APPLICANT: Chumakov, Ilya
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APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ily
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 Gaps
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) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: attenuation factor oligonucleotide US-09-888-413-147
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 64.8%; Score 16.2; DB 5; Length 46; larity 85.7%; Pred. No. 5.2e+02; Conservative 0; Mismatches 3; Indels
 61.6%; Score 15.4; DB 4; Length 25; 76.0%; Pred. No. 1.1e+03; ive 0; Mismatches 6; Indels
 Indels
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KRIS, RICHARD M.
APPLICANT: KRIS, RICHARD M.
TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM
FILER REFERENCE: NEOGRA-1 P4
CURRENT APPLICATION NUMBER: US/09/888,413
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 09/337,325
PRIOR APPLICATION NUMBER: 09/218,166
PRIOR APPLICATION NUMBER: 09/109,076
PRIOR PELING DATE: 1999-07-02
PRIOR PELING DATE: 1998-12-22
PRIOR PELING DATE: 1998-12-22
PRIOR PELING DATE: 1998-12-22
PRIOR PELING DATE: 1998-12-22
PRIOR SPLING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN VOIL: 2.1
SEQ ID NO H.
 0; Mismatches
 1 CAACTCATCACCACTCTTCCATC 25
 25 caccicaraaccacicicaaccacc 1
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 NUCLEIC ACID
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA primer TAFR01
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US91-07035-38
 US-09-888-413-147/c
; Sequence 147, Application US/0988413
; Patent No. 6759198
 4 CTCATCACCACTCTTCCAT 24
 17 crcatrcccacrcrrrrccar 37
 TYPE: DNA ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 76.0°
 Query Match
Best Local Similarity
Matches 18; Conservi
 US-09-641-638-1288
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Gaps

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Gaps

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Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
 17; Conservative
 APPLICANT: Bachmaier, Kurt
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 MOLECULE TYPE: DNA
 Query Match
Best Local Similarity
Matches 17; Conserv
 TYPE: DNA
ORGANISM: Human
 US-08-267-803B-41
 TOPOLOGY:
 US-09-133-774-24
 US-09-303-862-24
 US-09-133-774-24
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 ô
 APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
 Score 15.2; DB 1; Length 20;
Pred. No. 1.3e+03;
0; Mismatches 3; Indels
 ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Suite 203 CITY: Mn meapolis
 ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
 110.00030101
 Sequence 23, Application US/08469802B Patent No. 5741645 GENERAL INFORMATION:
 NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFRENCE/DOCKET NUMBER: 110,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
 20 caacreargaccerrerr 1
 60.8%;
 ATTORNEY/AGENT INFORMATION:
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Conservative
 NUMBER OF 'SEQUENCES: 4'
 Minneapolis
 Query Match
Best Local Similarity
Matches 17; Conserva
 USA
US-08-469-802B-23/c
 US-08-469-802B-23
 COUNTRY:
 쉱
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GENERAL INFORMATION:
APPLICANT: Bachmader, Kurt
APPLICANT: Bachmader, Kurt
APPLICANT: Hessel, Andrew J.
APPLICANT: Hessel, Andrew J.
APPLICANT: Neu M.D., Nikolaus
APPLICANT: Neu M.D., Nikolaus
APPLICANT: Penninger, Josef M.
TITLE OF INVENTION: D. 5962636el Peptides Capable of Modulating Inflammatory Heart
TITLE OF INVENTION: Disease
FILE REFERENCE: A-536
CURRENT APPLICATION NUMBER: US/09/133,774B
CURRENT FILING DATE: 1998-08-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
 Gaps
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 .
0
 Score 15.2; DB 2; Length 42;
Pred. No. 1.4e+03;
0; Mismatches 3; Indels
 MEDIUM.

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIPICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: MCCOTMack, Myra H.
REFISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 110.00030120
FELEPHONE: 612-305-1217
FELEPHONE: 612-305-1228
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TUDENGTH: 20 base pairs
 60.8%; Score 15.2; DB 2;
85.0%; Pred. No. 1.3e+03;
tive 0; Mismatches 3;
3: Floppy disk
IBM PC compatible
3YSTEM: PC-DOS/MS-DOS
 Sequence 24, Application US/09133774B Patent No. 5962636
 Sequence 24, Application US/09303862
Patent No. 6034230
GENERAL INFORMATION:
 1 CAACTCATCACCACTCTTT 20
 2 AACTCATCACCACTCTCTTC 21
 20 CAACTCATGACCCTCTCT 1
 60.8%;
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APPLICANT: ALA-KOKKO, LEENA, et al.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALITERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
TITLE OF INVENTION: 666
CORRESPONDENCE: 666
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
CITY: PHILADELPHIA
 Gaps
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 Query Match

59.2%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels
 STATE: PA
CUNNING: USA
ZIP: 19103-7086
COMPUTER READBLE FORM:
MEDIUW TYEE: FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHLIN RC-BOS/MS-DOS
SOFTWARE: PATCHLIN R-BOS WILLING DATE: US/08/943,731
FILING DATE: U3-OCT-1997
CLASSIFICATION NUMBER: US/08/943,731
FILING APPLICATION NUMBER: US/08/943,731
FILING APPLICATION NUMBER: US/08/943,731
FILING APPLICATION NUMBER: US/08/943,731
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/803,628
FILING BAPLICATION NUMBER: US 07/803,628
FILING BAPLICATION NUMBER: US 07/803,628
FILING BAPLICATION NUMBER: 35,317
RESERBENCE/DOCKET NUMBER: 9598-27
TELERDRAK: 215-965-1284
THERERAK: 215-965-1291
 US-09-396-196G-75841
; Sequence 75841, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
APPLICANT: Mitchael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: David Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FRASEG for Windows Version 4.0
; SEQ ID NO 75841
 TELEX: 811-494
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 8 TCACCACTCTCTTCCATC 25
 DNA (genomic)
 TCCCCACTCTTCCCTC
 linear
 TOPOLOGY: li
MOLECULE TYPE:
 d
 ð
APPLICANT: Hessel, Andrew J.
APPLICANT: New M.D., Nikolaus
APPLICANT: Penninger, Josefue
APPLICANT: Penninger, Josefue
TITLE OF INVENTION: No. 6034230el Peptides Capable of Modulating Inflammatory Heart
TITLE OF INVENTION: Disease
TITLE OF INVENTION: Disease
CURRENT APPLICATION NUMBER: US/09/303,862
CURRENT FILING DATE: 1999-05-03
EARLIER APPLICATION NUMBER: 09/133,774
EARLIER APPLICATION NUMBER: 09/133,774
EARLIER PILING DATE: 1998-08-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: ParentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 42
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 60.8%; Score 15.2; DB 3; Length 42; 85.0%; Pred. No. 1.4e+03; ive 0; Mismatches 3; Indels
 60.0%; Score 15; DB 4; Length 25; 78.3%; Pred. No. 1.6e+03; tive 0; Mismatches 5; Indels
 US-09-396-196G-7617

Sequence 7617, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: 05/09/396,196G
CURRENT FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FBALESQ for Windows Version 4.0

SEQ ID NO 7617

LUNGTH: 25
 PROCKOP, DARWIN J.
SPOTILA, LORETTA D.
DELTAS, CONSTANTINOS D.
SEREDA, LARISA
LARSON, ANDREA W.
PACK, MICHAEL
COLIGE, ALAIN
EARLY, JAMES
KORKKO, JARMO
 2 AACTCATCACCACTCTTCCAT 24
 3 AACTCATCCTGACTCTCACCCAT 25
 Sequence 312, Application US/08943731
Patent No. 6265157
GENERAL INFORMATION:
 2 AACTCATCACCACTCTTC 21
 8 AGCTCATGGCCACTCTTC 27
 Query Match
Best Local Similarity 78.3
Matches 18; Conservative
 Conservative
 TYPE: DNA
ORGANISM: Mus musculus
 Query Match
Best Local Similarity
Local 17; Conserv?
 TYPE: DNA
ORGANISM: Human
 US-09-396-196G-7617
 RESULT 14
US-08-943-731-312/c
 US-09-303-862-24
 APPLICANT:
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APPLICANT:
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| FALLER INCOMENTATION: BAPPLICANT: COhen, Daniel APPLICANT: Cohen, Daniel APPLICANT: Cohen, Daniel APPLICANT: Chen, Daniel APPLICANT: Chumakov, Ilya TITLE OF INVENTION: Biallelic markers for use in constructing a high density... FILE REFERENCE: GENSET.020CP1 CURRENT APPLICATION NUMBER: US/09/422,978
| CURRENT APPLICATION NUMBER: US/09/298,850 | EARLIER FILING DATE: 1999-04-21 | EARLIER PILING DATE: 1999-04-21 | EARLIER PILING DATE: 1999-11-23 | EARLIER FILING DATE: 1999-04-21 | NUMBER: OF SEQ ID NOS: 11796 | SEQ ID NO 1201 | LENGTH: 47
 APPLICANT: Prockop, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ritvaniemi, Pertti
APPLICANT: Baldwin, Clinton
APPLICANT: Baldwin, Clinton
APPLICANT: Ahmad, Nilofer Nina
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS: ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 55589881i8
STREET: One Liberty Place, 46th floor
STREET: One Liberty Place, 46th floor
 Indels
) OTHER INFORMATION: 99-21370-87 : polymorphic base C or T US-09-422-978-1201
 Query Match 57.6%; Score 14.4; DB 4; Best Local Similarity 83.3%; Pred. No. 3.2e+03; Matches 15; Conservative 1; Mismatches 2;
 ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,284A
 RESULT 19
US-07-977-284A-208/c
; Sequence 208, Application US/07977284A
; Patent No. 5558988
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
 ; Sequence 1201, Application US/09422978
; Patent No. 6537751
 4 CTCATCACCACTCTTC 21
 25 crccrcarcacrcrcrc 42
 FILING DATE: 13-NOV-1992
CLASSIFICATION: 435
 PRIOR APPLICATION DATA
 ORGANISM: Homo Sapiens
 NAME/KEY: allele
LOCATION: 24
 US-09-422-978-1201
 COUNTRY:
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 Query Match 58.4%; Score 14.6; DB 4; Length 25; Best Local Similarity 81.0%; Pred. No. 2.4e+03; Matches 17; Conservative 0; Mismatches 4; Indels
 58.4%; Score 14.6; DB 4; Length 25; 81.0%; Pred. No. 2.4e+03;
 58.4%; Score 14.6; DB 4; Length 25; 81.0%; Pred. No. 2.4e+03; Live 0; Mismatches 4; Indels
 4; Indels
 RESULT 17
US-09-196-100658

i Sequence 100658, Application US/09396196G

i Patent No. 6821724

i GENERAL INFORMATION:

APPLICANT: Mitchael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

ITILE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FRSESQ for Windows Version 4.0

SEQ ID NO 100658

LEAGTH: 25
 Sequence 75842, Application US/09396196G
Fatent No. 6821724
GENERAL INPORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
AITLE REFERENCE: 310.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 75842
LENGTH: 25
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 3 ACTCATCACCACTCTTCCA 23
 4 ACTCATGGCTACTCTCTTCAA 24
 3 ACTCATCACCACTCTTCCA 23
 5 TCATCACCACTCTCTTCCATC 25
 1 Acreargecraercrerrea 21
 17; Conservative
 Query Match 58.4
Best Local Similarity 81.0
Matches 17; Conservative
 ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-75842
 TYPE: DNA ORGANISM: mus musculus
; ORGANISM: mus musculus US-09-396-196G-75841
 Best Local Similarity
Matches 17; Conserv
 US-09-396-196G-100658
 RESULT 16
US-09-396-196G-75842
 Query Match
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Gaps

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 APPLICANT:
APPLICANT:
APPLICANT:
Ritvaniemi, Pertti
APPLICANT:
Ritvaniemi, Pertti
APPLICANT:
Baldwin, Clinton
APPLICANT:
Baldwin, Clinton
APPLICANT:
And, NinGer Nina
TITLE OF INVENTION:
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
ONE Liberty Place - 46th Floor
CITY:
Philadelphia
 ö
 56.8%; Score 14.2; DB 1; Length 24; 84.2%; Pred. No. 3.5e+03; Live 0; Mismatches 3; Indels
 COMPUTER READABLE FUKM:

MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORDERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,426B
FILING DATE: 03-FEB-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/93/10964
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,284
FILING DATE: 13-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MARK Delica
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1082
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFPAK: (215) 568-3439
INPORMATION FOR SEQ ID NO: 208:
 TJU-0697
 US-08-256-426B-208/c
; Sequence 208, Application US/08256426B
Septence 108, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
 APPLICANT: Prockop, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Williams, Charlene J.
 NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPAX: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
 6 CATCACCACTCTTCCAT 24
 24 cárcácccrcrrrcccar 6
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
 Conservative
 COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
APPLICATION NUMBER:
 ; TOPOLOGY: LINEAR; ANTI-SENSE: NO
US-07-977-284A-208
 Query Match
Best Local Similarity
Matches 16; Conserv
 엄
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Sequence 22, Application US/08810599
Fatent No. 5976798
GENERAL INFORMATION:
APPLICANT: PARKER, W. Davis
APPLICANT: HERNSTADT, Corinna
APPLICANT: FAHY, Eson Her S.
APPLICANT: FAHY, Eson Methods for Detecting Mitochondrial Mutations
TITLE OF INVENTION: Methods for Alzheimer's Disease and Methods for Determining
TITLE OF INVENTION: of Mitochondrial Nucleic Acid
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CTTY: Washington
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 56.8%; Score 14.2; DB 4; Length 25; 84.2%; Pred. No. 3.5e+03; ive 0; Mismatches 3; Indels
 Indels
 US-09-396-196G-75840

Sequence 75840, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Mitchael Mittmann
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 75840
 Query Match 56.8%; Score 14.2; DB 2; Best Local Similarity 84.2%; Pred. No. 3.5e+03; Matches 16; Conservative 0; Mismatches 3;
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.25" Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1 for Windows
CURRENT APPLICATION DATA:
 7 ACTCATGGCTACTCTTTC 25
 6 CATCACCACTCTCTTCCAT 24
 3 ACTCATCACCACTCTTC 21
 24 carcacccrcrrrcccar 6
 Ouery Match
Best Local Similarity 84.2
Matches 16; Conservative
 TYPE: DNA
CORGANISM: mus musculus
US-09-396-196G-75840
TYPE: NUCLEIC ACID
 STRANDEDNESS: SIN
TOPOLOGY: LINEAR
ANTI-SENSE: NO
 US-08-256-426B-208
 RESULT 22
US-08-810-599-22/c
 ZIP: 20036
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 Length 22;
 Query Match 56.0%; Score 14; DB 3; Length 22; Best Local Similarity 77.3%; Pred. No. 4.2e+03; Matches 17; Conservative 0; Mismatches 5; Indels
 Length 25;
 US-01.22196.1966-52198/c

Sequence 52198, Application US/09396196G

Sequence 52198, Application US/09396196G

Sequence 52198, Application US/09396196G

PAPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REPREBUCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678
 56.0%; Score 14; DB 4; I 77.3%; Pred. No. 4.3e+03; tive 0; Mismatches 5;
 4 CTCATCACCACTCTCTTCCATC 25
 2 ccarcagcarrerrercare 23
 22 crcaacaccaccrrcrrcaacc 1
 ATTORNEY AGENT INFORMATION:
NAME: ROSEDMEN, Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 6600!
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEPAX: (206) 622-6031
INFORMATION FOR SEQ ID No: 2:
SEQUENCE CHARACTER STICS:
LENGTH: 22 base pairs
 , MOLECULE TYPE: DNA (genomic) US-08-757-438-2
 27-NOV-1996
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Best Local Similarity 77.3;
Matches 17; Conservative
 TYPE: nucleic acid
STRANDEDNESS: double
 TYPE: DNA
CORGANISM: Mus musculus
US-09-396-196G-22970
 linear
 TOPOLOGY:
 LENGIH: 25
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 à
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 ö
 Length 22;
 5; Indels
 Sequence 2, Application US/08757438
Patent No. 6627883
GENERAL INFORMATION
APPLICANT: Hernstadt, Corinna
APPLICANT: Fahy, Eoin D.
APPLICANT: Fahy, Eoin D.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: OPTIMAL PROCEDURE FOR ISOLATION OF
 NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
 PatentIn Release #1.0, Version #1.30
 Score 14; DB 2;]
Pred. No. 4.2e+03;
 PRICE APPLICATION 1973

APPLICATION NUMBER: US 08/757,438

FILING DATE: 27 No. 5976798 1996

APPLICATION NUMBER: US 08/614,072

FILING DATE: 12 Nar 1996

APPLICATION NUMBER: US 08/536,036

FILING DATE: 29 SEP 1995

APPLICATION NUMBER: US 08/414,969

FILING DATE: 31 Mar 1995

APPLICATION NUMBER: US 08/413,740

FILING DATE: 30 Mar 1995

APPLICATION NUMBER: US 08/33,740

FILING DATE: 34 MARCH 1995

APPLICATION NUMBER: US 08/397,808

FILING DATE: 3 Mar 1995

APPLICATION NUMBER: US 08/397,808

FILING DATE: 3 MARCH 1995

APPLICATION NUMBER: US 08/397,808

FILING DATE: 3 MARCH 1995

APPLICATION NUMBER: US 08/397,808

FILING DATE: 3 MARCH 1994

ATTOCNEY AGENT INFORMATION:
NAME: TOFFENETI, JUMITH L.

REGISTATION NUMBER: 39,044

REGISTATION NUMBER: 39,041

REFERENCE NOCKET NUMBER: 3104/17
 CITY: Seattle
STATE: Mashington
CONTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
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COMP
APPLICATION NUMBER: US/08/810,599
 US/08/757,438
 2105/17
 MOLECULE TYPE: other nucleic acid HYPOTHETICAL: No
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TELECOMMUNICATION INFORMATION:
 TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 77.33
Matches 17; Conservative
 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
 linear
 ; ANTI-SENSE: NO
US-08-810-599-22
 TELEPHONE:
 US-08-757-438-2/c
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Query Match
Best Local Similarity 77.3'
Matches 17; Conservative
 linear
 MOLECULE TYPE: DNA
 RESULT 28
US-08-646-538-20/c
 US-09-503-222-20/c
 LENGTH:
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 Gaps
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 Score 14; DB 4; Length 25; Pred. No. 4.3e+03;
 56.0%; Score 14; DB 4; Length 25; 100.0%; Pred. No. 4.3e+03; ive 0; Mismatches 0; Indels
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 RESULT 27
US-09-396-196G-83551
iS-09-396-196G-83551, Application US/09396196G
j Patent No. 6821724
iGENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affwerrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 83551
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US-09-396-196G-52200/c
; Sequence 52200, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Mack
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: PASESEQ for Windows Version 4.0
 56.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52198
LENGTH: 25
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 Query Match
Best Local Similarity 100.
Matches 14; Conservative
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 TYPE: DNA
ORGANISM: mus musculus
 TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-52200
 TYPE: DNA
CORGANISM: mus musculus
US-09-396-196G-83551
 Query Match
Best Local Similarity
 US-09-396-196G-52198
 SEQ ID NO 52200
LENGTH: 25
 Matches
 g
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ö
 ö
 APPLICANT: Paviation:
APPLICANT: Paviation:
APPLICANT: Gaitanaris, George N.
APPLICANT: Stauber, Roland H.
APPLICANT: Stauber, Roland H.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREFT: Two Emparcadero Center, 8th Floor
CITY: San Francisco
STATE: California
 Gaps
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Score 14; DB 4; Length 25;
Pred. No. 4.3e+03;
0; Mismatches 5; Indels
 Length 40;
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 ; NAME/KEY: -
; LOCATION: 1..40
; OTHER INFORMATION: /note= "oligonucleotide #bio25"
US-08-646-538-20
 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

PILING DATE: No. 602/881 yet assigned

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REGISTRATION NUMBER: 31,677

REGISTRATION NUMBER: 31,677

TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0200

TELEPAK: (415) 576-0300

SEQUENCE CHARACTERISTICS:
 Query Match 56.0%; Score 14; DB 3; Le Best Local Similarity 77.3%; Pred. No. 4.7e+03; Matches 17; Conservative 0; Mismatches 5;
 COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 3 ACTCATCACCACTCTCCAT 24
 2 AACTCATCACCACTCTTCCA 23
 1 AACTCATAACCATCCTCTACAA 22
 33 ACTAGTCACTACTCTCTCAT 12
 Sequence 20, Application US/08646538 Patent No. 6027881 GENERAL INFORMATION:
 Sequence 20, Application US/09503222; Patent No. 6265548; GENERL INFORMATION:
APPLICANT: Pavlakis, George N. APPLICANT: Gaitanaris, George A.
56.0%;
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 TYPE: nucleic acid
STRANDEDNESS: single
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PatentIn Release #1.0, Version #1.25
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 SOFTWARE: Patentin release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FILING DATE: 19910544
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MALTANION NUMBER: 29,959
RESTERENCE/POCKET NUMBER: 4610-0011.40
TELEPAN: 706141
TELEPHONE: 415-327-7250
TELEPAN: 706141
TELERAX: 706141
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LOCATION: 1..4
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NAME/KEY: modified_base
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OTHER INFORMATION:
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OTHER INFORMATION:
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 TOPOLOGY: linear FEATURE:
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NAME/KEY:
LOCATION:
 PCT-US31-03680-144

| Sequence 144, Application PC/TUS9103680
| Sequence 144, Application PC/TUS9103680
| GENERAL INFORMATION:
| APPLICANT: Matteucci, Mark D. APPLICANT: Matteucci, Mark D. APPLICANT: Matteucci, Mark D. TITLE OF INVENTION: ERQUENCES-SPECIFIC NONPHOTOACTIVATED
| TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF TITLE OF INVENTION: DUPLEX DNA NUMBER OP SEQUENCES: 158
| NUMBER OP SEQUENCES: 158
| CORRESPONDENCE ADDRESS: SPECIFIC NONPHOTOACTIVATED
| STREET: 545 Midlefield Road, Suite 200 CITY: Menlo Park STATE: California CITY: Midlefield Road, Suite 200 CITY: Menlo Park STATE: California CIUNRY: USA
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STREET: California
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 Query Match 56.0%; Score 14; DB 3; Length 40; Best Local Similarity 77.3%; Pred. No. 4.7e+03; Matches 17; Conservative 0; Mismatches 5; Indels
 ; NAME/KEY: - ; LOCATION: 1..40 ; COTHER INFORMATION: /note= "oligonucleotide #bio25" US-09-503-222-20
 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/503,222
 CLASSICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,538
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-249000
TELECOMMUNICATION INFORMATION:
TELEFAK: (415) 576-0200
TELEFAK: (415) 576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
 3 ACTCATCACCACTCTTCCAT 24
 33 ACTAGTCACTACTCTCTCAT 12
 ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
 TYPE: nucleic acid
STRANDEDNESS: single
 TOPOLOGY: linear MOLECULE TYPE: DNA
 FILING DATE:
 CITY: San
STATE: Ca
COUNTRY:
 RESULT 30
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 Length 26;
 Indels
 OTHER INFORMATION: /mod base= OTHER OTHER INFORMATION: /note= "N4,N4-ethanocytosine"
 55.2%; Score 13.8; DB 5;
57.1%; Pred. No. 5.3e+03;
tive 6; Mismatches 3;
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 Sequence 13, Application US/09009893A
Patent No. 6623938
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
 1 CAACTCATCACCACTCTTC 21
 1 MAMMIMCTCTMCTCTCTTC 21
 NAME/KEY: modified_base LOCATION: 7
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OTHER INFORMATION: /mod
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 NAME/KEY: modified_base LOCATION: 12
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Best Local Similarity 57.15
Matches 12; Conservative
 LOCATION: 11
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OTHER INFORMATION:
OTHER INFORMATION:
 LOCATION: 9
OTHER INFORMATION:
OTHER INFORMATION:
 US-09-009-893A-13/C
 PCT-US91-03680-145
 LOCATION:
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 g
 Sequence 145, Application PC/TUS9103680
GENERAL INFORMATION:
APPLICANT: Matteucci, Mark D.
APPLICANT: Krawczyk, Steven
TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
TITLE OF INVENTION: CROSSIINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF TITLE OF INVENTION: DUPLEX DNA
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
 ö
 Query Match 55.2%; Score 13.8; DB 5; Length 26; Best Local Similarity 57.1%; Pred. No. 5.3e+03; Matches 12; Conservative 6; Mismatches 3; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FILING DATE: 19910524
CLASSIFICATION: 435.5.
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OTHER INFORMATION:
FEATURE:
NAME/KEY: modified_base
LOCATION: 24
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "5-methylcytosine"
 ACTORNEY AGENT INFORMATION:
NAME: Murashige, Kate H.
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4610-0011.40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-226
TELEFAX: 415-327-226
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
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TENGTH: 26 base pairs
TENGTH: ACTORNOLOGY: 110-027
 ADDRESSEE: Morrison & Poerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
 PEATURE:
NAME/KEY: modified_base
LOCATION: 26
OTHER INFORMATION: /mod_base= OTHER
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PCT-US91-03680-144
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 NAME/KEY: modified_base
LOCATION: 1...4
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 1 MAMMIMCICIMCICICITY 21
 1 CAACTCATCACCACTCTTC 21
 NAME/KEY: modified_base
 PCT-US91-03680-145
 COUNTRY:
 RESULT 31
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APPLICANT: Kenny, Joseph J.

TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
TITLE OF INVENTION: CD-95 Induced Apoptosis
FILE REFERENCE: 1488.0970002
CURRENT APPLICATION NUMBER: US/09/009, 893A
CURRENT APPLICATION NUMBER: US/09/009, 893A
PRIOR PILING DATE: 1998-02-21
PRIOR APPLICATION NUMBER: US 60/054, 800
PRIOR PILING DATE: 1997-00-5
PRIOR PILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 33
 APPLICANT: Rosen, Craig A.
APPLICANT: Bosen, Craig A.
APPLICANT: Bixit, Vishva M.
APPLICANT: Gixit, Vishva M.
APPLICANT: Gixit, Vishva M.
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
APPLICANT: Kenny, Joseph J.
TITLE OF INVENTION: I-FLICE, A No. 6680171e1 Inhibitor of Tumor Necrosis Factor Recepting OF INVENTION: 100-95 Induced Apoptosis
FILE REFERENCE: 1488.0970002
CURRENT APPLICATION NUMBER: US/09/489,155
CURRENT FILING DATE: 2000-01-21
PRIOR PILING DATE: 1998-01-21
PRIOR FILING DATE: 1998-01-21
PRIOR FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Version 3.0
SEQ ID NO 13
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 55.2%; Score 13.8; DB 4; Length 33; 88.2%; Pred. No. 5.5e+03; Live 0; Mismatches 2; Indels
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 Query Match 55.2%; Score 13.8; DB 4; Best Local Similarity 88.2%; Pred. No. 5.5e+03; Matches 15; Conservative 0; Mismatches 2;
 Sequence 13, Application US/09489155
Patent No. 6680171
GENERAL INFORMATION:
APPLICANT: Ni, Jian
 Sequence 19, Application US/09489155
Patent No. 6860171
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Dixit, Vishva M.
APPLICANT: Gentz, Reiner L.
 8 TCACCACTCTCTTCCAT 24
 8 TCACCACTCTCTTCCAT 24
 32 TCACCAATCTCTGCCAT
 32 rcaccaarcrcrccar
 Query Match
Best Local Similarity 88.2
Matches 15; Conservative
 ; ORGANISM: primer
US-09-009-893A-21
 TYPE: DNA

ORGANISM: primer
US-09-489-155-13
 US-09-489-155-13/c
 US-09-489-155-19/c
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UB-10-788

LICANT: Gentz, Neiner L.

APPLICANT: Gentz, Reiner L.

APPLICANT: Gentz, Reiner L.

TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Reconstruction of TUMENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Reconstruction INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Reconstruction Number: US/09/009,893A

CURRENT APPLICATION NUMBER: US 60/054,800

PRIOR PILING DATE: 1997-01-21

PRIOR FILING DATE: 1997-01-21

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin version

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 Sequence 19, Application US/0900983A

Patent No. 6623938

GENERAL INFORMATION:
APPLICANT: Bixit, Vishwa M.
APPLICANT: Conting A.
APPLICANT: Conting A.
APPLICANT: Conting A.
APPLICANT: Conting A.
APPLICANT: Conting A.
APPLICANT: Gent, Vishwa M.
APPLICANT: Gent, Vishwa M.
APPLICANT: Gent, Nemer I.
TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
TITLE OF INVENTION: I-PLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
TITLE OF INVENTION: I-PLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
TITLE OF INVENTION: UNBER: US 60/054,800
FRIOR FILING DATE: 1998-02-21
CURRENT FALLING DATE: 1997-08-05
FRIOR FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patent In version 3.0
SEQ ID NO 19
LENGTH: 33
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 55.2%; Score 13.8; DB 4; Length 33; 88.2%; Pred. No. 5.5e+03; live 0; Mismatches 2; Indels
 Score 13.8; DB 4; Length 33;
Pred. No. 5.5e+03;
0; Mismatches 2; Indels
 US-09-009-893A-21/c
; Sequence 21, Application US/09009893A
; Patent No. 6623938
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 8 TCACCACTCTCTTCCAT 24
 8 TCACCACTCTTTCCAT 24
 32 rcaccaarcrcrccar 16
 55.2%;
88.2%;
 Query Match
Best Local Similarity 88.23
Matches 15, Conservative
 Query Match
Best Local Similarity 88.29
 GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Dixit, Vishva M.
 ; TYPE: DNA
; ORGANISM: primer
US-09-009-893A-13
 TYPE: DNA
CRGANISM: primer
US-09-009-893A-19
 RESULT 33
US-09-009-893A-19/c
 RESULT 34
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0
 55.2%; Score 13.8; DB 1; Length 39; ilarity 88.2%; Pred. No. 5.7e+03; Conservative 0; Mismatches 2; Indels
 Sequence 107, Application PC/TUS9206821A
GENERAL INFORMATION:
APPLICANT: Shah, Jyotsna S.
APPLICANT: Nietupski, Raymond M.
APPLICANT: Liu, Jing
TITLE OF INVENTION: Oligonucleotides Complementary to
TITLE OF INVENTION: Mycobacterial Nucleic Acids
NUMBER OF SEQUENCES: 133
CORRESPONDENCE ADDRESS:
 CAPPER 10.39.1.

CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,282C
FILING DATE: August 13, 1991
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kevin M. Farrall
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: 35,505
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1870RMATION:
TELECOMMUNICATION:
TELECOMMUNICAT
 ADDRESSEE: Amoco Corporation
STREET: 200 East Randolph Drive, P.O. Box 87703
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06821A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/744,282
 NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
 NAME: Galloway, Norval B.
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: CN 5851
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-07-744-282C-64
 6 CATCACCACTCTCC 22
 CATCACCACCTCCTCC 18
 FILING DATE: 13-AUG-1991
ATTORNEY/AGENT INFORMATION:
 TYPE: nucleic acid
STRANDEDNESS: single
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 STREET: 200 Bast
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
 Query Match
Best Local Similarity
Matches 15; Conserv
 USA
 PCT-US92-06821A-107
 03911
 60680
 COUNTRY:
 셤
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 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Joseph J.
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: I-FLICE, A No. 6680171e1 Inhibitor of Tumor Necrosis Factor Recept TITLE OF INVENTION: I-FLICE, A PAPLICANTON WOMER: US/09/489,155
CURRENT PILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/09/09,893
PRIOR FILING DATE: 1998-01-21
PRIOR FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PALENTH Version 3.0
SEQ ID NO 21
LENGTH: 33
APPLICANT: Kenny, Joseph J.

TITLE OF INVENTION: 1-Files, A No. 6680171el Inhibitor of Tumor Necrosis Factor Receptivite OF INVENTION: 02-95 Induced Apoptosis
FILE REFERENCE: 1488.0970002
CURRENT APPLICATION NUMBER: US/09/489,155
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/009,893
PRIOR FILING DATE: 1998-01-21
PRIOR FILING DATE: 1998-01-21
NUMBER OF SEQ ID NOS: 35
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SOFTWARE: PATENTI VERSION 3.0
SEQ ID NO 19
LENGTH: 33
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 55.2%; Score 13.8; DB 4; Length 33; 88.2%; Pred. No. 5.5e+03; ive 0; Mismatches 2; Indels
 Score 13.8; DB 4; Length 33; Pred. No. 5.5e+03; 0; Mismatches 2; Indels
 APPLICANT: Shah, Jyotsna S.
APPLICANT: Nietupski, Raymond M.
APPLICANT: Liu, Jing
TITLE OF INVENTION: Oligonucleotides Complementary to
TITLE OF INVENTION: Mycobacterial Nucleic Acids
 US-07-744-282C-64; Sequence 64, Application US/07744282C; Patent No. 5521300; GENERAL INFORMATION:
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 32 rcaccaarcrcrccar 16
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88.2%;
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 Conservative
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Best Local Similarity
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Best Local Similarity
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; ORGANISM: primer
US-09-489-155-19
 ; TYPE: DNA
; ORGANISM: primer
US-09-489-155-21
 US-09-489-155-21/c
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RESULT 40

US-09-641-638-1287

i Sequence 1287, Application US/09641638

sequence 1287, Application US/09641638

sequence 1287, Application US/09641638

sequence 1287, Application US/09641638

sequence 1287, Application

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Chen, Annick

TITLE OF INVENTION: BLALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING

TITLE OF INVENTION: GENSEI 105/09/641,638

TITLE OF INVENTION: GENSEI 05/00-01-16

PRIOR PILING DATE: 2000-02-16

PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-05-07

PRIOR PLICATION NUMBER: US 60/133,200

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LOCATION: 24
CTHEN THORMATION: 10-507-353 : polymorphic base C or T
US-09-641-638-1287
TELECOMMUNICATION INFORMATION:
TELEPAX: 312-856-7180
TELEPAX: 312-856-4972
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGle
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGle
TYPE: MOLECULE TYPE: DNA
PCP-US92-06821A-107
 4 CTCATCACCACTCTTCC 22 ||:||||| ||||| ||||| 22 CTYATCACGCCTCCCTTCC 40
 ORGANISM: Homo Sapiens
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14, Appl 224994,

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381320, 754829,

Sequence Sequence

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US-09-978-192A-142

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US-09-978-192A-142

US-09-978-192A-142
 GENERAL INFORMATION:
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: SEIDMAN, JOHN
APPLICANT: WATKINS, HUGH
APPLICANT: ROSENZWEIG, ANTHONY
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
 US-09-978-585A-142
US-09-978-191A-142
US-09-978-403A-142
 ALIGNMENTS
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 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,172
FILLING DATE:
CLASSIFICATION:
 COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
 ADDRESSEE: LAHIVE & COCKFIELD STREET, 60 STATE STREET, Suite
 ; Sequence 9, Application US/08469172; Publication No. US20030054343A1
 Massachusetts: U.S.A.
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 STREET: 60 STJ
CITY: BOSTON
STATE: Massacl
COUNTRY: U.S.J
 02109
 US-08-469-172-9
 14.7.2
16.2
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16.2
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Sequence 3589, Ap
Sequence 879180,
Sequence 961186,
 Sequence 9, Appli
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(c) 1993 - 2005 Compugen Ltd.
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 25
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 Published_Applications_NA:*
 1 CAACTCATCACCACTCTTCCATC
 Post-processing: Minimum Match 0%
Maximum Match 100%
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 - nucleic search, using sw model
 IDENTITY NUC
Gapop 10.0 , Gapext 1.0
 Pred. No. is the number of res
score greater than or equal to
and is derived by analysis of
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26
 US-10-788-779-9
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 Length
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70.4
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Sequence 6576, Ap Sequence 6966, Ap Sequence 1, Appli Sequence 1372, Ap

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Gaps

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Sequence 1359, Application US/10349143
; Sequence 5189, Application US/10349143
; Publication No. US20040005584A1
GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/00/349,143
; TITLE OF INVENTION STEE: 2003-01-21
; CURRENT APPLICATION NUMBER: US/09/422,978
; PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1999-04-21
; PRIOR PILING DATE: EARLIER FILING DATE: 1999-04-21
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; PRIOR FILING DATE: EARLIER PILING DATE: 1998-04-21
; NUMBER: OF SEQ ID NOS: 11796
; SEQ ID NO 3589
 Sequence 879180, Application US/11036317
| Publication No. US20050214823A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Alan
| APPLICANT: Williams, Alan
| TITLE OF INVENTION: Wethod of Analysis of Alternative Splicing in Mouse
| FILE REPERBNCE: 3654.1
| CURRENT FILING DATE: 2005-01-13
| PRIOR APPLICATION NUMBER: US 60/536,639
| PRIOR APPLICATION NUMBER: US 60/536,639
| PRIOR APPLICATION NUMBER: 2004-01-13
| NUMBER OF SEQ ID NOS: 991174
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
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 Length 47;
 Score 25; DB 20; Length 25; Pred. No. 0.8;
 Indels
 Indels
 LOCATION: 24
OTHER INFORMATION: 99-6834-307 : polymorphic base G or A
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 72.8%; Score 18.2; DB 18;
80.0%; Pred. No. 5.9e+02;
 0; Mismatches
 1; Mismatches
 TOPOLOGY: linear

MOLECULE TYPE: CDNA
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Best Local Similarity 100.0%;
Matches 25; Conservative 0
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Best Local Similarity 80.0'
Matches 20; Conservative
 TYPE: DNA ORGANISM: Homo Sapiens
 TYPE: DNA ORGANISM: Mus musculus
 US-11-036-317-879180/c
 JS-10-349-143-3589/c
 NAME/KEY: allele
 US-10-349-143-3589
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 Gaps
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0
 DB 8; Length 25;
 RESULI 4
US-10-788-779-9
US-10-788-779-9
; Sequence 9, Application US/10788779
; Publication No. US20040152121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
 0; Indels
 STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 102109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/788,779
FILING DATE: 27-Feb-2004
CLASSIFICATION: <Unknown>
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100.0%; Pred. No. 0.8;
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/469,172
FILING DATE: «Unknown»
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELLZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
TELECOMMUNICATION INFORMATION:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
 0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 35.505
REFERENCE/DOCKET NUMBER: GML-111
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDENESS: single
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 (617) 227-7400
 TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
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 Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
 BOSTON
 TELEPHONE:
 linear
 TOPOLOGY: 11
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 US-08-469-172-9
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Gaps

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; ORGANISM: Mus musculus
US-10-719-900-264364
 ; ORGANISM: Mus musculus
US-10-719-900-381320
 US-10-719-900-754829
 TYPE: DNA
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 Sequence 979596, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
ITITLE OF INVENTION Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.11
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PLING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOUTHARD SEQ ID NOS: 991174
SEQ ID NO 979596
LENGTH: 25
 ö
 APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
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 70.4%; Score 17.6; DB 26; Length 25; 83.3%; Pred. No. 1e+03; 1ive 0; Mismatches 4; Indels
 Length 25;
 Length 25;
 NUMBER OF SEQ ID NOS: 991174
SOFTWARE Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 961186
LENGTH: 25
 Indels
 Indels
 Score 17.6; DB 26;
Pred. No. 1e+03;
0; Mismatches 4;
 Query Match 68.8%; Score 17.2; DB 26; Best Local Similarity 86.4%; Pred. No. 1.5e+03; Matches 19; Conservative 0; Mismatches 3;
 Sequence 961186, Application US/11036317, Publication No. US20050214823A1 SENERAL INFORMATION: APPLICANT: Williams, Alan
 2 AACTCATCACCACTCTTCCATC 25
 2 AACTCATCACCACTCTCTTCCATC 25
 25 AACTCATCACCACTGATTTCCAAC 2
 24 AACTCATCACCACTGATTTCCAAC 1
 2 AACTCATCACCACTCTTCCA 23
 22 AACTCATCACCACTGATTTCCA 1
 70.4%;
 Query Match
Best Local Similarity 83.33
Matches 20; Conservative
 Query Match
Best Local Similarity 83.3
Matches 20; Conservative
 TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-961186
 TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-979596
 RESULT 5
US-11-036-317-961186/c
 US-11-036-317-979596/c
US-11-036-317-879180
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Sequence 264364, Application US/10719900
| Publication No. US20050026164A1
| GENERAL INFORMATION:
| APPLICANT: You Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVENTION: WHERE: US/10/719,900
| CURRENT APPLICATION NUMBER: US/10/719,900
| PRIOR PAPLICATION NUMBER: 60/427,808
| PRIOR PRILING DATE: 2002 11.20
| WINHER OF SEQ ID NOS: 982914
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
 Sequence 381320/c
; Sequence 381320/c
; Sequence 381320, Application US/10719900
; Publication No. US2050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: WHERE: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 381320
 Length 25;
 Length 25;
 APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11.20
PRIOR APPLICATION NUMBER: 00/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTHARE: Microarray Probe Sequence Listing Generator V 1.1
ENGTH: 25
 Indels
 64.8%; Score 16.2; DB 22;
85.7%; Pred. No. 3.9e+03;
ative 0; Mismatches 3;
 64.8%; Score 16.2; DB 22;
85.7%; Pred. No. 3.9e+03;
tive 0; Mismatches 3;
 Sequence 754829, Application US/10719900
, Publication No. US20050026164A1
, GENERAL INFORMATION:
 4 CTCATCACCACTCTCCAT 24
 2 AACTCATCACCACTCTTCC 22
 21 crcarcaccacerrerecear 1
 AACTGATGACCACTGTCTTCC 5
 Query Match
Best Local Similarity 85.79
Watches 18; Conservative
 Query Match
Best Local Similarity 85.7
Matches 18; Conservative
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US-10-719-900-264364/c

RESULT 7

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Query Match
Best Local Similarity 89.5⁵
Matches 17; Conservative
 TYPE: DNA
COCGANISM: Mus musculus
US-10-719-900-224994
 US-10-719-900-224994
 RESULT 14
US-10-681-773-71822
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 Sequence 961185, Application US/11036317
; Sequence 961185, Application US/11036317
; Publication No. US20050214823A1
; GENREAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; FILE REFERENCE: 3654.1
; CURRENT APLICATION NUMBER: US/11/036,317
; CURRENT PILING DATE: 2005-01-13
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFFWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 961185
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 RESULT 10

(WS-11-036-317-879179/C

(WS-11-036-317-879179), Application US/11036317

(Sequence 879179, Application US/11036317

(SENDEAL INCOMMATION:

(APPLICANT: Williams, Alan

(APPLICANT: Williams, Alan

(APPLICANT: Blune, John

(APPLICANT: MUNBER: US/11/036,317

(APPLICANT FILING DATE: 2005-01-13

(APPLICANT FILING DATE: 2004-01-13

(APPLICANT FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILIN
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 Length 25;
 64.0%; Score 16; DB 26; Length 25; larity 79.2%; Pred. No. 4.8e+03; Conservative 0; Mismatches 5; Indels
 64.0%; Score 16; DB 26; Length 25; 79.2%; Pred. No. 4.8e+03; ive 0; Mismatches 5; Indels
 Indels
 64.8%; Score 16.2; DB 22;
85.7%; Pred. No. 3.9e+03;
ive 0; Mismatches 3;
 2 AACTCATCACCACTCTTCCATC 25
 2 AACTCATCACCACTCTTCCATC 25
 25 AACTCATCACCAGTGATTTCCAAC 2
 24 AACTCATCACCTCTGATTTCCAAC 1
 5 TCATCACCACTCTCCATC 25
 1 TAATAACCACTCTCTTCCCTC 21
 Query Match
Best Local Similarity 85.7
Matches 18; Conservative
 19; Conservative
; ORGANISM: Mus musculus
US-10-719-900-754829
 ORGANISM: Mus musculus
 TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-961185
 Query Match
Best Local Similarity
Matches 19; Conservi
 Best Local Similarity
 US-11-036-317-961185/c
 Query Match
 TYPE: DNA
 Matches
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RESULT 12

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US-10-226-844-14

| Sequence 14, Application US/10226844
| Publication No. US20030113764A1
| GENERAL INFORMATION:
| APPLICANT: Bodary, Sarah C. |
| APPLICANT: Bodary, Sarah C. |
| APPLICANT: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMORS |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMORS |
| TITLE OF INVENTION: UNMBER: US/09/627,202 |
| PRIOR APPLICATION NUMBER: US/09/627,202 |
| PRIOR APPLICATION NUMBER: US 60/146,217 |
| PRIOR FILING DATE: 1999-07-28 |
| NUMBER OF SEQ ID NOS: 22 |
| SEQ ID NO 14 |
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 Gaps
 Sequence 71822, Application US/10681773
Publication No. US20040146890A1
GENERAL INFORMATION:
APPLICANT: Matsuzaki, Hajime
APPLICANT: Shen, Mei-Mei
APPLICANT: Kennedy, Giulia
TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
FILE REPERENCE: 3522.2
CURRENT APPLICATION NUMBER: US/10/681,773
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 Length 25;
 Query Match 64.0%; Score 16; DB 16; Length 42; Best Local Similarity 79.2%; Pred. No. 4.9e+03; Matches 19; Conservative 0; Mismatches 5; Indels
 APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 35281
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
 Indels
 Score 15.8; DB 22;
Pred. No. 5.8e+03;
0; Mismatches 2;
 Sequence 224994, Application US/10719900 Publication No. US20050026164A1 GENERAL INFORMATION:
 2 AACTCATCACCACTCTTCCATC 25
 6 AATGCATCAAGACTCTCTGCCATC 29
 1 ATAACCACTCTCTTCCCTC 19
 7 ATCACCACTCTCTTCCATC 25
 63.2%;
89.5%;
 FEATURE:
COTHER INFORMATION: PCR primer
US-10-226-844-14
 TYPE: DNA ORGANISM: Artificial sequence
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-853737
 TYPE: DNA
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 Sequence 853737, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION UNMBER: US 60/536,639

PRIOR APPLICATION UNMBER: US 60/536,639

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEG ID NO 853737
 Sequence 105909, Application US/1068173
; Sequence 105909, Application US/1068173
; Publication No. US20040146890A1
; GRNERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Rennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; TITLE OF INVENTION: 2022.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2002-05-14
; PRIOR FILING DATE: 2002-05-14
; PRIOR PRING DATE: 2002-05-14
; PRIOR PILING DATE: 2002-06-14
; PRIOR PRING DATE: 2002-06-14
; PRIOR PILING DATE: 2002-06-14
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105909
 Gaps
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 62.4%; Score 15.6; DB 24; Length 25; 81.8%; Pred. No. 7e+03; ive 0; Mismatches 4; Indels (
 Query Match 62.4%; Score 15.6; DB 24; Length 25; Best Local Similarity 81.8%; Pred. No. 7e+03; Matches 18; Conservative 0; Mismatches 4; Indels
 PRIOR APPLICATION NUMBER: 60/470,475
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 124031
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 71822
LENGTH: 25
 1 CAACTCATCACCACTCTTCC 22
 3 caaarcarragererereree 24
 1 CAACTCATCACCACTCTTCC 22
 4 CAAATCATTAGCTCTCTCTTCC 25
 2003-10-07
 Best Local Similarity 81.6
Matches 18; Conservative
 ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-71822
 ; ORGANISM: Homo sapien
US-10-681-773-105909
CURRENT FILING DATE:
 US-11-036-317-853737/c
 US-10-681-773-105909
 Query Match
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Sequence 979595, Application US/11036317

Publication No. US2005021482341

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVERTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT PILING DATE: 2005-01-13

FRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOSTWARE MICROARRAY Probe Sequence Listing Generator V 1.1
 Gaps
 CTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: attenuation factor oligonucleotide US-09-888-413-147
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 Length 25;
 Length 25;
 Indels
 Indels
 7e+03;
 APPLICANT: KRIS, RICHARD M.
APPLICANT: KRISK, RICHARD M.
TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM
FILE REFERENCE: NEGGEN-1 P4
CURRENT APPLICATION NUMBER: US/09/886,413
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 09/337,325
PRIOR PILING DATE: 1998-06-21
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-10-32
PRIOR FILING DATE: 1998-10-32
PRIOR FILING DATE: 1998-10-32
PRIOR FILING DATE: 1998-10-35
SOFTWARE: PALENTION NUMBER: 60/068,291
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PALENTIN Ver. 2.1
Score 15.6; DB 26;
Pred. No. 7e+03;
0; Mismatches 4;
 DB 26;
 Pred. No. 7e+0
0; Mismatches
 Query Match 62.4%; Score 15.6; Best Local Similarity 81.8%; Pred. No. 7e Matches 18; Conservative 0; Mismatche
 Sequence 147, Application US/0988413
Publication No. US20030096232A1
GENERAL INFORMATION:
 4 CICATCACCACTCTTCCATC 25
 2 AACTCATCACCACTCTCTACA 23
 25 crcarcaccacrantriccaac 4
 22 AACTCATCACCTCTGATTTCCA 1
Query Match 62.4%;
Best Local Similarity 81.8%;
Matches 18; Conservative (
 ORGANISM: Artificial Sequence
) ORGANISM: Mus musculus
US-11-036-317-979595
 RESULT 17
US-11-036-317-979595/c
 US-09-888-413-147/c
 SEQ ID NO 979595
LENGTH: 25
```

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Indels

Length 47;

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APPLICANT: Blumented, marta
APPLICANT: Blumented, marta
APPLICANT: Buguelett, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
ITILE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
ITILE OF INVENTION: CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GEN-TIAXC2D1
CURRENT APPLICATION NUMBER: US/10/170,097
PRIOR APPLICATION NUMBER: US/10/170,097
PRIOR PRILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR PILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR PILING DATE: 1999-03-03
PRIOR PILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 1288
 ; OTHER INFORMATION: 10-507-364 : polymorphic base C or T
US-10-926-684-1288
 NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 10-507-364 : polymorphic base C or
 Score 15.4; DB 18;
Pred. No. 8.8e+03;
1; Mismatches 2;
 Query Match 61.6%; Score 15.4; DB 22; Best Local Similarity 84.2%; Pred. No. 8.8e+03; Matches 16; Conservative 1; Mismatches 2;
 US-10-926-684-1288; Sequence 1288, Application US/10926684; Sequence 1288, Conference 1288; Publication No. US20050014190A1; CENERAL INFORMATION: APPLICANT: Blumenfeld, Marta
 RESULT 22
US-10-719-956-5098/c
; Sequence 5098, Application US/10719956
 11 CTCATCACGCCTCYCTTCC 29
 4 CTCATCACCACTCTCTTCC 22
 4 CICATCACCACTCTTCC 22
 crcarcacecrcycrrcc 29
 Query Match 61.6%;
Best Local Similarity 84.2%;
Matches 16; Conservative
 PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 1288
LENGTH: 47
 TYPE: DNA
ORGANISM: Homo Sapiens
 TYPE: DNA ORGANISM: Homo Sapiens FEATURE:
 US-10-170-097-1288
 LOCATION: 24
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 Sequence 1288, Application US/10170097

Publication No. US20030228582A1

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

APPLICANT: Chamakov, Ilya

APPLICANT: Chamakov, Ilya

APPLICANT: Chumakov, Ilya

APPLICANT: Chinakov, Ilya

APPLICANT: Chinakov, Ilya

APPLICANT: Chinakov, Ilya

APPLICANT: Chinakov, Ilya

CURRENT ELING DATE: 2002-06-10

FRIOR APPLICATION NUMBER: US 09/641,638

PRIOR PRILING DATE: 2000-02-11

PRIOR PRILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: US 09/502,330

PRIOR APPLICATION NUMBER: US 09/502,330

PRIOR APPLICATION NUMBER: US 09/275,267

PRIOR APPLICATION NUMBER: US 09/275,267

PRIOR APPLICATION NUMBER: US 60/119,917
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 OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: attenuation factor oligonucleotide US-10-865-853-147
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 61.6%; Score 15.4; DB 10; Length 25; 76.0%; Pred. No. 8.5e+03; ive 0; Mismatches 6; Indels (
 Query Match 61.6%; Score 15.4; DB 22; Length 25; Best Local Similarity 76.0%; Pred. No. 8.5e+03; Matches 19; Conservative 0; Mismatches 6; Indels C
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KRIS, RICHARD M.
APPLICANT: FELDER, STEPHEN
TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM
FILLE REFERENCE: NEOGEN-1 P4
CURRENT APPLICATION NUMBER: US/09/888,413
FRIOR APPLICATION NUMBER: US/09/888,413
FRIOR APPLICATION NUMBER: 09/337,325
FRIOR PLILNG DATE: 2001-06-26
FRIOR PLILNG DATE: 1999-06-21
FRIOR PLILNG DATE: 1999-06-21
FRIOR PLILNG DATE: 1999-06-21
FRIOR PLILNG DATE: 1999-06-21
FRIOR PLILNG DATE: 1999-06-21
FRIOR FILING DATE: 1999-06-21
FRIOR PLILNG DATE: 1998-07-02
FRIOR FILING DATE: 1998-07-02
FRIOR FILING DATE: 1999-12-19
SEQ ID NO 147
LENGTHER FRIENTING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 147
 1 CAACTCATCACCACTCTTCCATC 25
 1 CAACTCATCACCACTCTTCCATC 25
 25 CACCTCATAAGCACTCTCAACCACC 1
 25 CACCTCATAAGCACTCTCAACCACC 1
 ; Sequence 147, Application US/10865853; Publication No. US20050026193A1; GENERAL INFORMATION:
 ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 76.0°
Matches 19; Conservative
 US-10-865-853-147/c
 RESULT 20
US-10-170-097-1288
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Length 47; Indels

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US-10-719-956-691491
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 GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT PILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 5098
LENGTH: 25
 GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILER REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
 GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FITE REPRENCE: 3527,
CURRENT FILING DATE: 2003-11-20
FRIOR PILICATION NUMBER: 06/427,836
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR PILING DATE: 2002 11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
 Score 15.2; DB 24; Length 25; Pred. No. 1e+04; 0; Mismatches 3; Indels (
 Score 15.2; DB 24; Length 25; Pred. No. 1e+04;
 Indels
 le+04;
 0; Mismatches
 ; Sequence 666093, Application US/10719956
; Publication No. US20040146910A1
 Sequence 691491, Application US/10719956
Publication No. US20040146910A1
 5 TCATCACCACTCTTCCAT 24
 5 TCATCACCACTCTCCAT 24
 2 rcarcardacrererrerrerrerre
 24 rearcaccacrereacear s
 60.8%;
 60.8%;
85.0%;
Publication No. US20040146910A1
 ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-5098
 TYPE: DNA
ORGANISM: Rattus norvegicus
 TYPE: DNA
ORGANISM: Rattus norvegicus
 Best_Local Similarity 85.0
Matches 17; Conservative
 Query Match 60.8
Best Local Similarity 85.0
Matches 17; Conservative
 RESULT 23
US-10-719-956-666093
 US-10-719-956-666093
 RESULT 24
US-10-719-956-691491
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Sequence 29428, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT PAPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
 Sequence 76601, Application US/11036317
; Sequence 76601, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Williams, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TITLE OF INVENTION NUMBER: US/11/036,317
; CURRENT APPLICATION NUMBER: US 60/536,639
; PRIOR PILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOGTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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0
 Score 15.2; DB 24; Length 25; Pred. No. 1e+04;
 DB 26; Length 25;
 Length 25;
 Indels
 Indels
 Score 15.2; DB 26;
Pred. No. 1e+04;
 le+04;
 0; Mismatches
 0; Mismatches
 0; Mismatches
 Score 15.2;
Pred. No. 1e
 RESULT 27
US-10-891-260-7937
; Sequence 7937, Application US/10891260
 23
 1 TCATCAACTCTCTCTTCAAT 20
 4 CTCATGACTACTTTCTTCCA 23
 5 TCATCACCACTCTCTTCCAT 24
 5 AAGTAATCACCACTTTCTTC 24
60.8%;
 60.8%;
85.0%;
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Matches 17; Conserv
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; ORGANISM: probe
US-11-060-756-294238
 US-11-036-317-768601
 US-11-060-756-294238
 SEQ ID NO 294238
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHAITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION WHUBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
 DETECTING GENE EXPRESSION ASSOCIATED WITH
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 Publication No. US20050118625A1
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: WOUNTS, William
TITLE OF INVENTION: WUCLEIC ACID ARRAYS FOR DETECTING GENE EXI
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILLING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
 Length 25;
 Length 25;
 Length 25;
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 Score 15; DB 22; L
Pred. No. 1.2e+04;
0; Mismatches 5;
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60.0%; Score 15; DB 22;
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5;
 60.0%; Score 15; DB 22; 78.3%; Pred. No. 1.2e+04;
 0; Mismatches
 Sequence 53605, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
 1 CAACTCATCACCACTCTTTCCA 23
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 1 CAACTCATCACCACTCTTTCCA 23
 24 CATCTCATTAACACTCTGGTCCA 2
 carcicarraacacrciggrcca 1
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 53600
LENGTH: 25
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Best Local Similarity 78.3%;
Matches 18; Conservative
 SOFTWARE: PatentIn version 3.2
 Best Local Similarity 78.3
Matches 18; Conservative
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 RESULT 31
US-10-956-157-53605/c
 SEQ ID NO 53604
 SEQ ID NO 53605
LENGTH: 25
 TYPE: DNA
 TYPE: DNA
 Query Match
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 APPLICANT: Wyeth
APPLICANT: Mounts, William
TITLE OF INVENTION: HUCKLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 011896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
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 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Mateuzaki, Hajime
APPLICANT: Mei, Rui
TILE OF INVENTION: Methods of Analysis of Human Polymorphisms
FILE REFERENCE: 352.3
CURRENT APPLICATION NUMBER: US/10/891,260
CURRENT FILING DATE: 2004-07-13
PRIOR PILING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 10244
SOFTWARE: Patentin Version 3.2
LENGTH: 33
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 Length 33;
 60.0%; Score 15; DB 22; Length 25;
Llarity 78.3%; Pred. No. 1.2e+04;
Conservative 0; Mismatches 5; Indels
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 DB 24;
 Score 15.2; DB 24;
Pred. No. 1e+04;
1; Mismatches 4;
 US-10-809-189-7617

Sequence 7617, Application US/10809189

PUBLICATION NO. US20050048531A1

GENERAL INFORMATION

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
 US-10-956-157-53600/c
... Sequence 53600, Application US/10956157
... Publication No. US20050118625A1
... GENERAL INFORMATION:
 2 AACTCATCACCACTCTTCCAT 24
 AACTCATCCTGACTCTCACCCAT 25
 11 caaarckrragcrcrcrcrrcc 32
 1 CAACTCATCACCACTCTTTCC 22
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Matches 17; Conservative
 ORGANISM: Mus musculus US-10-809-189-7617
 TYPE: DNA
CORGANISM: homo sapien
US-10-891-260-7937
 Query Match
Best Local Similarity
Matches 18; Conserv
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APPLICANT: LYNGOCOTE TITLE OF INVENTIONS METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILE REFERENCE: 506612000120

CURRENT PELLING DATE: 2002-09-06

PRIOR PELLING DATE: 2001-00-29

PRIOR PELLING DATE: 2001-06-08

NUMBER: OF SEQ ID NOS: 9090

SOUTWARE: PATENTING DATE: 201-06-08

NUMBER: OF SEQ ID NOS: 9090

SOUTWARE: PATENTING DATE: 201-06-08

NUMBER: OF SEQ ID NOS: 9090

SEQ ID NO 6966

LENGTH: 50

THE CONTRACT PATENTING DATE: 201-06-08

NUMBER: OF SEQ ID NOS: 9090

SEQ ID NO 6966
 Sequence 1, Application US/10861304

Sequence 1, Application No. US20050014697A1

GENERAL INFORMATION:

APPLICANT: Stander, Jonathan S.

APPLICANT: Liu, Limin

TITLE OF INVENTION: Compositions and Methods for Modulating S-Nitrosoglutathione

TITLE OF INVENTION: Compositions and Methods for Modulating S-Nitrosoglutathione

TITLE OF INVENTION: Compositions and Methods for Modulating S-Nitrosoglutathione

TITLE OF INVENTION: Compositions and Methods for Modulating S-Nitrosoglutathione

TITLE OF INVENTION: Compositions and Methods for Modulating S-Nitrosoglutathione

TITLE OF INVENTION: Compositions and Methods for Modulating S-Nitrosoglutathione

TITLE OF INVENTION: Compositions and Methods for Modulating S-Nitrosoglutathione

TITLE OF INVENTION NUMBER: US 60/550,833

PRIOR PILING DATE: 2004-02-18

PRIOR APPLICATION NUMBER: US 60/545,965

PRIOR APPLICATION NUMBER: US 60/476,055

PRIOR APPLICATION NUMBER: US 60/476,055

PRIOR PILING DATE: 2003-06-04

NUMBER OF SEC ID NOS: 31

SEC ID NO 1

LENGTH: 21
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 Length 21;
 Score 15; DB 18; Length 50;
Pred. No. 1.3e+04;
0; Mismatches 5; Indels
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 59.2%; Score 14.8; DB 22; 88.9%; Pred. No. 1.5e+04;
 0; Mismatches
 24 AACTCATCTCGAATCTCTCAT 46
 Sequence 1372, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
 2 AACTCATCACCACTCTTCCAT 24
 OTHER INFORMATION: Oligonucleotide
 8 TCACCACTCTCTTCCATC 25
 18 rcrccacacrcrrccarc 1
 60.08;
 Query Match
Best Local Similarity 78.34
Matches 18; Conservative
 Query Match
Best Local Similarity 88.9°
Matches 16; Conservative
 TYPE: DNA
CORGANISM: Homo sapiens
US-10-131-827-6966
 ORGANISM: Artificial
 US-10-861-304-1
 TYPE: DNA
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 Sequence 6576, Application US/10131827

Sequence 6576, Application US/20140009479A1

Sequence 6576, Application NO. US20040009479A1

SENDICATION NO. US20040009479A1

APPLICANT: Wohlgemuth, Jay

APPLICANT: Woodward, Robert

APPLICANT: Woodward, Robert

APPLICANT: US NGOC

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING CONTREMY PILITE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILE REFERENCE: 506612000120

CURRENT FILING DATE: 2002-09-06

PRIOR APPLICATION NUMBER: US 60/296,764

PRIOR PPLICATION NUMBER: US 60/296,764

PRIOR PPLING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 9090

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6576
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 GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
CURRENT FILIGE S27.1
CURRENT PRILICATION NUMBER: US/10/719,956
CURRENT PILIGE DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR PILIGE DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
 Length 25;
 60.0%; Score 15; DB 18; Length 50; llarity 78.3%; Pred. No. 1.3e+04; Conservative 0; Mismatches 5; Indels
 Ouery Match 60.0%; Score 15; DB 24; Length 25
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels
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US-10-719-956-602018
; Sequence 602018, Application US/10719956
; Publication No. US20040146910A1
 3 AAATCATCAGCATTTTCTTCTT 25
 2 AACTCATCACCACTCTTCCAT 24
 Sequence 6966, Application US/10131827
Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
 2 AACTCATCACCACTCTCTTCCAT 24
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 27 AACTCATCTCGAATCTCTCAT 5
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; ORGANISM: Homo sapiens
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 Query Match
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 RESULT 33
US-10-131-827-6576/c
 US-10-131-827-6966
 RESULT 34
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Pan, James;
 APPLICANT
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 ; OTHER INFORMATION: Description of Artificial Sequence: Ag4532 Forward
US-10-072-012-1372
 - See File Wrapper or PALM.
 APPLICANT: Alsobrook 11, John F.
APPLICANT: Alsobrook 11, John F.
APPLICANT: Riegley, Denise M.
APPLICANT: Riegley, Denise M.
APPLICANT: Burgese, Catcherine E.
TILE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: 00/201-31
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-31
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-02
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PRIOR APPLICATION NUMBER: 60/267,459
PRIOR PLING DATE: 2001-02-07
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 Ouery Match 59.2%; Score 14.8; DB 19; Length 22; Best Local Similarity 88.9%; Pred. No. 1.5e+04;
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US-09-978-295A-142/C
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Sequence 142, Application US/09978295A
Fatent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
 Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
Colman, Steven D.
Wolenc, Adam R.
 Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
 Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P.
 8 TCACCACTCTCTTCCATC 25
 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
 Shimkets, Richard
 Patturajan, Meera
Zerhusen, Bryan
 16; Conservative
 Matches
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APPLICANT: Ferrar, Applicant APPLICANT: Effect, Ellan APPLICANT: Ellavacíff, Ellan APPLICANT: Geograf, Ellan APPLICANT: Geograf, Ellan APPLICANT: Geograf, Sherman APPLICANT: Geograf, Sherman APPLICANT: Geograf, Part Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colonal Colona
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R FILING DATE: 1998-04-15

R APPLICATION NUMBER: 60/082568

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R APPLICATION NUMBER: 60/08269

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R APPLICATION NUMBER: 60/082004

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082707

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082797

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082797

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082797

R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/083336

R FILING DATE: 1998-04-27

R APPLICATION NUMBER: 60/083322

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083495

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R FILING DATE: 1998-04-29
 RELING DATE: 1998-03-31

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R APPLICATION NUMBER: 60/080165

R FILING DATE: 1998-03-31

R RELING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080194

R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080327

R FILING DATE: 1998-04-01

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R FILING DATE: 1998-04-01

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R FILING DATE: 1998-04-01
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/081955
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FILING DATE: 1998-04-15
 APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/079920
 60/079923
 APPLICATION NUMBER: 60/080105
 FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
 FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081229
 APPLICATION NUMBER: 60/081838
 APPLICATION NUMBER: 60/083499
 APPLICATION NUMBER: 60/083545
 APPLICATION NUMBER: 60/083558
 APPLICATION NUMBER: 60/083554
 FILING DATE: 1998-03-30
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Gaps ö Score 14.8; DB 9; Length 24; Pred. No. 1.5e+04; 0; Mismatches 2; Indels Sequence 142, Application US/09978697
Fatent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Beterin, David
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Persara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Fivaroff, Ellen
APPLICANT: Fivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR APPLICATION NUMBER: 60/08436
PRIOR APPLICATION NUMBER: 60/084414
PRIOR PILING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-06
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 Nicholas F.
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 Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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|        | ٣   | 14.6  | 58.4       | 29              | 9  | AR526910  | AR526910 Sequence  |
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| υ      | 19  | 13.8  | 55.2       | 33              | 9  | AX787202  | AX787202 Sequence  |

| AX787209 Sequence AX78711 Sequence CQ003302 Sequence CQ003302 Sequence CQ003302 Sequence AX294559 Sequence AX29926 Sequence CQ620790 Sequence CQ620791 Sequence CQ620791 Sequence CQ620791 Sequence CQ620792 Sequence CQ620793 Sequence CQ620794 Sequence AX461855 Sequence AX461855 Sequence AX461855 Sequence AX461855 Sequence AX42169 Sequence AX42169 Sequence AX42169 Sequence AX42169 Sequence AX42169 Sequence AX42169 Sequence AX42169 Sequence AX42169 Sequence AX42169 Sequence AX42169 Sequence AX42169 Sequence AX421365 Sequence AX467369 Sequence AX467369 Sequence AX467369 Sequence AX467369 Sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | DNA linear PAT 26-JUL-1995 and Rosenzweig, A. ardiomyophathy associated                                                                                                | Length 25; 0; Indels 0; Gaps 0; linear PAT 06-MAR-2004 waeter, F.                                                                                         |
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| 33 6 AX787209 49 6 CQ848511 50 6 CQ848580 20 6 CQ848580 21 6 AX28926 22 6 AX28926 25 6 CQ620790 25 6 CQ620790 25 6 CQ620790 25 6 CQ620792 25 6 CQ620792 25 6 AR461852 25 6 AR461855 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 25 6 AR461856 | ALIGNMENTS  25 bp  25 bp  1910880  to 25) Seidman, J., Watkins, H. etecting hypertrophic c 429923-A 10 04-JUL-1995 ation/Qualifiers 25 25 25 21 Ltype="unassigned DNA" | 100.0%; Score 25; DB 6; 100.0%; Pred. No. 0.066; 110e 0; Mismatches AGATTCATGGCAC 25                                                                      |
| 133 9 8 9 12 13 13 13 13 13 13 13 13 13 13 13 13 13                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 112903 Sequence 112903 112903.1 Unknown. Unclassi 1 (base Seidman, Method f mutation Patent:                                                                           | 1 1 1 25 CQ CQQ CQQ CQQ CQQ CQQ CQQ CQQ CQQ CQQ                                                                                                           |
| 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | RESULT 1 112903 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE SOURCE                                     | Query Ma<br>Best Loc<br>Matches<br>Qy<br>Db<br>Dc CQ774405/C<br>LOCUS<br>DEFINITION<br>ACCESSION<br>VERSION<br>VERSION<br>VERSION<br>REYERENCE<br>AUTHORS |

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 AR481983.1 GI:47243890
 A83424
A83424.1 GI:6732762
 (bases 1 to 39)
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Best Local Similarity 84.2
Matches 16; Conservative
 Conservative
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Best Local Similarity
Thes 16; Conserve
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 Unknown.
 Unknown
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 DEFINITION
 ORGANISM
 DEFINITION
 SOURCE
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AUTHORS
TITLE
JOURNAL
 TITLE
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KEYWORDS
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AR481983
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A83424
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 PAT 08-OCT-2004
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 PAT 03-APR-2003
 Li,L., Ballinger,R.A., Padigaru,M., Kekuda,R., Colman,S.D., Spytek,K.A., Casman,S.J., Vernet,C.A., Shenoy,S.G., Gusev,V., Malyankar,U.M., Edinger,S., Gerlach,V., Smithson,G., Stone,D.J., Sciore,P., Macdougal,J.R., Gunther,E., Peyman,J.A., Ellerman,K., Gangolli,E.A. and Millet,I.
Gaprotein coupled receptors and nucleic acids encoding same Patent: WO 02059313-A 546 01-AUG-2002;
Curagen Corporation (US)
 Gaps
 Gaps
 Unclassified.

1 (bases 1 to 29)
Mang, W., Gish, K.C., Schall, T.J., Vicari, A. and Zlotnik, A. Antibodies that bind chemokine teck
Patent: US 6723520-A 24 20-APR-2004;
Location/Qualifiers
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 ö
 58.4%; Score 14.6; DB 6; Length 25; larity 81.0%; Pred. No. 1.8e+04; Conservative 0; Mismatches 4; Indels
 6; Length 29;
Corn root preferential promoters and uses thereof Patent: WO 2004013169-A 10 12-FEB-2004;
Bayer BioScience N.V. (BE)
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Sequence 24 from patent US 6723520.
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AUTHORS
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VERSION
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 REFERENCE
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 FEATURES
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unidentified
unidentified
unclassified.

(base 1 to 25)

Goebel, W. and Demuth, A.

USE OR A SECRETION VECTOR FOR FERTILITY CONTROL BY ORAL VACCINATION
Patent: WO 9850067-A 10 12-NOV-1998;
GOEBEL WERNER (DE); SCHERING AG (DE)
Location/Qualifiers
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 PAT 21-JAN-2000
 PAT 14-MAY-2004
 Ono, K., Ohtomo, T., Tsuchiya, M., Yoshimura, Y., Koishihara, Y. and
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84.2%; Pred. No. 2.9e+04;
iive 0; Mismatches 3;
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Reshaped human anti-HM 1.24 antibody
Patent: US 6699974-A 50 02-MAR-2004;
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A18467.1 GI:641203

DEFINITION ACCESSION VERSION

A18467

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ORGANISM

REFERENCE AUTHORS

TITLE

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PAT 07-SEP-2000
 PAT 20-FEB-2004
 1 (bases 1 to 41)
Waldmann,H., Sims,M.J. and Crowe,J.S.
Labeled humanized anti-CD18 antibodies and fragments and kits
 Crowe, J. Scott. and Lewis, A. Peter. Preparation of chimaeric antibodies using the recombinant PCR
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 mRNA
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 1 (bases 1 to 41)
Waldmann, H., Sims, M. and Crowe, S.
Humanized antibody against CD18
Patent: US 5982279-A 22 16-NOV-1999;
Location/Qualifiers
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Patent: US 6689869-A 22 10-FEB-2004;
Location/Qualifiers
 Patent: US 5858725-A 17 12-JAN-1999;
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Sequence 22 from patent US 5985279.
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AR085792
 RESULT 11
AR474145
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 PAT 29-SEP-1999
 PAT 28-OCT-1994
 PAT 04-DEC-1994
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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 PREPARATION OF CHIMAERIC ANTIBODIES USING THE RECOMBINANT PCR
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1 (bases 1'to 41)
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Patent: WO 9302191-A 22 04-FEB-1993;
Location/Qualifiers
 Patent: WO 9207075-A 35 30-APR-1992;
Location/Qualifiers

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A24273.1 GI:817928

Rattus rattus

VERSION KEYWORDS SOURCE ORGANISM

Oligonucleotide. A24273

DEFINITION ACCESSION

A24273

RESULT 8 A24273

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1 (bases 1 to 41)

REFERENCE AUTHORS

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Unknown. Unknown. Unclassified.

AR028581.1

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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RESULT 9 AR028581

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AUTHORS TITLE

REFERENCE

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RESULT 12 I03017

PAT 16-JAN-2004

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Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 Shimkets, R.A. and Leach, M.

Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

Patent: WO 014794A 7710 05-JUL-2001;

Curagen Corporation (US)

Location/Qualifiers
 Shimkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide polymorphisms and
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Patent: WO 0147944-A 1688 05-JUL-2001;
 25.7.26
/note="Nucleotide deleted between bases 25 and
Accession number cg43950029"
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Unclassified.
1 (bases 1 to 49)
1 (bases 1 to 49)
Maldmann, H., Clark, M.R., Winter, G.P. and Riechmann, L.
Antibodies to the antigen Campath-1
Patent: US 6569430-A 41 27-MAY-2003;
Location/Qualifiers
 Length 49;
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 PAT 10-SEP-1993
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 PAT 17-AUG-2003
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 l (bases 1 to 48)
Burke, R.L., Urdea, M.S. and Valenzuela, P.D.T.
Expression of glycoprotein D of herpes simplex virus
Patent: US 4618578-A 7 21-OCT-1986;
Chiron Corporation; Emeryville, CA
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Best Local Similarity
Matches 18; Conserv
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AX787202/c
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AX787209/c
LOCUS
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 BD134567 2102 Method for assaying an enzyme perticipating in conjugation with sulfuric acid in human beings, and probe and kit therefor.
 Human CHST4 gene
JP 200208567-A/17
26-MAR-2002
ASP-2000 JP 2000272229
MASUHINO NISHIMURA, HIROSHI YAGUCHI, SHINSAKU NAITO, ISAO HIRAOKA
C12N15/09, C12Q1/25, C12Q1/68, G01N21/64, G01N21/78, G01N33/53, PC
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 PAT 17-JUL-2003
 G01N33/566,
PC C12N15/00
CC Method for assaying an enzyme perticipating in conjugation with sulfuric
CC acid in human beings, and probe and kit therefor FH Key
 1 (bases 1 to 21)
Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.
Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.
Method for assaying an enzyme perticipating in conjugation with
sulfuric acid in human beings, and probe and kit therefor
Patent: JP 2020886667-A 17 26-WAR-2002;
OTSUKA PHARMACEUTICAL FACTORY INC
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Curagen Corporation (US)
 BD134567.1 GI:23229512
JP 2002085067-A/17.
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Means for improving immune response
Patent: WO 03031469-A 7 17-APR-2003;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ; Lopez,
Sonia Moreno (ES) ; Jimenez, Marcos Timon (ES)
Location/Qualifiers
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 Lopez, S.M. and Jimenez, M.T.
Means for improving immune response
Patent: WO 03031469-A 9 17-APR-2003;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ; Lopez,
Sonia Moreno (ES) ; Jimenez, Marcos Timon (ES)
Location/Qualifiers
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 Fuertes, L.L. and Jimenez, M.T. Dna-expression construct for treatment of infections with
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 PAT 17-JUL-2003
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 PAT 19-AUG-2004
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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leishmaniasis
Patent: Wo 03031470-A 6 17-APR-2003;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE)
Location/Qualifiers
 Fuertes, L.L. and Jimenez, M.T.
Dna-expression construct for treatment of infections with leishmaniasis
Patent: WO 03011470-A B 17-APR-2003;
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Location/Qualifiers
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 Quantitative multiplex detection of nucleic acids Patent: WO 2004065628-A 39 05-AUG-2004; Fu, Guoliang (GB) Location/Qualifiers
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 PAT 19-AUG-2004
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Gaps
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 Shimkets,R.A. and Leach,M.

Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
methods of use thereof
Curagen Corporation (US)
Location/Qualifiers
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches

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Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R. Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction Patent: WO 0179548-A 1688 25-0CT-2001; CORNELL RESEARCH FOUNDATION, INC. (US)
 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W.
 Myosin-like gene expressed in human heart and muscle Patent: WO 0192524-A 5529 06-DEC-2001;
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Matches 16, Conservative
 Shannon, M.E.
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 Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R. Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction Patent: WO 0179548-A 6321 25-OCT-2001; CORNELL RESEARCH FOUNDATION, INC. (US)
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 PAT 21-NOV-2001
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 PAT 08-AUG-2001
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 PAT 21-NOV-2001
 1 (bases 1 to 21)
Ballinger, D.G., Ding, W., Wagner, S. and Hess, M.A.
Chromosome 11-linked coronary heart disease susceptibility gene
 Gaps
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 Patent: US 6225451-A 104 01-MAY-2001;
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 Query Match
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 AX289926
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AX294559/c
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 RESULT 26
AR148747/c
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Location/Qualifiers
 22 GCCCAGCATCTCCATGGCAC 3
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 Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
 Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
 Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Myosin-like gene expressed in human heart and muscle Patent: WO 0192524-A 5532 06-DEC-2001; Acomica, Inc. (US)
 Myosin-like gene expressed in human heart and muscle Patent: WO 0192524-A 5530 06-DEC-2001; Acomica, Inc. (US)
 Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 5531 06-DEC-2001;
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 23 GCCCAGCATCTCCATGGCAC 4
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 Query Match
Best Local Similarity 80.0
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 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 5533 06-DEC-2001;
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 Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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Polymonication encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 5532 03-FEB-2004;
 Polymuciectide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 5531 03-FEB-2004; Location/Qualifiers
 1 (bases 1 to 25)
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
 1 (bases 1 to 25)
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
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 (bases 1 to 25) Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
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 Polymuciectide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 5529 03-FEB-2004;
 Polymucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 5530 03-FEB-2004; Location/Qualifiers
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 1 (bases 1 to 25)
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
 1 (bases 1 to 25)
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
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 PAT 20-JUN-2002
 (bases 1 to 25)

(bases 1 to 25)

(bases 1 to 25)

(c) 'Y. Ji'Y. Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shamon,M.E.

Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
Patent: US 668188-A 5334 03-FEB-2004;

Location/Qualifiers
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 668188-A 5533 03-FEB-2004; Location/Qualifiers
 Gaps
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 Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
Plant cell death system
Patent: WO 0233106-A $ 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
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 54.4%; Score 13.6; DB 6; Length 25; 80.0%; Pred. No. 6.1e+04; Live 0; Mismatches 4; Indels
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 linear
 1.43
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ProRIPBF primer"
1.19
/note="Introduced restriction sites"
 Sequence 5534 from patent US 6686188. AR461857
 DNA
 other sequences; artificial sequences.
 Sequence 5 from Patent WO0233106. AX427664
 1. .25
/organism="unknown"
/mol_type="genomic DNA"
 /mol_type="genomic DNA"
 Location/Qualifiers
 1. .25
/organism="unknown"
 6 GCCTAGCAGATTCATGGCAC 25
 6 GCCTAGCAGATTCATGGCAC 25
 20 GCCCAGCATCTCCATGGCAC 1
 AX427664.1 GI:21537783
 synthetic construct
synthetic construct
 Query Match
Best Local Similarity 80.0°
Matches 16; Conservative
 Unknown.
Unclassified.
 Unknown.
 misc_feature
 DEFINITION
ACCESSION
VERSION
 LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
 source
 RESULT 39
AR461857/c
LOCUS
 source
 ORGANISM
 ORGANISM
 JOURNAL
FEATURES
 REFERENCE
AUTHORS
 REFERENCE
AUTHORS
 JOURNAL
 RESULT 40
 JOURNAL
 KEYWORDS
 AX427664
 FEATURES
 FEATURES
 TITLE
 TITLE
 ORIGIN
 ORIGIN
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 8
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RESULT 1
 Ado59185 PCR prime
Adk70978 Corn root
Abx95944 Human CRA
Adq67857 Human CRA
 Aah47313 Mouse MCH
Aaq34493 Human ant
Aat38608 Chimaeric
Aaq12689 Rei light
Aav39382 Humanised
Aax59432 Primer us
Aax59432 Primer us
 Adr05306 Human bet
 Human G-p
Human ZPA
 Adb67035 Mouse Gal
 Primer us
PCR prime
 Aaq91130 Beta-card
 Abz01194 Human leu
 DC3 promo
 Human rea
 Aca63120 Human bet
 November 18, 2005, 05:29:23 ; Search time 172.148 Seconds (without alignments) 859.686 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 Abx95944 I
Adq67857 I
Abq76852 DG
Aad31605 Hi
 Abs59198 | Aav65080 |
 4167226
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 4390206 seqs, 2959870667 residues
 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 SUMMARIES
 Listing first 45 summaries
 - nucleic search, using sw model
 ABX95944
ADQ67857
ABQ76852
AAD31605
ABS59198
 ADR05306
 AD059185
 ADK70978
 ADB67035
 AAQ94493
AAT38608
 AAQ12689
AAV39382
 AAX59432
AAQ24659
 AAQ91130
 ACA63120
 AAV65080
 AAH47313
 Gapop 10.0 , Gapext 1.0
 geneseqn2003cs:*
 geneseqn2003ds:*
 geneseqn2001bs:*
geneseqn2002as:*
 N Geneseg 16Dec04:*
 geneseqn2000s:*
geneseqn2001as:*
 geneseqn2002bs:*
 geneseqn2003as:*
 geneseqn2003bs:*
 geneseqn2004bs:
 Minimum Match 0%
Maximum Match 100%
 geneseqn2004as
 geneseqn1980s:*
 geneseqn1990s:*
 US-10-788-779-10
25
 DB
 Query
Match Length
 IDENTITY NUC
 Copyright
 Minimum DB seq length: 0 Maximum DB seq length: 50
 Post-processing:
 Scoring table:
 Perfect score:
 Score
 OM nucleic
 Database :
 Sequence:
 Searched:
 Run on:
 Result
 Š.
 UU
 υυ
```

| 21 14.2 56.8 41 2 AAQ35184 23 14.2 56.8 50 4 AAL34502 24 14 56.0 41 12 ADH91221 25 14 56.0 47 2 AAK5256 26 14 56.0 47 2 AAK5256 27 14 56.0 50 6 AAL24480 28 13.8 55.2 21 6 ARX7035 29 13.8 55.2 22 9 ACK70180 29 13.8 55.2 22 9 ACK70180 29 13.8 55.2 33 10 ADC21315 29 13.8 55.2 33 10 ADC21315 29 13.8 55.2 33 10 ADC21316 29 13.8 55.2 33 10 ADC21316 29 13.8 55.2 33 10 ADC21316 20 39 13.6 54.4 20 6 AB194601 20 39 13.6 54.4 21 2 AAZ5629 20 41 13.6 54.4 21 2 AAZ5629 20 41 13.6 54.4 22 6 ABIN05539 21 13.6 54.4 22 6 ABIN05539 22 13.6 54.4 25 6 ABIN05539                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Aaq35184 Light cha<br>Aal34502 Human SNP<br>Adh05434 Gene poly<br>Adh91221 1-bete-me | Aax52556 Human gen<br>Aax68752 Human map<br>Aal28480 Human SNP<br>Abz05331 Human leu<br>Abk70835 PCR prime | Ack02180 Human mic<br>Adc21315 Plasmid p<br>Adc21307 Plasmid p<br>Adc21307 Plasmid p<br>Adc21305 Plasmid p<br>Adq31581 Multiplex | Aal28734 Human SNP<br>Add31582 Multiplex<br>Abi94601 Capture o<br>Aa26929 Human chr<br>Aaf95928 Human gen<br>Abi85772 Capture o<br>Abi85773 Capture o<br>Abi85773 Capture o | Human<br>Human       |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------|
| 21 14.2 56.8 41 25.0 41 25.0 41 25.0 41 25.0 41 25.0 41 25.0 41 25.0 41 25.0 41 25.0 13.8 55.2 21 33 25.2 33 13.8 55.2 23 33 13.8 55.2 23 33 13.8 55.2 23 33 13.8 55.2 25 25 25 25 25 25 25 25 25 25 25 25 25                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 44                                                                                   |                                                                                                            | ∢ '                                                                                                                              | ল<br>অ                                                                                                                                                                      | ABN05540<br>ABN05539 |
| 22 23 14.2 24.4 114.2 25.4 114.2 25.4 114.2 25.4 114.2 25.4 114.2 25.4 114.2 25.4 113.8 25.4 113.8 25.4 113.8 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 25.4 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 113.6 11 |                                                                                      |                                                                                                            |                                                                                                                                  |                                                                                                                                                                             | 25 6 25 6            |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 4.2 56.<br>14 56.<br>14 56.                                                          | ທທທທທ                                                                                                      |                                                                                                                                  |                                                                                                                                                                             | 54.                  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                      | 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                    | 2 H 21 W 44 W 1                                                                                                                  | 8 8 8 8 4 4 4<br>9 7 8 8 9 1 1 2 6                                                                                                                                          | 44                   |

## ALIGNMENTS

```
AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), associated involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing
 Non-invasive method for diagnosis of hypertrophic cardio-myopathy useful for testing asymptomatic individual(8).
 Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy; diagnosis; primer; mutation; detection; ss.
 Ä
 Beta-cardiac myosin heavy chain PCR primer B9.1R.
 Watkins H, Rosenzweig
 (GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA
 (HARD) HARVARD COLLEGE.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
 Example 1; Col 10; 22pp; English
 멾.
 92US-00989160.
 92US-00989160
 AAQ91130 standard; cDNA; 25
 (first entry)
 Seidman C,
 WPI; 1995-245715/32.
 19-FEB-1996
 11-DEC-1992;
 11-DEC-1992;
 US5429923-A.
 04-JUL-1995.
 Seidman J,
 Synthetic.
 AAQ91130;
AAQ91130
```

oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain DNA. The method is useful for detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy. This method is especially useful for diagnosing SHC and FHC, as well as for determining the estimated the life expectancy of a person with familial hypertrophic cardiomyopathy. In particular, the method is useful for determining an individual's genetic information, and diagnosing e.g. Gaucher's disease, haemophilia, buchenne's muscular dystrophy, sickle cell anaemia, Taysachs disease, phenylectonuria or cystic fibrosis. The present sequence is a PCR primer used to amplify a region of the beta cardiac myosin heavy chain gene containing an FHC-associated mutation

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Gaps

.. 0

0; Indels

0; Mismatches

100.0%;

25; Conservative

Similarity

Query Match Best Local 8

Matches

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1 GCTGAGCCTAGCAGATTCATGGCAC 25 GCTGAGCCTAGCAGATTCATGGCAC 25

ADR05306 standard; DNA; 25

ADR05306 RESULT 3

ADR05306;

21-OCT-2004 (first entry)

100.0%; Score 25; DB 9; Length 25; 100.0%; Pred. No. 0.026;

Sequence 25 BP; 6 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

```
ö
asymptomatic individuals suspected of having the disease. The method has a broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 familial hypertrophic cardiomyopathy; SHC; Gaucher's disease; sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia; buchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease; phenylketonuria; cystic fibrosis.
 Gaps
 ;
0
 Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
 Length 25;
 0; Indels
 Human beta cardiac myosin heavy chain PCR primer B9.1R.
 Sequence 25 BP; 6 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
 Rosenzweig A;
 , DB 2;
. 0.026;
 anaemia, Tay-Sachs disease and phenylketonuria
 Mismatches
 Score 25;
Pred. No.
 25
 GCTGAGCCTAGCAGATTCATGGCAC 25
 Watkins H,
 1 GCTGAGCCTAGCAGATTCATGGCAC
 .;
0
 100.0%;
 ACA63120 standard; DNA; 25 BP.
 92US-00989160.
 95US-00469172.
 (first entry)
 25; Conservative
 Seidman C, Seidman J,
 ROSENZWEIG A.
 Similarity
 SEIDMAN C. SEIDMAN J.
 US2003054343-A1.
 WATKINS
 06-JUN-1995;
 11-DEC-1992;
 28-AUG-2003
 20-MAR-2003
 ACA63120;
 Query Match
Best Local 8
 (SEID/)
 ROSE/)
 WATK/)
 Homo
 Matches
 RESULT 2
 ACA63120
 888888
 8
 g
```

Human beta cardiac myosin heavy chain mutation detection primer B9.1R.

Human, beta cardiac myosin, heavy chain, PCR; primer, ss, FHC, SHC, familial hypertrophic cardiomyopathy, sporadic hypertrophic cardiomyopathy.

27-FEB-2004; 2004US-00788779.

US2004152121-A1.

05-AUG-2004.

Homo sapiens

92US-00989160. 95US-00469172.

11-DEC-1992;

06-JUN-1995;

```
Detecting mutations associated with hypertrophic cardiomyopathy to diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac myosin heavy-chain DNA and detecting the mutation in the amplified
 The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (familial or sporadic, FHC, SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy, comprising amplifying beta-cardiac myosin heavy-chain DNA forming an amplified product, and detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy in the amplified product, thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also included are a set of DNA oligomolectide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two oligomucleotides
 Watkins H, Rosenzweig A;
 Claim 18; SEQ ID NO 10; 22pp; English.
 Seidman J,
 ROSENZWEIG A.
 WPI; 2004-592586/57
 SEIDMAN C.
SEIDMAN J.
 WATKINS
 Seidman C,
 product.
 (SEID/)
 (ROSE/)
 (SEID/
 WATK/
```

The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (sporadic or familial, SHC and FHC) comprises detecting a mutation associated with hypertrophic cardiomyopathy in an amplified product of a beta cardiac myosin heavy chain DNA. The mutations associated with SHC/FHC are detected in the myosin gene isolated from blood, by detecting mis-matched areas in RNA-DNA hybrid double strands (RNA from the normal gene, DNA from the suspect determine life expectancy in affected individuals e.g. using a Kaplan-Meier curve for the classified type of FHC causing point mutation. Also included are an RNA probe comprising ribonucleotides arranged in a sequence which is complementary to at least a portion of beta-cardiac myosin heavy-chain DNA and a set of DNA oligonucleotide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or hemophilia, by detecting a mutation in an amplified product of a beta cardiac myosin heavy-chain DNA.

Example 1; Page 5; 22pp; English.

a presence or absence of a mutation associated with

WPI; 2003-512374/48.

Detecting

Claim 1; Page 362; Opp; English.

```
which amplify beta-cardiac myosin heavy-chain DNA (the set of oligonucleotide primers being useful for facilitating the diagnosis of hypertrophic cardiomyopathy by being capable of detecting a hypertrophic cardiomyopathy kit for facilitating the diagnosis of hypertrophic cardiomyopathy (comprising a first container and an RNA probe completely hybridisable to the beta-cardiac myosin heavy chain DNA, where the RNA probe is capable of detecting a hypertrophic cardiomyopathy associated mutation, a second container by pertrophic cardiomyopathy-associated mutation in a second container or absence of a hypertrophic cardiomyopathy-associated mutation in container or absence of a hypertrophic cardiomyopathy-associated mutation in appertrophic cardiomyopathy for facilitating the diagnosis of individuals hypertrophic cardiomyopathy relies on the presence of the formal propertrophic cardiomyopathy relies on the presence of typical clinical symptoms and the demonstration of unexplained ventricular cardiomyopathy that the diagnosis of individuals by hypertrophy. The present invention is non-invasive and based, at least in contained ships which established that there are no extensive studies involving a large number of familiar mutations in the beta cardiac myosin heavy-chain gene. Prior and consider who may contain and demonstration and the diagnosis of familiar mutations in the beta cardiac myosin heavy-chain gene. Prior are reveals that there are no extensive studies involving a large number of caused by nother mutations in the beta cardiac myosin heavy-chain gene. Prior and
 ö
 caused by point mutations in the beta cardiac myosin heavy-chain gene. The present sequence is a PCR primer used to amplify a region of the beta
 17; leukocyte; gene expression profiling; allograft rejection;
atherosclerosis; congestive heart failure; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 Gaps
 cardiac myosin heavy chain having a disease-related point mutation.
 ö
 Human leukocyte gene expression profiling probe SEQ ID NO 1185.
 / Match 100.0%; Score 25; DB 13; Length 25; Local Similarity 100.0%; Pred. No. 0.026; nes 25; Conservative 0; Mismatches 0; Indels
 Sequence 25 BP; 6 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 GCTGAGCCTAGCAGATTCATGGCAC 25
 ABZ01194 standard; DNA; 50
 (first entry)
 WO200257414-A2.
 Homo sapiens.
 09-JAN-2003
 25-JUL-2002.
 ABZ01194;
 Query Match
 Matches
 ABZ01194
 8
 셤
```

New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.

Prentice J, Phillips J;

Wohlgemuth J, Fry K, Matcuk G, Altman P, P) Ly N, Woodward R, Quertermous T, Johnson F;

WPI; 2002-636525/68.

(BIOC-) BIOCARDIA INC

22-OCT-2001; 2001WO-US047856. 20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P.

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ö
 This invention relates to a novel melanin-concentrating hormone receptor protein antagonist, a heterocyclic ring derivative or a salt thereof. Specifically, it refers to the development of a drug that contains this nitrogen-containing heterocyclic ring as the main skeleton of the antagonist compound, that works as the active ingredient. The present invention describes this antagonist as a melanin-concentrating hormone receptor inhibitor that exhibits anorectic activities and as such can be used to treat and/ or prevent obesity. This oligonucleotide sequence is a PCR primer used in an exemplification of the invention.
 The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 Gaps
 pharmaceuticals for preventing obesity, contains heterocyclic ring derivative or its salt as active ingredient.
 human; SLC-1; primer; ss; melanin-concentrating hormone receptor; antagonist; heterocyclic ring; anorectic; obesity; PCR.
 ;
 Melanin concentrating hormone receptor antagonist useful in
 60.0%; Score 15; DB 6; Length 50; 78.3%; Pred. No. 2.3e+03; ive 0; Mismatches 5; Indels
 Ē
 Iwasaki
 Sequence 50 BP; 21 A; 9 C; 11 G; 9 T; 0 U; 0 Other;
 PCR primer used to amplify human SLC-1 DNA SeqID 7.
 Kamikubo T,
 Example 359; SEQ ID NO 7; 155pp; Japanese.
 3 TGAGCCTAGCAGATTCATGGCAC 25
 14 TGAGCCGAGCAGTTACAAGACAC 36
 Hayashibe S, I
a Y, Kurama T;
 (YAMA) YAMANOUCHI PHARM CO LTD
 ADO59185 standard; DNA; 37 BP.
 14-NOV-2003; 2003WO-JP014534.
 15-NOV-2002; 2002JP-00332950.
 26-AUG-2004 (first entry)
 18; Conservative
 Kimura Y,
 WPI; 2004-440938/41.
 Local Similarity
 Kondoh Y,
 WO2004046110-A1
 Homo sapiens.
 Matsumoto S,
 03-JUN-2004.
 ADO59185;
 Query Match
 Kaku H,
 Matches
 ADO59185/
 RESULT 5
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Matches

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The invention relates to nucleic acids encoding the chemokines TECK, MIP-3beta, DC CR and MDC CR. The polypeptide sequences are useful in isolating DNA clones encoding the chemokines, for generating antibodies, and for predicting oligonuclectides for screening a library to isolate species variants. A nucleic acid encoding a chemokine polypeptide can be used to identify genes, mRNA and cDNA species which encode related or homologous ligands, as well as DNA encoding homologous proteins from different species. The chemokines and antibodies which bind to the polypeptides are useful in the treatment of conditions associated with abnormal physiology or development, including inflammatory conditions such as asthma, abnormal proliferation, regeneration, adegeneration and arrophy. This sequence receptor of activated monocytes (CRAM) polypeptide, used in the scope of the invention
 Human; PCR; ss; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma; monocyte/dendritic cell receptor for chemokine; inflammatory condition; abnormal physiology; abnormal proliferation; degeneration; atrophy; antilasthmatic; cytostatic; primer; CRAM; chemokine receptor of activated monocytes.
 New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions (e.g. asthma), and
 Zlotnik A;
 Sequence 29 BP; 11 A; 8 C; 8 G; 2 T; 0 U; 0 Other;
 58.4%; Score 14.6; DB 10;
81.0%; Pred. No. 3.3e+03;
 0; Mismatches
 Vicari A,
 5 AGCCTAGCAGATTCATGGCAC 25
 AGCAGAGCAGAGTGATGGCAC 28
 Example; Page 32; 54pp; English.
 96US-0021664P.
96US-0028329P.
97US-0048593P.
97US-00887977.
 Human CRAM cDNA PCR primer #3.
 Gish KC, Schall TJ,
 03-JAN-2002; 2002US-00039659
 ADQ67857 standard; DNA; 29
 (first entry)
 07-OCT-2004 (first entry)
 Conservative
 abnormal proliferation.
 (SCHE) SCHERING CORP
 WPI; 2003-416900/39.
 Query Match
Best Local Similarity
Matches 17; Conserv
 US2003018167-A1.
 11-OCT-1996;
04-JUN-1997;
03-JUL-1997;
 05-JUL-1996;
 23-JUL-2003
 23-JAN-2003
 ABX95944;
 ADQ67857;
 Wang W,
 RESULT 8
 ADQ67857
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 The invention relates to a corn root preferential promoter fragment. The corn root preferential promoter is useful for the preferential expression of a biologically active RNA in roots of a plant, wherein the plant is a corn plant. The biologically active RNA encodes a protein of interest, which when expressed in the calls of a plant confers pest or pathogen resistance to the plant, wherein the protein is ISPAl or ISPA2 from Brevibeaillus laterosporus. An isolated DNA molecule encoding a GL4 or GL5 protein is useful for the isolation of a corn root preferential promoter region. SequencesADK70975-ADK70978 represent PCR primers for isolating corn root preferential GL5 promoter fragment.
 New corn root preferential promoters useful for the preferential and/or selective expression of a biologically active RNA in roots of a plant,
 Gaps
 Gaps
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0
 ch 59.2%; Score 14.8; DB 12; Length 37; 1. Similarity 80.0%; Pred. No. 2.8e+03; 16; Conservative 1; Mismatches 3; Indels (
 58.4%; Score 14.6; DB 12; Length 25; 81.0%; Pred. No. 3.3e+03; ive 0; Mismatches 4; Indels (
 GL4; GL5; corn; root preferential promoter; pest resistance; pathogen resistance; plant; ISPA1; ISPA2; PCR; primer; ss.
 Corn root preferential GL5 promoter amplifying primer GVK30.
Sequence 37 BP; 7 A; 10 C; 11 G; 8 T; 0 U; 1 Other;
 Sequence 25 BP; 5 A; 8 C; 5 G; 7 T; 0 U; 0 Other;
 Meulewaeter F;
 Claim 1; SEQ ID NO 10; 76pp; English.
 4 GAGCCTAGCAGATTCATGGCA 24
 4 GAGCCTAGCAGATTCATGGC 23
 GAGCATAGTCGATCCATGGCA 3
 ABX95944 standard; cDNA; 29 BP
 Vanderkimpen G, Van Eldik G,
 ADK70978 standard; DNA; 25 BP
 28-JUL-2003; 2003WO-EP008367
 31-JUL-2002; 2002US-0399383P.
 (FARB) BAYER BIOSCIENCE NV.
 (first entry)
 17; Conservative
 preferably a corn plant
 WPI; 2004-157099/15.
 Best Local Similarity
 Best Local Similarity
 WO2004013169-A1.
 06-MAY-2004
 12-FEB-2004
 Zea mays.
Synthetic.
 ADK70978;
 Query Match
 Query Match
 RESULT 6
ADK70978/c
```

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Gaps

. 0

Matches

RESULT 7
ABX95944
ID ABX9
XX

Length 29; Indels Promoter; expression cassette; structural gene; plant; transgenic; linseed; fatty acid ester; polyunsaturated fatty acid; pUFA; cosmetic; animal nutrition; human nutrition; pharmaceutical; cholesterol; blood; heart disease; seed specific; PCR; primer; ss.

DC3 promoter associated oligonucleotide DC3a #4

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%XCCCCCCCCCCCCCX8X414X8X1X28X412X8X8X8X8X8X8X8X8X8X8X8
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 The invention relates to a substantially pure or isolated polypeptide comprises the mature protein of human TECK (thymus expressed chemokine) whose full larght sequence appears as ADOG7837. Also included are an isolated or recombinant nucleic acid encoding mature TECK, an expression vector comprising the nucleic acid, a host cell comprising the expression vector and a method for producing the polypeptide. Also disclosed are the mouse TECK CDNA and protein, human chemokines MIP-3alpha and MIP-3beta (and their encoding CDNAs), and the CDNAs and encoded proteins (and their encoding CDNAs), and the CDNAs and encoded proteins (corresponding to human chemokine receptors DCCR (dendritic cell receptor for chemokine) and M/DCCR (Monocyte/dendritic cell receptor for chemokine). The polypeptide is useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions, e.g. asthma. An experiment was performed analysing the expression of human CRAM (not defined, unclear what its relation to TECK is). The present sequence is a reverse transcriptase (RT)-PCR primer used
 Human; 88; PCR; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; chemokine receptor; DCCR; dendritic cell receptor for chemokine; M/DCCR; Monocyte/dendritic cell receptor for chemokine; M/DCCR; development; inflammatory condition; asthma; RT-PCR; reverse transcriptase PCR; primer; CRAM.
 New substantially pure or isolated Thymus Expressed Chemokine (TECK) useful for treating conditions associated with abnormal physiology o
 development, including inflammatory conditions, e.g. asthma
 Vicari A, Zlotnik A;
 Sequence 29 BP; 11 A; 8 C; 8 G; 2 T; 0 U; 0 Other;
 Example 6; SEQ ID NO 24; 54pp; English
CRAM RT-PCR primer for exon 3,
 Schall TJ,
 96US-0021664P.
96US-0028329P.
97US-0048593P.
97US-00887977.
 2004US-00754071
 03-JAN-2002; 2002US-00039659
 in the above analysis.
 WANG W.
GISH K C.
SCHALL T J.
VICARI A.
 WPI; 2004-533376/51.
 ZLOTNIK A.
 Gish KC,
 US2004137578-A1.
 09-JAN-2004;
 05-JUL-1996;
11-OCT-1996;
 03-JUL-1997;
 04-JUN-1997;
 15-JUL-2004
 (GISH/) (SCHA/) (VICA/) (VICA/) (ZLOT/) (
 Wang W,
 WANG/)
 Mus sp.
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transgenic

New expression cassette for plant genes, useful for preparing transg plants that have increased production of polyunsaturated fatty acids

Example 13; Page 40; 188pp; German.

Drexler H, Scheffler J;

m

Bischoff F, Heinz

Lerchl J, Duwenig E, WPI; 2002-675961/73.

19-JAN-2001; 2001DE-01002338. 19-JAN-2001; 2001DE-01002338. (BADI ) BASF PLANT SCI GMBH.

DE10102338-A1

Synthetic.

25-JUL-2002.

```
This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SG) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites.

The EC has the structure (L1-P-SG-12) n where L1 = is a polylinker (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker sequences reproduced (ABQ7699-ABQ76801) or equivalent RE-site-containing sequences and n = 1-3. The invention discloses a vector containing this EC, an organism containing the EC or the vector and a transgenic plant containing a (non-) functional nucleic acid in the vector. Transgenic plants e.g linesed can be prepared with improved production of fatty acid esters with an increased content of polyunsaturated fatty acids (BURA), useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. protect against heart disease. The expression cassettes of the invention provide increased and more efficient production of fine chemicals
 ;
0
 Human, reaper protein, Rpr, detection, purification, screening, therapy, tumour, cytostatic, open reading frame, ORF, PCR primer, ss.
 (especially PUFA), including seed-specific production. This sequence represents a PCR primer used to illustrate the method of the invention
 Gaps
 ..
 57.6%; Score 14.4; DB 6; Length 29; 75.0%; Pred. No. 4.2e+03; ive 0; Mismatches 6; Indels
 Sequence 29 BP; 4 A; 7 C; 8 G; 10 T; 0 U; 0 Other;
 Human reaper (hRpr) ORF amplifying primer, Fwd13.
 24
 25
 1 GCTGAGCCTAGCAGATTCATGGCA
 2 GCGGATCCTAGCTTTTTCTTGGCA
 AAD31605 standard; DNA; 33
 Query Match
Best Local Similarity 75.0°
Matches 18; Conservative
 18-JUN-2002 (first entry)
 Homo sapiens
 AAD31605;
 AAD31605/c
ID AAD31
 RESULT 10
```

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Gaps

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Query Match 58.4%; Score 14.6; DB 12; Length 29; Best Local Similarity 81.0%; Pred. No. 3.3e+03; Matches 17; Conservative 0; Mismatches 4; Indels

5 AGCCTAGCAGATTCATGGCAC 25 

ВР

ABQ76852 standard; DNA; 29

RESULT 9 ABQ76852

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8

25-MAR-2003 (first entry)

ABQ76852;

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us-10-788-779-10.rng

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Homo sapiens
 05-FEB-1999
 Peyman JA,
 in humans.
 Gerlach V,
 Synthetic
 ო
 AAV65080;
 Query Match
 Matches
 RESULT 12
 AAV65080
8
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 Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis; diabetes; cell signal processing; metabolic pathway modulation; cancer; adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma; immune response; neurodegenerative disorder; inflammatory disorder; Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;
 The invention relates to human homologue of Drosophila melanogaster Reaper protein (hRpr) and its corresponding nucleic acid. The hRpr polypeptides are useful for generating antibodies, which can be used in detection or purification protocools designed to detect or purify the polypeptide to which the antibody is directed. These sequences are also used for screening compounds, which can enhance or inhibit hRpr and for treating tumours. The hRpr polynucleotides are useful as a probe or primer. The present sequence is a PCR primer used to amplify human hRpr open reading frame (ORF)
 New human homologue of Drosophila melanogaster reaper protein (hRpr), useful for generating antibodies and for screening compounds, which can inhibit or enhance hRpr activity.
 Gaps
 ;
0
 Human G-protein coupled receptor, forward primer #116.
 Sequence 33 BP; 4 A; 12 C; 11 G; 6 T; 0 U; 0 Other;
 1 GCTGAGCCTAGCAGATTCATGGCA 24
 32 GCTGGGCCACGCAGCACCATGGCA 9
 Example 1; Page 24; 45pp; English.
 2000US-025743P.
2001US-0259743P.
2001US-0260718P.
2001US-0261498P.
2001US-0263489P.
 BP
 08-AUG-2001; 2001WO-US024765.
 2000US-0256635P
 08-AUG-2000; 2000US-0223699P
 18-DEC-2001; 2001WO-US049394
 ABS59198 standard; DNA; 22
 (first entry)
 ပဲ
 Kornbluth SA, Holley
 WPI; 2002-241769/29.
 Best Local Similarity
Matches 18; Conserv
 (UYDU-) UNIV DUKE.
 primer; PCR; ss
WO200212540-A2
 WO200259313-A2
 21-DEC-2000;
04-JAN-2001;
10-JAN-2001;
 12-JAN-2001; 24-JAN-2001; 308-FEB-2001;
 Homo sapiens.
 18-DEC-2000;
 05-NOV-2002
 01-AUG-2002
 ABS59198;
 Query Match
 ABS59198/c
```

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The invention relates to novel isolated G-protein coupled receptor (GPCR) polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid and antibody are useful for treating, preventing or alleviating a GPCR-associated disorder or a pathological state in a subject, particularly a channer. In particular, the disorder is cardiomyopathy, atherosclerosis, adiabetes, or a disorder related to cell signal processing and metabolic pathway modulation. The GPCR polypeptide and nucleic acid are also useful or diagnosing the presence of or predisposition to a disease associated with altered levels of GPCR, polypeptide and nucleic acid are also useful on polypeptide are especially useful in therapeutic or prophylactic applications for disorders associated with aberrant GPCR expression or creating the above conditions. Furthermore, the nucleic acids and polypeptides are useful in treating adenocarcinoma lymphoma, prostate cancer, uterus cancer, immune response, neurodespenerative disorders, asthma, inflammatory disorders. Crohn's disease, multiple sclerosis or horight hereditary osteodystrophy. These are also useful in developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. ABSS9431 represent human GPCR coding sequences, primers and probes of the invention
 ū
 digaru M, Kekuda R, Colman SD, Spytek KA;
Shenoy SG, Gusev V, Malyankar UM, Edinger S;
Stone DJ, Sciore P, Macdougall JR, Gunther E,
Gangolli EA, Millet I;
 New G protein coupled receptor polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing cardiomyopathy, atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
 ZPA; human; vector; expression; secretion; fertility control antigen; attenuated Salmonella; Gram-negative; oral vaccine; haemolysin operon; hly specific promoter; hlyR enhancer-like regulator; contraception;
 Gaps
 ..
0
 DB 6; Length 22;
 3; Indels
 Sequence 22 BP; 7 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 56.8%; Score 14.2; DB 6
84.2%; Pred. No. 5e+03;
Live 0; Mismatches
 Claim 1; Page 617; 685pp; English.
 Padigaru M,
 21
 Human ZPA PCR primer huZPA5 #2.
14-MAR-2001; 2001US-0275946P.
23-MAR-2001; 2001US-0278150P.
18-ARR-2001; 2001US-0284591P.
23-ARR-2001; 2001US-0285718P.
19-UIN-2001; 2001US-0299377P.
16-AUG-2001; 2001US-0312902P.
 21 TGGTCCTACCAGATTCATG 3
 ВР
 TGAGCCTAGCAGATTCATG
 AAV65080 standard; DNA; 25
 (first entry)
 Local Similarity 84.3
 Li L, Ballinger RA, Pa
Casman SJ, Vernet CAM,
 Smithson G,
Ellerman K,
 (CURA-) CURAGEN CORP.
 WPI; 2002-599789/64.
 hly specific pro-
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Mus
 RESULT 14
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 AAV65071-V65104 are PCR primers used in the construction of a novel vector for expression and secretion of a fertility control antigen in attenuated salmonella or other attenuated Gram-negative vaccine strains
 to produce an oral vaccine. The vector comprises a gene encoding the fertility control antigen under the control of a complete haemolysin operon, including the hly specific promoter and the hlyR enhancer-like regulator but excluding most of the hlyA gene. The vector is used for immunological contraception by oral administration
 Oral contraceptive vaccine containing recombinant salmonella -
transformed with vector containing gene for fertility control antigen.
 Gaps
 Cytostatic, Anorectic, Antidiabetic, Nootropic, Neuroprotective, Gynaecological; mouse, Galanin-like Peptide; GALP; prostate cancer; ovarian cancer; gynaecological disorder; diabetes; dementia;
 Kaufmann S;
 ö
 25;
 Mouse Galanin-like Peptide, GALP, primer mG-300R, SEQ ID 3.
 3; Indels
 Length
 Hess J,
 Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;
 Score 14.2; DB 2;
Pred. No. 5.1e+03;
 Gentschev I,
 0; Mismatches
 Ohtaki T;
 Disclosure; Page 6; 17pp; German.
 Demuth A,
 GCCTAGAGGATGCATGGCA 19
 6 GCCTAGCAGATTCATGGCA 24
 BP
 97DE-01020761.
 56.8%;
 22-FEB-2002; 2002JP-00047006.
24-APR-2002; 2002JP-00123170.
 97DE-01020761
 20-FEB-2003; 2003WO-JP001856.
 disorder; primer; ss
 (TAKE) TAKEDA CHEM IND LID
 ADB67035/c
ID ADB67035 standard; DNA; 28
 (first entry)
 16; Conservative
 Kobayashi H,
 Goebel W,
 SCHERING AG.
 WPI; 1998-596140/51
 WPI; 2003-671814/63
 Query Match
Best Local Similarity
 WO2003070950-A1.
 DE19720761-A1
 07-MAY-1997;
 07-MAY-1997;
 04-DEC-2003
 12-NOV-1998.
 28-AUG-2003
 Kumano S,
 Donner P,
 ADB67035;
 (SCHD)
 Mus sp.
 eating
 Best Loca
Matches
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Novel DNA for constructing knockout animals applicable in clarifying

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The invention provides melanin concentrating hormone (MCH) receptor (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise MCHR polypeptide regions from different species. The MCHR fusion protein comprise MCHR polypeptide region a fluorescent polypeptide region joined directly, or via a linker, to the carboxy side of the MCHR polypeptide region. The MCHR fusion proteins can be expressed by standard recombinant methodology. MCH action promotes feeding (orexigenic) and up regulation of MCH activity stimulates food intake. Sequences AAH7313-14 represent PCR primers for amplifying mouse MCHIR cDNA, used in the construction of mouse MCHIR-linker-green fluorescent protein (GFP)
 constructing
 sequences (ADB67033-ADB67032). The sequences are useful for constructin knockout animals which are useful in clarifying the physiological function of GALP and in screening preventives or remedies for diseases due to hypo- or hyporescretion of LH, e.g. prostate cancer, ovarian cancer, gynaecological disorders, diabetes, dementia and eating disorders, e.g. obesity and other disorders. The present sequence is a primer for mouse GALP, which was used in an example from the invention.
 Gaps
 Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion; fluorescent polypeptide; orexigenic; anabolic; food intake; MCH1R; green fluorescent protein; GFP; PCR primer; ss.
 ဌ
 Fusion proteins comprising melanin concentrating hormone receptor peptides and fluorescent proteins, useful for identifying appetite stimulants.
 The present invention relates to mouse Galanin-like Peptide (GALP)
 and
 ;
 membrane transporter
 56.8%; Score 14.2; DB 10; Length 28; 84.2%; Pred. No. 5.2e+03; ive 0; Mismatches 3; Indels
 screening preventives or remedies for diseases, e.g. cancer
 Mouse MCH1R cDNA amplifying primer MCH1R (Eco RI).
 Sequence 28 BP; 5 A; 7 C; 9 G; 7 T; 0 U; 0 Other;
 galactose
 Example 1; Page 36; 118pp; Japanese.
 Example 2; Page 33; 71pp; English.
 1 GCTGAGCCTAGCAGATTCA 19
 22 GCTGAGCCTGGCAGAACA 4
physiological function of the
 뮵
 14-MAR-2001; 2001WO-US008071.
 15-MAR-2000; 2000US-0189698P.
 AAH47313 standard; DNA; 29
 (first entry)
 variant fusion constructs
 Conservative
 (MERI) MERCK & CO INC
 WPI; 2001-565791/63.
 Local Similarity
les 16; Conserv
 WO200168706-A1.
 30-NOV-2001
 20-SEP-2001
 Marsh DJ;
 AAH47313;
 Query Match
 Best Loc
Matches
 AAH47313/c
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The present sequence is a primer for the chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. was prepd, and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded FV region. The reshaped FV region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
Murine, human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; PCR; low human antigenicity; diagnosis; treatment; cerebral tumour; reshaped; primer; polymerase chain reaction;
 Monoclonal antibody; complementarity determining region; CDR; integrin;
hybridoma 184; protein RBI; Ig; ss.
 Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma.
 56.8%; Score 14.2; DB 2; Length 38; 84.2%; Pred. No. 5.5e+03; rative 0; Mismatches 3; Indels
 Sequence 38 BP; 8 A; 9 C; 12 G; 9 T; 0 U; 0 Other;
 Rei light chain variable region primer #R4.
 Example 5; Page 23; 45pp; Japanese.
 1 GCTGAGCCTAGCAGATTCA 19
 34
 94JP-00252166.
 94JP-00285057.
 93JP-00291078
 90US-00467700.
 91EP-00300362
 (CHUS) CHUGAI PHARM CO LID.
 AAQ12689 standard; DNA; 39
 01-OCT-1991 (first entry)
 Local Similarity 84.2
nes 16; Conservative
 WPI; 1996-358509/36.
 JP08169900-A.
 19-NOV-1993;
 18-OCT-1994;
 17-JAN-1991;
 19-JAN-1990;
20-DEC-1990;
 02-JUL-1996
 24-JUL-1991
 EP438310-A.
 Synthetic.
 Synthetic.
 16
 AAQ12689;
 Query Match
 Matches
 RESULT 17
 AAQ12689
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 AAQ94492-Q94497 are human antibody ONS-M21 CDR PCR primers. The cDNA encoding the CDRs was used in the construction of an expression vector, contg. -CDNA encoding a human/murine chimeric antibody, reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease
 Reconstituted antibody against human medullo:blastoma cells - contains high proportion of human antibody origin and has low antigenicity.
 Gaps
 Gaps
 Human, ONS-M21 antibody; chimeric protein; CDR; medulloblastoma;
brain tumour; treatment; diagnosis; PCR primer C;
complementarity determining region; ss.
 ö
 ö
 56.8%; Score 14.2; DB 4; Length 29;
larity 84.2%; Pred. No. 5.2e+03;
Conservative 0; Mismatches 3; Indels
 56.8%; Score 14.2; DB 2; Length 38; 84.2%; Pred. No. 5.5e+03;
 3; Indels
 Sequence 38 BP; 8 A; 9 C; 12 G; 9 T; 0 U; 0 Other;
Sequence 29 BP; 7 A; 9 C; 7 G; 6 T; 0 U; 0 Other;
 Chimaeric human/murine MAb ONS-M21 PCR primer D.
 0; Mismatches
 Human antibody ONS-M21 CDR PCR primer C.
 Example 5; Page 62; 120pp; Japanese.
 4 GAGCCTAGCAGATTCATGG 22
 1 GCTGAGCCTAGCAGATTCA 19
 28 dadecirrecadarccarde 10
 16 GGTGTGCCAAGCAGATTCA 34
 Ohtomo T, Sato K, Tsuchiya M;
 AAQ94493 standard; DNA; 38 BP
 AAT38608 standard; DNA; 38 BP.
 94WO-JP001763
 93JP-00291078
 (first entry)
 (first entry)
 (CHUS) CHUGAI SEIYAKU KK.
 16; Conservative
 WPI; 1995-200347/26.
 Query Match
Best Local Similarity
Matches 16; Conser
 Local Similarity
 WO9514041-A1
 19-OCT-1994;
 19-NOV-1993;
 09-DEC-1996
 16-JAN-1996
 26-MAY-1995
 Synthetic.
 AAQ94493;
 Query Match
 Matches
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AAT38608

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Gaps

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The specification describes a reconstituted human antibody recognizing the peptide antigen HM1.24. This human antibody contains natural human tramework regions modified by amino acid substitutions to provide homogeneity with a previously designed framework region (which may arise from a human or non-human source); and complementary determining regions (CDR) derived from a non-human anti-HM1.24 antibody. The reconstituted antibody is useful in the treatment of diseases in which the surface antigen HM1.24 is implicated such as myeloma. The present sequence is used in the creation of the antibodies of the invention
of the H chain V region are derived from human subtype HSG1 (e.g. FR1-3 from human antibody HG3 and FR4 from human antibody JH6). The present sequence represents a PCR primer used in an example from the present invention. The antibodies are used for the treatment of myeloma, especially by injection, intravenously, intramuscularly or subcuteneously. The antibodies are used at 0.01-1000 (especially 5-100) mg/Kg body weight. The humanised antibody has low antigenicity and is therefore effective therapeutically in humans
 Reconstituted human antibody; peptide antigen HMI.24; framework region; complementary determining region; CDR; anti-HMI.24 antibody; myeloma; humanised antibody; primer; ss.
 Reconstituted human antibody useful in the treatment of myeloma
 Primer used in construction of humanised anti-HM1.24 antibody
 56.8%; Score 14.2; DB 2; Length 39;
84.2%; Pred. No. 5.5e+03;
tive 0; Mismatches 3; Indels
 56.8%; Score 14.2; DB 2; Length 39; larity 84.2%; Pred. No. 5.5e+03; Conservative 0; Mismatches 3; Indels
 Sequence 39 BP; 10 A; 12 C; 10 G; 7 T; 0 U; 0 Other;
 Sequence 39 BP; 10 A; 12 C; 10 G; 7 T; 0 U; 0 Other;
 Disclosure; Page 114; 256pp; Japanese.
 1 GCTGAGCCTAGCAGATTCA 19
 19 derereceadedarrea 37
 1 GCTGAGCCTAGCAGATTCA 19
 19 GGTGTGCCAAGCAGATTCA 37
 98WO-JP004469
 97JP-00271726
 AAX59432 standard; DNA; 39
 16-JUL-1999 (first entry)
 Ouery Match
Best Local Similarity 84.2°
Matches 16; Conservative
 (CHUS) CHUGAI SEIYAKU KK
 WPI; 1999-277273/23.
 Best_Local Similarity
Matches 16; Conserv
 03-OCT-1997;
 02-OCT-1998;
 WO9918212-A1
 15-APR-1999.
 Tsuchiya M;
 Synthetic.
 AAX59432;
 Query Match
 RESULT 19
 AAX59432
 8888888888
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0
 A humanised anti-HM1.24 antibody has been developed which comprises human L and H Chain C regions, and L and/or H chain V regions containing material originating in mouse anti-HM1.24 antibody. The V regions contain framework (FR) regions of human origin and complimentarity determining regions (CDR) of mouse origin, leading to a reshaped humanised antibody. The C regions are human Ck (L-chain) and human C gamma (especially C gamma 1) (H-chain). The RR regions of the L chain V region are derived from human subtype HSG1 (e.g. from human antibody RE1) and the FR regions
 The sequences in AAQ12685-Q12692 are primers for PCR mutagenesis and amplification of the Rei light chain variable region texmplate so as to graft the CDRs of murine 1B4 into the Rei light chain variable region.
 Kosaka M;
 of humanised recombinant immunoglobulin - including polymerase reaction amplification of murine antibody light and heavy chain
 Gaps
 Mouse; human; humanised; anti-HM1.24 antibody; myeloma; FR; CDR; framework region; complimentarity determining region; antigenicity;
 .;
0
 Koishihara Y,
 56.8%; Score 14.2; DB 2; Length 39;
84.2%; Pred. No. 5.5e+03;
ive 0; Mismatches 3; Indels
 Humanised anti-HM1.24 antibody - for treatment of myeloma
 Humanised anti-HM1.24 antibody PCR primer SEQ ID NO:50.
 Sequence 39 BP; 11 A; 11 C; 9 G; 8 T; 0 U; 0 Other;
 Yoshimura Y,
 Example 9; Page 134; 210pp; Japanese.
 Law MF, Mark GE, Williamson AR;
 Disclosure, Fig 4; 78pp; English.
 1 GCTGAGCCTAGCAGATTCA 19
 19 GCTGTGCCAAGCAGATTCA 37
 Ohtomo T, Tsuchiya M,
 BP.
 97WO-JP003553.
 96JP-00264756
 AAV39382 standard; DNA; 39
 (first entry)
 (CHUS) CHUGAI SEIYAKU KK.
 Local Similarity 84.2
les 16; Conservative
 (MERI) MERCK & CO INC.
 WPI; 1991-216983/30.
 WPI; 1998-286421/25.
 See also EP-438312
 variable portions
 PCR primer; ss
 Homo sapiens.
 WO9814580-A1
 03-OCT-1997;
 04-OCT-1996;
 21-SEP-1998
 09-APR-1998.
 Synthetic.
 AAV39382;
 Query Match
 Prodn.
 Ono K,
 Mus sp
 Matches
 18
 RESULT 11
AAV39382
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Gaps

; 0

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Light chain primer EL.
 Query Match
 AAL34502/c
 Matches
 RESULT 22
XXXXXXXXXXXXX
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 The YFC51.1.1 rat anti-human -CD18 light chain was humanised as follows: brimer EL (AAQ24659) was used with Primer FL (AAQ24660) in a PCR reaction using as template CAMPATH-1H light chain (i.e. humanised CAMPATH-1 on REI framework; Biotechnology 9:64-68 (1991) to produce fragment EFL. Three other PCR reactions were performed on the same template, generating fragments ABL, CDL and GHL. Fragments EFL and GHL were combined and used as the template for a PCR reaction with primers EL and HL (AAQ24662) to produce fragment EHL. Similarly, fragment ADL was produced from ABL and CDL using the primers AL and DL (AAQ24655 and AAQ24658, respectively). The products ADL and EHL were purified and combined in a recombinant PCR reaction using primers AL and HL. The final humanised light chain product, AHL, was cloned into the HindIII site of pUCL8 (primers AL and HL both contain HindIII sites). (Updated on 25-MAR-2003 to correct PN
 chimeric humanised antibodies - using a new polymerase chain
 Gaps
 Polymerase chain reaction, humanised antibody, CAMPATH-1H, rat anti-human CD18 light chain, YFC51.1.1; human IgG1 heavy chain;
 ö
 Score 14.2; DB 2; Length 41; Pred. No. 5.6e+03; 0; Mismatches 3; Indels
 Sequence 41 BP; 9 A; 8 C; 12 G; 12 T; 0 U; 0 Other;
 PCR primer EL for CAMPATH-1H light chain.
 Example 2; Page 45; 67pp; English.
 22 GGTGTGCCAAGCAGATTCA 40
 1 GCTGAGCCTAGCAGATTCA 19
 BP
 56.8%; S
 AAQ24659 standard; DNA; 41 BP.
 91WO-GB001744.
 90GB-00022011
 AAQ35184 standard; cDNA; 41
 (WELL) WELLCOME FOUND LTD
 (revised)
(first entry)
 (revised)
(first entry)
 16; Conservative
 Lewis AP;
 WPI; 1992-167155/20.
 reaction technique.
 Query Match
Best Local Similarity
 PCR grafting; ss.
 WO9207075-A1.
 10-OCT-1990;
 08-OCT-1991;
 25-MAR-2003
08-JUN-1993
 25-MAR-2003
10-NOV-1992
 30-APR-1992.
 Crowe JS,
 Synthetic.
 Prepn. of
 AAQ35184;
 AAQ24659;
 field.)
 Matches
 RESULT 20
 AAQ35184
ID AAQ3
XX AC AAQ3
XX DT 25-N
DT 08-3
 AAQ24659
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The sequences given in AAQ35180-87 are primers which were used to amplify and humanise the light chain isolated from the rat antibody YFC51.1.1 The light chain of YFC51.1.1 was isolated using a non-radioactively labelled clone of the light chain from rat myeloma Y3-Ag 1.2.3. The isolated sequences were amplified, humanised and constructed into the light chain genes using these primers. The gene construction, and a corresponding one for the heavy chain (see also AAQ35188-95) were transformed into COS cells which transiently expressed the humanised transformed into COS cells which transiently expressed the humanised cransformed into COS cells which transiently expressed the humanised transiently expressed the humanised transiently expressed the humanised antibody with specificity for CD18 antigen. The arbibody may be useful in treating leukcoytes—mediated conditions, such as inhibiting influx of leukcoytes into the lung and other organs during inhibiting influx of leukcoytes into the lung and other organs during cepsis, endotoxic shock or adult respiratory distress syndrome. The arbibodies may also be used to treat asthms and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflammation and may form the lung and inflamm
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 Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; coyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; colony stimulating factor; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
 New humanised antibody specific for human CD-18 antigen - inhibits influx of leukocytes into the lungs, useful for treating endotoxic shock, adult
Probe; myeloma; Y3-Ag 1.2.3; primer; rat; monoclonal; antibody; COS; YFC51.1.1; CD18; humanised; antigen; leukocyte; lung; sepais; asthma; endotoxic shock; adult respiratory distress syndrome; inflammation; immunotoxin; transient expression; PCR; polymerase chain reaction; ss.
 Gaps
 .
0
 Score 14.2; DB 2; Length 41; Pred. No. 5.6e+03;
 3; Indels
 Sequence 41 BP; 9 A; 8 C; 12 G; 12 T; 0 U; 0 Other;
 respiratory distress syndrome, asthma, etc.
 Mismatches
 Disclosure; Page 47; 59pp; English.
 ..0
 Human SNP oligonucleotide #7710.
 19
 GGTGTGCCAAGCAGATTCA 40
 Crowe S;
 92WO-GB001289.
 91GB-00015364.
 56.8%;
 1 GCTGAGCCTAGCAGATTCA
 (WELL) WELLCOME FOUND LTD.
 AAL34502 standard; DNA; 50
 (first entry)
 Local Similarity 84.2
 Sims M,
 WPI; 1993-058788/07.
 16-JUL-1991;
 WO9302191-A1
 15-JUL-1992;
 04-FEB-1993.
 24-JAN-2002
 Waldmann H,
 Synthetic.
 AAL34502;
 22
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17-MAY-2002; 2002JP-00143185.
17-OCT-2002; 2002JP-00303528.
 14; Conservative
 Kobayashi Y, Ashida Y,
 Nakamura Y, Sekine A,
 (SANY) SANKYO CO LTD
 WPI; 2004-012542/01.
 WPI; 2004-081882/08.
 (RIKE) RIKEN KK.
(NAKA/) NAKAMURA Y.
(SEKI/) SEKINE A.
 Sest Local Similarity
 (IIDA/) IIDA A. (SAIT/) SAITO S.
 WO2003095454-A1
 Homo sapiens
 20-NOV-2003.
 ADH91221;
 Query Match
 of the
 Matches
 RESULT 24
ADH91221
 ð
 셤
 The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cytlin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, coupled receptors and thioesterases. The present sequence is one protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and treatment of diseases them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, lengthistics.
 ö
 Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
 Gaps
 ö
 Gene polymorphism detection method-related primer/probe #400
 gene polymorphism detection; primer; probe; SNP analysis; single nucleotide polymorphism analysis; drug selection; ss.
 Score 14.2; DB 4; Length 50;
Pred. No. 5.8e+03;
0; Mismatches 3; Indels
 Sequence 50 BP; 5 A; 8 C; 15 G; 22 T; 0 U; 0 Other;
 Claim 1; Page 3617; 4143pp; English
 1 GCTGAGCCTAGCAGATTCA 19
 GCAGAGCCTAGCAGACACA 7
 ΒÞ
 28-DEC-2000; 2000WO-US035498
 28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
 56.8%;
 16-MAY-2003; 2003WO-JP006141.
 nervous system disease; ss.
 ADH05434 standard; DNA; 41
 (first entry)
 Conservative
 Shimkets RA, Leach M;
 (CURA-) CURAGEN CORP.
 Query Match
Best Local Similarity
 WPI; 2001-465210/50.
 WO2003097877-A1.
 WO200147944-A2
 Homo sapiens.
 Unidentified
 05-JUL-2001
 11-MAR-2004
 27-NOV-2003
 organisms
 ADH05434;
 25
 RESULT 23
 ADH05434
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 The invention comprises a method for detecting gene polymorphisms, the method involves constructing an oligonucleotide primer and/or probe containing the polymorphism site in a receptor gene or its complementary sequence, amplifying that pand detecting it with the probe and/or primer. The method of the invention is useful for the analysis of SNPs and in drug selection. The present DNA sequence represents a primer/probe
 New carbapenem compounds resistant to beta-lactamase (except metallo-beta -lactamase), useful for treating microbial infections especially respiratory infections.
 Detecting gene polymorphism for single nucleotide polymorphism analysis and drug selection.
 1-beta-methylcarbapenem compound; antimicrobial; bacterial infection;
 Gaps
 1-beta-methylcarbapenem compound-related human DNA sequence #400.
 ö
 56.0%; Score 14; DB 12; Length 41; B7.5%; Pred. No. 7e+03;
 1; Indels
 Sequence 41 BP; 14 A; 11 C; 8 G; 7 T; 0 U; 1 Other;
 Uchida T, Kojima K;
 1; Mismatches
 Disclosure; SEQ ID NO 400; 726pp; Japanese
Saito S;
 Claim 2; SEQ ID NO 400; 166pp; Japanese
 respiratory infection; human; ds
Iida A,
 ADH91221 standard; DNA; 41 BP
 4 GAGCCTAGCAGATTCA 19
 14-MAY-2003; 2003WO-JP006028
 14-MAY-2002; 2002JP-00138448
 06-MAY-2004 (first entry)
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Gaps

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Indels

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Mismatches

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Conservative

17;

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Matches
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 This invention describes a novel method for obtaining a set of biallelic markers represented in AAX2533-X52612 and AAX2533-X52843 for use in constructing a high density equilibrium map of the human genome. The method involves (a) obtaining a nucleic acid library comprising genome. DNA fragments comprising the full genome or a portion (b) determining the sequence of selected regions of the genomic DNA fragments and (d) identifying nucleotides in the genomic DNA fragments and (d) identifying nucleotides in the genomic DNA fragments which vary between individuals, thereby defining a set of biallelic markers. The methods can be used for identifying traits such as disease (e.g. Alzheimer's disease), drug response, drug efficacy and drug toxicity. They can be used for selecting an individual for inclusion in a clinical trial. The method is used to map the position of genes in a genome (preferably the human genome). The sequences described in AAX52633-X52832 and AAX52844-
 useful as antimicrobials to treat bacterial infections, especially respiratory infections in warm-blooded animals (e.g. humans). The present human DNA sequence is included in the sequence listing of this patent.
 Biallelic marker; human; high density disequilibrium map; disease; trait; identification; Alzheimer's disease; drug response; drug efficacy; drug toxicity; ss.
 Production of biallelic markers - by obtaining a genomic DNA library, determining the order and sequence of DNA fragments and identifying nucleotides which vary between individuals.
 Gaps
The invention comprises 1-beta-methylcarbapenem compounds which are
 ö
 human genome). The sequences described in AAX52633-X52832 and
X52868 represent primers used in the method of the invention
 56.0%; Score 14; DB 12; Length 41; 87.5%; Pred. No. 7e+03; ive 1; Mismatches 1; Indels
 Sequence 47 BP; 13 A; 11 C; 10 G; 13 T; 0 U; 0 Other;
 Sequence 41 BP; 14 A; 11 C; 8 G; 7 T; 0 U; 1 Other;
 Tchoumakov I;
 Example 6; Page 134; 288pp; English.
 Human genome biallelic marker 24
 AAX52556 standard; DNA; 47 BP
 used rot commethod is used to map the permethod is used to map the sequences
 97EP-00401740.
 4 GAGCCTAGCAGATTCA 19
 98WO-IB001193
 (first entry)
 Query Match
Best Local Similarity 87.5.
Best Local 4; Conservative
 Cohen D, Blumenfeld M,
 WPI; 1999-132278/11.
 (GEST) GENSET
 Homo sapiens
 WO9904038-A2
 17-JUL-1998;
 18-JUL-1997;
21-APR-1998;
 30-JUN-1999
 28-JAN-1999
 AAX52556;
 RESULT 25
 AAX52556
ន្តដូន្តនូន
 8
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Length 47;

Score 14; DB 2; I Pred. No. 7.2e+03;

56.0%;

Query Match Best Local Similarity

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ö
 AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and dispossition are posses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3000, and actually given a sequence in the Sequence Listing from the
 Human genome; biallelic marker; high density disequilibrium map;
genomic map; haplotype; phenotype; polymorphic base; genotyping;
haplotyping; hybridisation; identification; characterisation; diagnosis;
single nucleotide polymorphism; SNP; ds.
 Novel biallelic markers used to construct a high density disequilibrium map of the human genome.
 Gaps
 /standard name= "single nucleotide polymorphism"
 ö
 Length 47;
 56.0%; Score 14; DB 3; Length 47; 77.3%; Pred. No. 7.2e+03; tive 0; Mismatches 5; Indels
 Sequence 47 BP; 13 A; 11 C; 10 G; 13 T; 0 U; 0 Other;
 Human map-related biallelic marker SEQ ID NO:3104.
 Chumakov I;
 Location/Qualifiers
replace(24,T)
 Claim 3; Page 892; 2745pp; English.
 25
 24
 4 GAGCCTAGCAGATTCATGGCAC 25
 GAGCCTTGGACTTTCATGACAC
GAGCCTAGCAGATTCATGGCAC
 ВР
 98US-0082614P.
98US-0109732P.
 99WO-IB000822
 Local Similarity 77.3%;
les 17; Conservative
 AAZ68752 standard; DNA; 47
 (first entry)
 Blumenfeld M,
 WPI; 2000-013267/01
 present invention
 (GEST) GENSET
 Homo sapiens
 WO9954500-A2
 21-APR-1999;
 21-APR-1998;
 23-NOV-1998;
 10-SEP-2001
 28-OCT-1999
 Key
variation
 AAZ68752;
 Cohen D,
 Query Match
 Best Loc
Matches
 RESULT 26
 AAZ68752
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(first entry)

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요
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17; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
 Human leukocyte gene expression profiling probe SEQ ID NO 5324.
 Claim 1; Page 500; Opp; English.
 22-OCT-2001; 2001WO-US047856.
 20-OCT-2000; 2000US-0241994P.
08-JUN-2001; 2001US-0296764P.
 ABZ05333 standard; DNA; 50
 (BIOC-) BIOCARDIA INC.
 WPI; 2002-636525/68.
 T7; leukocyte;
 WO200257414-A2.
 Wohlgemuth J,
 Homo sapiens.
 09-JAN-2003
 25-JUL-2002
 ABZ05333;
 Ly N,
 RESULT 28
 ABZ05333
 셤
 ð
 The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apposais related proteins, cadherin, cyclin, polymerase, oncogenes, histories, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, Groproteins cytochromes, kinesins, cytokines, interferons, interleukins, Groproteins cytochromes, kinesins, cytokines, interferons, interleukins, Groproteins cuped and thioseterases. The present sequence is one such oligonuclectide. The oligonuclectides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases. Since associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukamenia), diseases of the nervous system and an infection of pathogenic
 Immunosuppressive, immunostimulatory, antiinflammatory, cytostatic, neuroprotective; antimicrobial; gene therapy, vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cyckine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation;
 Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
 56.0%; Score 14; DB 4; Length 50; 77.3%; Pred. No. 7.3e+03;
 multifactorial disease; autoimmune disease; infection nervous system disease; ss.
 Sequence 50 BP; 13 A; 22 C; 8 G; 7 T; 0 U; 0 Other;
 Claim 1; Page 1863; 4143pp; English.
GAGCCTTGGACTTTCATGACAC 24
 Human SNP oligonucleotide #1688.
 BP
 28-DEC-2000; 2000WO-US035498
 28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
 AAL28480 standard; DNA; 50
 (first entry)
 Shimkets RA, Leach M;
 (CURA-) CURAGEN CORP.
 WPI; 2001-465210/50.
 WO200147944-A2
 Homo sapiens.
 24-JAN-2002
 05-JUL-2001.
 organisms
 AAL28480;
 RESULT 27
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Fry K, Matcuk G, Altman P, Prentice J, Phillips J; I R, Quertermous T, Johnson F;

Woodward R,

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The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 Gaps
 ;
0
 Query Match 56.0%; Score 14; DB 6; Length 50; Best Local Similarity 77.3%; Pred. No. 7.38+03; Matches 17; Conservative 0; Mismatches 5; Indels
 Sequence 50 BP; 14 A; 14 C; 10 G; 12 T; 0 U; 0 Other;
 PCR primer for human gene CHST4 #2.
 24
 24
 3 TGAGCCTAGCAGATTCATGGCA
 3 readcccadegerrrcardaca
 ABK70835 standard; DNA; 21
 15-JUL-2002 (first entry)
 ABK70835;
 RESULT 29
 ABK70835
ID ABK7
XX
AC ABK7
XX
DT 15-J
XX
DE PCR
XX
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Gaps ; 0

5; Indels

77.3%; Pred. ....tive 0; Mismatches

17; Conservative

Best Local Similarity Matches 17; Conserv

Query Match

1 GCTGAGCCTAGCAGATTCATGG 22

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26 GCTGGGCCTAGCACGGACATGG 5

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02-OCT-2001; 2001DE-01048697.
12-NOV-2001; 2001DE-01056678.
 WO2003031469-A2.
 Mittmann MP;
 17-APR-2003
 Synthetic.
 ADC21315;
 RESULT 31
 ADC21315/
 셤
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 The invention relates to classification and quantitative determination of enzymes participating in sulphuric acid conjugation comprising using oligonucleotide probes hybridising to the following regions: (a) 885-911 region of CHST1 gene; (b) 174-197 region of CHST3 gene; (c) 1003-1032 region of CHST4 gene; (d) 322-346 region of CHST5 gene; (e) 737-765 region of SULT2A1 gene; (l) 703-732 region of HNK-1ST gene; (g) 299-325 region of SULTZA1 gene; (l) 358-182 region of SULTZB1 gene; (l) 514-478 region of SULTZB1 gene; (l) 554-582 region of SULTX3 gene; (j) 451-478 region of SULTZB1 gene; (l) 652-677 region of TPST2 gene. Also included are PCR primers for the above genes, are used in the determination. The probes, primers and the method are used in the determination of sulphuric acid conjugation for confirmation of the aafety of investigational drugs. The present sequence is a PCR primer for one of the above listed genes
Human, sulphuric acid conjugation, ss, PCR, CHST1, CHST3, primer, CHST4,
CHST5, CST, HNK-1ST, SULTA1, SULTB1, SULTX3, STE, TPST2.
 Determination of enzymes participating in sulfuric acid conjugation in humans, useful for confirmation of safety of investigational drugs, comprises using oligonucleotide probes.
 Gaps
 expressed sequence tag; microarray; gene expression; on; biallelic marker; polymorphism; human;
 ö
 55.2%; Score 13.8; DB 6; Length 21; 88.2%; Pred. No. 7.8e+03; ive 0; Mismatches 2; Indels
 Human microarray DNA oligonucleotide SEQ ID NO 102161.
 Sequence 21 BP; 6 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
 Claim 8; Page 11; 13pp; Japanese.
 (SAKA) OTSUKA SEIYAKU KOGYO KK.
 21
 BP
 21
 07-SEP-2000; 2000JP-00272229.
 16-MAR-2001; 2001US-0276759P.
 07-SEP-2000; 2000JP-00272239
 15-MAR-2002; 2002US-00098263
 5 AGCCTAGCAGATTCATG
 AGCCCAGCAAATTCATG
 ACK02180 standard; DNA; 25
 (first entry)
 Conservative
 cross-species comparison
 (AFFY-) AFFYMETRIX INC
 Query Match
Best Local Similarity
 WPI; 2002-378272/41.
 ss; probe; exp
 US2003104410-A1
 JP2002085067-A.
 Homo sapiens.
 26-MAR-2002
 14-OCT-2003
 05-JUN-2003
 ACK02180;
 genetic
 Homo
 RESULT 30
 셤
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018 500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in bybridisation to a DNA library, in anoticoring gene expression levels by hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are strached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dottor by the any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening CDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html
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 expression construct; vaccine; intradermal injection; type 1 cell-mediated immune response; antiviral; hepatotropic; antifilammatory; protozoacide; MIDGE; minimalistic immunologically defined gene expression vector; hepatitis B surface antigen; p36 antigen; Leishmania major; ss; primer;
 New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
 Gaps
 ;
0
 55.2%; Score 13.8; DB 9; Length 25; 88.2%; Pred. No. 8e+03; ive 0; Mismatches 2; Indels
 Sequence 25 BP; 5 A; 5 C; 7 G; 8 T; 0 U; 0 Other;
 Claim 1; SEQ ID NO 102161; 9pp; English.
 Plasmid pMOKp36 PCR primer #3.
 25
 BP
 02-OCT-2002; 2002WO-DE003798
 9 TAGCAGATTCATGGCAC
 TAGCGGATTAATGGCAC
 ADC21315 standard; DNA; 33
 Query Match
Best Local Similarity 88.2.
 18-DEC-2003 (first entry)
WPI; 2003-567953/53.
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 X L X D X B X S X M X B X L X Y X
 ઠે
 This invention describes a novel DNA expression construct, functional in eukaryotic cells, to prepare a vaccine, for intradermal injection, to generate a type 1 cell-mediated immune response. The construct encodes one or more antigens (Ag) under control of a promoter and, to improve transfection efficiency, is covalently linked to one or more oligopetides. The products of the invention have antiviral, were immunized intradermally (twice at an interval of 11 weeks) with a MIDGE (minimalistic immuniologically defined gene expression vector) that encoded hepatitis B surface antigen. The resulting antibody titer (expressed as optical density in enzyme linked immunosorbent assay) was concoded hepatitis B surface antigen. The interval of 12 was over 0.9. The MIDGE used was modified by binding the Tat protein-derived peptide Tyr-Gly-Arg-(Lys)_2-(Arg)_2-cln-(Arg)_3 the optical density was over 0.9. The constructs are used, particularly in human medicine, to generate a Tyr-Gly-Arg-(Lys)_2-chro) particularly in human medicine, to generate a type 1 cell-mediated immune response, specifically against hepatitis B virus surface antigen, but also against the p36 antigen of Leishmania modicine. Attachment of the oligopeptides increases transport of the moderate of the constructs are used, particularly in human medicine, to feel manner and medicine the p36 antigen of Leishmania.
 ö
 construct to the nucleus, resulting in a stronger immune response. This sequence represents a PCR primer used in the construction of construct pMOKp36 used to make the vaccines described in the disclosure of the
 expression construct; vaccine; intradermal injection; type 1 cell-mediated immune response; antiviral; hepatotropic; antiinflammatory; protozoacide; MIDGE; minimalistic immunologically defined gene expression vector; hepatitis B surface antigen; p36 antigen; Leishmania major; ss; primer;
 Use of a DNA expression construct encoding one or more antigens and covalently linked to oligopeptides for preparing intradermal vaccine, useful for treating e.g. hepatitis and leishmaniosis.
 Gaps
 ;
0
 55.2%; Score 13.8; DB 10; Length 33; 72.0%; Pred. No. 8.4e+03; ive 0; Mismatches 7; Indels (
 Sequence 33 BP; 10 A; 7 C; 7 G; 9 T; 0 U; 0 Other;
 (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(LOPE/) LOPEZ S M.
(JIME/) JIMENEZ M T.
 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 Example 4; SEQ ID NO 9; 32pp; German.
 32 gergaccercerargricardes
 Plasmid pMOKp36 PCR primer #1.
 ADC21313 standard; DNA; 33 BP
 02-OCT-2002; 2002WO-DE003798.
 (first entry)
 Query Match
Best Local Similarity 72.0
Matches 18; Conservative
 Jimenez MT;
 WPI; 2003-372085/35.
 WO2003031469-A2.
 18-DEC-2003
 17-APR-2003
 Synthetic.
 invention.
 Lopez SM,
 ADC21313;
 RESULT 32
 ADC21313,
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The inventor describes a novel base expression construct, functional incomparation describes a novel base expression construct, the construct cells, to prepare a vaccine, for intradermal injection, to generate a type I cell-mediated immune response. The construct encodes one or more antigens (Ag) under control of a promoter and, to improve can entigency is covalently linked to one or more inproved in transfection efficiency, is covalently linked to one or more inproved in transferrably defined by the activity. Mice were immunised intradermally (twice at an interval of 11 weeks) with a MIDGE (minimalistic immunologically defined gene expression vector) that encoded hepatitis B surface antigen. The resulting antibody titer (expressed as optical density in enzyme linked immunosorbent assay) was boout 0.45, about the same as when using a plasmid for expression. When the MIDGE used was modified by binding the Tat protein-derived peptide the moder (Lyp 1 cell-mediated immune response, specifically against hepatitis B virus surface antigen, but also against the p36 antigen of Leishmania construct to the nucleus, resulting in a stronger immune response. This sequence represents a PCR primer used in the construct to the nucleus, resulting in a stronger immune response.
 This invention describes a novel DNA expression construct, functional in
 Use of a DNA expression construct encoding one or more antigens and covalently linked to oligopeptides for preparing intradermal vaccine, useful for treating e.g. hepatitis and leishmaniosis.
 Gaps
 used to make the vaccines described in the disclosure of the
 immunization; leishmaniosis; vaccine; protozoacide; p36 antigen;
TAT peptide; ss; primer; PCR.
 ö
 55.2%; Score 13.8; DB 10; Length 33; 72.0%; Pred. No. 8.4e+03; ive 0; Mismatches 7; Indels (
 Sequence 33 BP; 10 A; 7 C; 7 G; 9 T; 0 U; 0 Other;
 (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
(LOPE/) LOPEZ S M.
(JIME/) JIMENEZ M T.
 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 Example 4; SEQ ID NO 7; 32pp; German.
 32 GGTGACCCTCGTATGTTCATGGTAC
 Plasmid pMOKp36 PCR primer #3.
02-OCT-2001; 2001DE-01048697.
12-NOV-2001; 2001DE-01056678.
 02-OCT-2002; 2002WO-DE003799
 ADC21307 standard; DNA; 33
 18-DEC-2003 (first entry)
 Best Local Similarity 72.0
Matches 18; Conservative
 Lopez SM, Jimenez MT;
 WPI; 2003-372085/35.
 WO2003031470-A2
 17-APR-2003.
 Synthetic.
 ADC21307;
 Query Match
 RESULT 33
ADC21307/c
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Fu G;
 RESULT 35
 ADQ3158
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 This invention describes a novel DNA expression construct for immunization against leishmaniosis which is covalently linked to one or more oilgopeptides to improve transfection efficiency. The construct consists of covalently closed DNA molecules which include a doublestranded (ds) region. The ds-forming single strands (la) antenin only the stranded raingle-stranded loops of DNA mucleotides and (la) contain only the coding region, under control of a promoter functional in the animal being immunized, and a terminator sequence. The construct is covalently linked coding region, under control of a promoter functional in the animal being immunized, and a terminator sequence. The construct is covalently linked con one or more oilgopeptides (II) to improve transfection efficiency. The products of the invention are incorporated into a vaccine which has products of the invention are incorporated into a vaccine which has a daministered intradermally (twice at 54.8 mug) to mice. Three weeks after the second injection, the animals were challenged with 50000 Leishmania and major promoastigates, injected subcutenaeously into a hind paw. After 8 weeks, the mean lesion size was 1 mm compared with over 4 mm for control animals given phosphate buffer only. The constructs of the invention constructs and without the difficulties associated with using eukaryotic expression vectors. Preparation of the vaccine is simpler and construction of pubmics.
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 New DNA expression construct, useful in vaccines against leishmaniosis, comprises antigen-encoding sequence linked to oligopeptides that increase transfection efficiency.
 Gaps
 immunization; leishmaniosis; vaccine; protozoacide; p36 antigen;
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 55.2%; Score 13.8; DB 10; Length 33; 72.0%; Pred. No. 8.4e+03; ive 0; Mismatches 7; Indels (
 Sequence 33 BP; 10 A; 7 C; 7 G; 9 T; 0 U; 0 Other;
 (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
 Example 1.1; SEQ ID NO 8; 22pp; German.
 25
 32 GGTGACCCTCGTATGTTCATGGTAC 8
 1 GCTGAGCCTAGCAGATTCATGGCAC
 Plasmid pMOKp36 PCR primer #1.
 .305/c
ADC21305 standard; DNA; 33 BP.
02-OCT-2001; 2001DE-01048732.
12-NOV-2001; 2001DE-01056679.
 02-OCT-2002; 2002WO-DE003799.
 02-OCT-2001; 2001DE-01048732.
12-NOV-2001; 2001DE-01056679.
 (first entry)
 Local Similarity 72.0 tes 18; Conservative
 Jimenez MT;
 construction of pMOKp36.
 WPI; 2003-372086/35.
 WO2003031470-A2.
 18-DEC-2003
 Fuertes LL,
 17-APR-2003
 Synthetic
 ADC21305;
 Query Match
 Matches
 ADC21305/
XX ADC2
XX ADC2
XX ADC2
XX IMMU
XX IMMU
XX IMMU
XX IMMU
XX SYNT
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 RESULT 34
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This invention describes a novel DNA expression construct for immunization against leishmaniosis which is covalently linked to one or more obligopeptides to improve transfection efficiency. The construct consists of covalently closed DNA molecules which include a double-construct consists of covalently closed DNA molecules which include a double-stranded (ds) region. The ds-forming single strands (Ia) are linked by short single-stranded loops of DNA muclectides and (Ia) contain only the coding region, under control of a promoter functional in the animal being immunized, and a terminator sequence. The construct is covalently linked to one or more oligopeptides (II) to improve transfection efficiency. The products of the invention are incorporated into a vaccine which has protozoacide activity. An expression construct, MIDGE 936-NLS (expressing the Leishmania p36 antigen linked to nuclear localization signals) was administered intradermally (twice at 54.8 mug) to mice. Three weeks after the second injection, the animals were challenged with 50000 Leishmania major promastigotes, injected subcutaneously into a hind paw. After 8 cekeks, the mean lesion size was 1 mm compared with over 4 mm for control animals given phosphate buffer only. The constructs of the invention provide a safe, effective and productive vaccine with greater activity than the main and packet the difficulties associated with using the constructs of the invention the control of the invention than the difficulties associated with using the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
 New DNA expression construct, useful in vaccines against leishmaniosis, comprises antigen-encoding sequence linked to oligopeptides that increase
 eukaryotic expression vectors. Preparation of the vaccine is simpler and less expensive. This sequence represents a PCR primer used in the construction of pMOKp36.
 Gaps
 .
0
 Human, Multiplex nucleic acid detection, ss; PCR; primer; SNP; single nucleotide polymorphism.
 Query Match 55.2%; Score 13.8; DB 10; Length 33; Best Local Similarity 72.0%; Pred. No. 8.4e+03; Matches 18; Conservative 0; Mismatches 7; Indels C
 Sequence 33 BP; 10 A; 7 C; 7 G; 9 T; 0 U; 0 Other;
(MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
 Multiplex detection of human SNPs, primer F10A.
 Example 1.1; SEQ ID NO 6; 22pp; German.
 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 32 GGTGACCCTCGTATGTTCATGGTAC 8
 24-JAN-2003; 2003US-00349780.
 24-JAN-2003; 2003US-00349780
 ADQ31581 standard; DNA; 49
 21-OCT-2004 (first entry)
 Fuertes LL, Jimenez MT;
 transfection efficiency.
 WPI; 2003-372086/35.
 JS2004146866-A1
 (FUGG/) FU G.
 Homo sapiens
 29-JUL-2004.
 ADQ31581;
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0;

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The invention relates analysing multiple targets in polynuclectide, involves providing a set or sets of multiple primers with target nucleic acids in separate reactions of primer extension or amplification, where the reactions produce nucleic acid products in that each nucleic acid fragments comprise at least one restriction site, digesting nucleic acid fragments comprises, joining digested products derived from the separate reactions on the restriction sites with cognate restriction enzymes, joining digested products derived from the separate reactions are created, amplifying the joined products, and detecting the amplified products. Also included are an oligonucleotide primer for detecting traget nucleic acid sequence (comprising a subject nucleic acid sequence (comprising a subjection comprises a restriction enzyme site, where the creatriction site acts as detection marker in the process of detecting tratest nucleic acid sequence, where the detection signal generated from enzyme site acts as detection on restriction site of reaction product is indicative of the presence of target nucleic acid sequence) and a kit for use in analysis and detection of multiple targets in a polynucleotide comprising a set or sets of multiple primers, universal primers, creatriction enzymes, DNA polymerase, ddyrp, buffers for all enzymes, and dNTPS). The method is useful for analysing multiple targets in a polynucleotide and for genotyping mutations, preferably single cucle cacid acids from any source. The method enablysing differential gene expression profiles, genonic methylation patterns and any specific contents and any source. The method enablysing differential gene expression profiles, genonic methylation patterns and any specific.
 ö
 Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; appoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interleaving Grotein cytochrome; kinase; cytokine; interferon; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.
 targets quantitatively. An experiment was performed, using the method of the invention, where 8 SNPs were detected in human genomic DNA, simultaneously. The present sequence is a primer used in the above
 Analyzing multiple targets in polynucleotide, by providing multiple primers with target nucleic acids, digesting nucleic acid products with cognate restriction enzymes, amplifying digested products, and detecting
 Gaps
 ;
0
 Score 13.8; DB 13; Length 49;
Pred. No. 9.1e+03;
0; Mismatches 2; Indels C
 Sequence 49 BP; 15 A; 11 C; 13 G; 10 T; 0 U; 0 Other;
 Example 1; SEQ ID NO 39; 65pp; English
 Human SNP oligonucleotide #1942.
 ;
0
 22
 44
 55.2%;
88.2%;
 28 GACTAGCAGATTCACGG
 AAL28734 standard; DNA; 50
 6 GCCTAGCAGATTCATGG
 24-JAN-2002 (first entry)
 Query Match 55.2
Best Local Similarity 88.2
Matches 15; Conservative
WPI; 2004-552653/53
 amplified products.
 WO200147944-A2
 Homo sapiens
 AAL28734;
 RESULT 36
 AAL28734
à
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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins coupled receptors and thioseterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune consenses (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lugue erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
 ö
 Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
 Gaps
 ..
0
 Human; Multiplex nucleic acid detection; 88; PCR; primer; SNP;
 55.2%; Score 13.8; DB 4; Length 50; 72.0%; Pred. No. 9.1e+03; tive 0; Mismatches 7; Indels
 Sequence 50 BP; 6 A; 15 C; 19 G; 10 T; 0 U; 0 Other;
 Multiplex detection of human SNPs, primer F10G.
 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 41
 Claim 1; Page 1936; 4143pp; English.
 17 derredeczekackereckadadece
 single nucleotide polymorphism.
 ADQ31582 standard; DNA; 50 BP
 24-JAN-2003; 2003US-00349780.
 24-JAN-2003; 2003US-00349780.
 28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
 28-DEC-2000; 2000WO-US035498
 21-OCT-2004 (first entry)
 Local Similarity 72.0
es 18; Conservative
 Leach M;
 (CURA-) CURAGEN CORP.
 WPI; 2001-465210/50.
 US2004146866-A1
 Shimkets RA,
 Homo sapiens.
 29-JUL-2004.
05-JUL-2001
 (FUGG/) FU
 organisms
 ADQ31582;
 Query Match
 Fu G;
 fatches
 RESULT 37
 ADQ31582
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The invention relates analysing multiple targets in polynucleotide, involves providing a set or sets of multiple primers with target nucleic acids in separate reactions of primer extension or amplification, where the reactions produce nucleic acid products in that each nucleic acid fragments comprise at least one restriction site, digesting nucleic acid fragments comprises at least one restriction sites with cognate of products of the separate reactions on the restriction sites with cognate reactions together, where randomly joining nucleic acid fragments from the separated reactions are created, amplifying the joined products, and detecting the amplified products. Also included are an oligonucleotide of primer for detecting traget nucleic acid sequence (comprising as in compressed acid sequence (comprising as restriction marker in the process of detecting traster nucleic acid sequence, where the detection site acids sequence, where the detection signal generated from enzymestic manipulation on restriction marker in the process of detecting traster nucleic acid sequence, where the detection signal generated from enzymesting as est or sets of multiple targets in a polynucleotide (comprising as est or sets of multiple targets in a polynucleotide (comprising as est or sets of multiple targets in a polynucleotide coide school of targets in a polynucleotide polymorphisms (SNPs), and for analysing multiple targets in a polynucleotide polymorphisms (SNPs), and for analysing and any specific cold acids from any source. The method enables analysis of multiple experience acids from any source. The method enables analysis of multiple targets in a primer acids from any source. The method enables and enablysis of multiple experience acids from any source. The method enables analysis of multiple experience the invention, where 8 SNPs were detected in human genomic DNA.
 Analyzing multiple targets in polynucleotide, by providing multiple primers with target nucleic acids, digesting nucleic acid products with cognate restriction enzymes, amplifying digested products, and detecting
 Human, K-ras, PCR primer, probe, capture probe, mutation detection, ligase detection reaction, LDR, p53; BRCA1; BRCA2; infectious disease; infection; 21 hydroxylase deficiency; Turner Syndrome, obsity; cancer, oncogene, tumour suppressor; human papillomavirus; forensic; environmental monitoring; food industry; feed industry; ss.
 55.2%; Score 13.8; DB 13; Length 50; 88.2%; Pred. No. 9.1e+03; ive 0; Mismatches 2; Indels C
 Sequence 50 BP; 16 A; 10 C; 15 G; 9 T; 0 U; 0 Other;
 Capture oligonucleptide Zip ID#1688 oligo #9.
 Example 1; SEQ ID NO 40; 65pp; English.
 22
 29 GACTAGCAGATTCACGG 45
 ABI94601 standard; DNA; 20 BP
 6 GCCTAGCAGATTCATGG
 (first entry)
 Query Match
Best Local Similarity 88.2
Matches 15; Conservative
 WPI; 2004-552653/53
 amplified products.
 WO200179548-A2.
 16-FEB-2002
 25-OCT-2001
 experiment
 Synthetic
 ABI94601;
 RESULT 38
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The present invention describes a method (M1) for designing capture oligonucleotide probes (I) for use on a support to which complementary oligonucleotide probes (II) will hybridse with little mismatch, where (I) have melting temperatures within a narrow range. The method is useful for detecting infectious diseases caused by bacterial infectious agents e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal infectious agents e.g. Cryptococcus neoformans, Candida albicans and Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus, Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus, Comptenin Bar virus and pollo virus, and parasitic infectious agents eslected from Onchoverva volvulus, Entamobal histolytica and Dracunculus medinesis. The method is also useful for detecting genetic diseases such as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

Concerning cancer involving oncogenes, tumour suppressor genes, or genes involved in DNA amplification, replication, recombination or repair, the cancer is specifically associated with a gene selected from BRCAI gene, p53 gene, human papillomavirus types 16 and 18 and liver cancers. The method is also used for environmental monitoring, forensics and the food and feed industry, detecting comprises scanning (using e.g. a scanning electron microscope and infrared microscope) the support at the particular sites and identifying if ligation of the oligonucleotide probesed entry in a computer) identified ligation to a presence or absence of the target uncleotide sequences. All Sally to the semplification.
 Human, coronary heart disease susceptibility gene, CHD1, mutation, chromosome 11; diagnosis; screening; PCR primer; metabolic disorder; detection; hypoalphalipoproteinaemia; familial combined hyperlipidaemia; insulin resistant syndrome X; multiple metabolic disorder; obesity; diabetes; dyslipidaemic hypertension; ss.
 Designing capture oligonucleotide probes for use on a support to which complementary oligonucleotides hybridize with little mismatch.
 Human chromosome 11 linked CHD1 gene mutation screening PCR primer #67.
 Gaps
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0
 54.4%; Score 13.6; DB 6; Length 20; 80.0%; Pred. No. 9.7e+03; ive 0; Mismatches 4; Indels
 Favis R, Kliman R;
 Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 Example 5; Fig 29; 300pp; English.
 6 GCCTAGCAGATTCATGGCAC 25
 20 GTCCCGCAGATTCAAGGCAC 1
 Gerry NP,
 ВЪ.
 (CORR) CORNELL RES FOUND INC
04-APR-2001; 2001WO-US010958.
 14-APR-2000; 2000US-0197271P.
 Local Similarity 80.0%;
ses 16; Conservative
 AAZ26929 standard; DNA; 21
 18-NOV-1999 (first entry)
 of the present invention
 Barany F, Zirvi M,
 WPI; 2002-034366/04.
 Homo sapiens
 WO9945112-A2
 Synthetic
 AAZ26929;
 Query Match
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Matches
 RESULT 39
 AAZ26929/
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Gaps

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10-SEP-1999

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completed: November 18, 2005, 11:52:38 ne : 175.148 secs
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 요
 The present invention describes the human chromosome 11-linked coronary heart disease susceptibility gene (GHDI). Mutations in the CHDI locus in the grandline are indicative of a predisposition to coronary heart disease or to metabolic disorders related to lipid metabolism. Products from the present invention can be used in the diagnosis of predisposition to coronary heart disease and to metabolic disorders, including hypoalphalipoproteinaemia, familial combined hyperlipidaemia, insulin resistant syndrome X or multiple metabolic disorder, obesity, diabetes and dysalipidaemic hypertension. CHDI proteins can be used for treating coronary heart disease and metabolic disorders. The products can also be used for detection and drug screening. AAZ26832 to AAZ26841 and AAZ27027 coronary heart buman CHDI nucleotide sequences taged in the exemplification of the present invention. AAZ26842 to AAZ26862 represent exemplification of the present invention. AAZ26843 to AAZ26863 to AAZ27014 represent PCR primers used in the acreening of mutations in human CHDI; AAZ27015 represent PCR primers used in the AAZ27014 represent plannal closing of mutations in human CHDI; AAZ27015 represent closing and proteins and proteins in human CHDI; AAZ27015 represent plannal closing and proteins in human CHDI; AAZ27015 represent plannal closing and proteins and proteins in human CHDI; AAZ27015 represent plannal closing and proteins and proteins in human CHDI; AAZ27015 represent plannal closing and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins anead in the apagement proteins and proteins and proteins and prote
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 New isolated coronary heart disease susceptibility gene, used to develop products for diagnosis and treatment of coronary heart disease and metabolic disorders.
 Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
polymorphism; vascular disease; coronary artery disease; forensics;
myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
pulmonary embolism; paternity test; ds.
 Gaps
 /*tag= a
/standard_name= "Single nucleotide polymorphism"
 .;
0
 54.4%; Score 13.6; DB 2; Length 21; 80.0%; Pred. No. 9.8e+03; tive 0; Mismatches 4; Indels
 AAZ27015 to AAZ27026 represent oligonucleotides used in the exemplification of the present invention
 Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 Human gene single nucleotide polymorphism #689.
 Hess MA;
 Location/Qualifiers
 Example 6; Page 98; 297pp; English.
 Wagner S,
 6 GCCTAGCAGATTCATGGCAC 25
 21 GCTTAGAAGAGTGATGGCAC 2
 AAF95928 standard; DNA; 21 BP
 99WO-US004682.
 98US-00034941
 98US-0080934P
 (MYRI-) MYRIAD GENETICS INC
 (first entry)
 16; Conservative
 Ding W,
 (revised)
 WPI; 1999-540844/45.
 Local Similarity
 Ballinger DG,
 WO200118250-A2
 Homo sapiens
Unidentified
 04-MAR-1999;
 04-MAR-1998;
 06-APR-1998;
 18-NOV-2004
 06-JUN-2001
 variation
 AAF95928;
 Query Match
 Matches
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21 AGCCTAGCACATAGATGTCA 2

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The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also correlations to diseases. The present sequence is and phenotype the human gene SNPS shown in the specification
 Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
 Gaps
 Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
 Revised record issued on 18-NOV-2004 : The variantion feature was incorrectly given a captial \boldsymbol{V}
 ö
 Ouery Match

54.4%; Score 13.6; DB 4; Length 21;
Best Local Similarity 80.0%; Pred. No. 9.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels
 Sequence 21 BP; 4 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
 (WHED) WHITEHEAD INST BIOMEDICAL RES. (MILL-) MILLENNIUM PHARM INC.
 Example; Page 95; 242pp; English
 S AGCCTAGCAGATTCATGGCA 24
 10-SEP-1999; 99US-0153357P.
26-JUL-2000; 2000US-0220947P.
16-AUG-2000; 2000US-0225724P.
 07-SEP-2000; 2000WO-US024503
 Gargill M,
 WPI; 2001-226749/23.
 atherosclerosis.
15-MAR-2001
 Lander ES,
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EST.
 RESULT 1
AI789860
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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 REFERENCE
AUTHORS
TITLE
 JOURNAL
 FEATURES
 ORIGIN
 A1789860 ue65dl2.r
A1256664 ui29h04.y
AU102770 AU102770
AU102772 AU102772
AL932459 AL932459
AZ829250 ZM0106K17
 AU103585 AU103585
BI824288 603040689
BI824288 603040689
BAL491482 T. brucei
BE732614 601571185
AA715909 nv76g04.r
AU105060 AU105060
AU105081 AU105083
AU105081 AU105081
AU105081 AU105081
 603040689
SALK 0571
T. brucei
601571185
 2M0022K09
Arabidops
 AL496098 T. brucei
T65804 yc11h12.s1
AZ824424 2M0099D06
 AZ480878 1M0302I22
 D12221 HUM000S362
 (without alignments)
795.779 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 November 18, 2005, 11:22:09 ; Search time 1195.82 Seconds
 Description
 AZ782156 :
AL757317 /
 159776
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
 34239544 seqs, 19032134700 residues
 Total number of hits satisfying chosen parameters:
 US-10-788-779-10
25
1 GCTGAGCCTAGCAGATTCATGGCAC 25
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM nucleic - nucleic search, using sw model
 TA317F10Q
 FA372A04P
 AL932459
AZ829250
 AZ782156
AL757317
AU103585
 AU105060
AU105083
AU105084
AU105091
 BI824288
BH790466
 AU105049
 AU102772
 AA715909
 IDENTITY NUC Gapop 10.0 , Gapext 1.0
 Length DB
 Copyright
 Minimum DB seq length: 0 Maximum DB seq length: 50
 Query
Match
 EST: *
 Perfect score:
 Scoring table:
 14.2
13.8
13.8
13.4
13.2
13.2
 Score
 Database :
 Sequence:
 Searched:
 Run on:
 Result
 Š.
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| 25   | 12.4 | 49.6 |    | AL938370   | 370   | AL938370 Arabidops | abidops    |
|------|------|------|----|------------|-------|--------------------|------------|
|      | 12.4 | 49.6 |    | 7 H97155   | 2     | H97155 yv91        | yv91f07.81 |
| c 27 |      | e,   |    | 3 AZ491459 | 459   | AZ491459 1M        | 1M0325H05  |
| 28   |      | ٠.   |    | 1 BG405996 | 966   | BG405996 Ba        | Bac40g01.  |
| c 53 |      | 48.8 |    | L AI182198 | 198   | AI182198 uc        | uc64f11.r  |
|      |      | 48.8 |    | L AU102762 | 762   | AU102762 AU        | AU102762   |
|      |      | •    |    | L AU102764 | 764   | AU102764 AU        | AU102764   |
|      |      |      |    | L AU102765 | 765   | AU102765 AU        | AU102765   |
|      | •    | •    |    | L AU102768 | 768   | AU102768 AU        | AU102768   |
|      |      | •    |    | L AU102771 | 771   | AU102771 AU        | AU102771   |
|      |      | ٠    |    | L AU102773 | 773   | AU102773 AU        | AU102773   |
|      |      | 48.8 |    | L AU102775 | 775   | AU102775 AU        | AU102775   |
|      |      |      |    | L AU102777 | 777   | AU102777 AU        | AU102777   |
| ი 38 | 12.2 | 48.8 | 20 | 1 AU102778 | 778   | AU102778 AU        | AU102778   |
|      |      |      |    | L AU102782 | 782 . | AU102782 AU        | AU102782   |
|      |      |      |    | L AU102784 | 784   | AU102784 AU        | AU102784   |
|      |      | •    |    | L AU102785 | 785   | AU102785 AU        | AU102785   |
|      | •    |      |    | L AU102786 | 786   | AU102786 AU        | AU102786   |
|      |      |      |    | L AU102787 | 787   | AU102787 AU        | AU102787   |
|      |      | 48.8 |    | L AU102788 | 788   | AU102788 AU        | AU102788   |
|      | •    |      |    | AU1        | 02789 | AU102789 AU        | AU102789   |

## ALIGNMENTS

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49 bp mRNA linear EST 02-JUL-1999 ue65612.rl Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:1495991 5' Similar to SW:RCIA_CHICK P70065 CASEIN KINASE I, ALPHA ISOFORM ;, mRNA sequence.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
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Location/Qualifiers
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 Contact: Robert Strausberg, Ph.D.
 Mus musculus (house mouse)
 AI789860.1 GI:5337576
 Tumor Gene Index
Unpublished (1997)
 1.49
 Mus musculus
 MGI:933595
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DEFINITION

RESULT 2 AI256664

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ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

ORIGIN

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AU102770 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CASCTIS, mRNA sequence.
 Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Brail: yauzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
Inength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
 50 bp mRNA linear EST 28-JAN-2004 AU102772 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS01205, mRNA sequence.
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1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, Sugano, J. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Bata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S., Okubo,K.,
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
 Department of Virology
Institute of Medical Science, University of Tokyo
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 Contact: Yutaka Suzuki
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 AU102772/c
 JOURNAL
MEDLINE
PUBMED
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 8
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 ö
 ö
 This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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The washurmy Mouse EST Project
Unpublished (1996)
Contact: Marra MyMouse EST Project
Washurmy Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
 ö
 ;
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 5; Indels
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3e+04;
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Mus musculus
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 Unpublished (2000)
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University of Utah Genome Center
University of Utah
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| Corganism="RAnopheles gambiae" |
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| Clone="Vector: p
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
 ö
 AL932459 AP1 Anopheles gambiae cDNA clone NAP1-P95-D-09-5, mRNA
 ö
 1 (bases 1 to 23)
Christophides, G.K., Blass, K., Zdobnov, E.M., Carmouche, R., Benes, V.
 Gaps
 Gaps
 Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazcoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Unpublished (2002)
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 Length 50;
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 Indels
 Buropean Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany
Tel: +49 6221 387-440
Fax: +49 6221 387-306
Faxi: t49 6221 387-306
Faxi: christop@embl-heidelberg.de
Plate: P95 row: D column: 09.
Location/Qualifiers
 Ouery Match 55.2%; Score 13.8; DB 1; Best Local Similarity 72.0%; Pred. No. 1.1e+05; Matches 18; Conservative 0; Mismatches 7;
 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 Ŋ
 Location/Qualifiers
 29 GCGGAGACTGGCGGATACAAAGCAC
 Contact: Christophides GK
Fotis C. Kafatos laboratory
 AL932459.1 GI:24974439
 Conservative
 and Kafatos, F.C.
 Query Match
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KEYWORDS
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DEFINITION
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JOURNAL
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 AL932459
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(http://www.ndues_DNa.resbources/documents/dhares/). The DNA.was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreasis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 gip hR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
 5
 ö
 GSS 20-FEB-2001
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 3).

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
 chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
AZB29250
2M0106K17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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 S. 2030 E., SLC,
 Gaps
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 Rm. 308, Biomedical Polymers Research Bldg., 20
 Tel: 801 585 506
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0106 row: K column: 17
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Class: plasmid ends
High quality sequence stop: 34.
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 à
 D12221 47 bp mRNA linear BST 02-DEC-1992 HUW0008362 Liver HepG2 cell line. Homo sapiens cDNA clone s362,
 ö
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 Mus musculus
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I (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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Niederhausern, A. and Wright, D., Weiss, R.
 Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 47)
Okubo, K., Hori, N., Matoba, R., Niiyama, T., Fukushima, A., Kojima, Y.
and Matsubara, K.
 Gaps
 Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression Nat. Genet. 2, 173-179 (1992)
 Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki Nijyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara Institute for Molecular and Cellular Biology Osaka University
1-3 Yamada-oka, Suita, Osaka 565, Japan.
Location/Qualifiers
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Unpublished (2000)
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 D12221.1 GI:2148401
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 Query Match 52.8
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Matches 15, Conservative
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 Homo sapiens
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 EST.
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5
 AL757317 35 bp DNA linear GSS 01-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-120G10-012516,
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 Arabidopsis thaliana
Warayota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis thaliana
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 Bioinformatics 19 (11), 1441-1442 (2003) 22755829
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 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunm@enetics.utah.edu
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 27 ACCCTAGCCGACTCACAGCAC 7
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 ð
 Zuechtungsforsching, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene Atig05890. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: Location/Qualifiers
 /note_"PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced teatermine the genomic sequence flanking the insertion. T-DNA derived sequences were removed.
 Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 ö
 EST 28-JAN-2004
 AU103585 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone AU103585 sugano Homo sapiens cDNA library Homo sapiens cDNA clone autores
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
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 4 (Dases 1 to 35)
Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
 Gaps
 Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
 High-throughput generation of sequence indexes from T-DNA mutegenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 ö
 52.0%; Score 13; DB 9; Length 35; 76.2%; Pred. No. 2.6e+05; ive 0; Mismatches 5; Indels
 flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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 /ecotype="Col-0"
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 Weisshaar, B.
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 VERSION
KEYWORDS
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 COMMENT
 TITLE
```

```
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatcku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 ö
 BI824288 50 bp mRNA linear EST 04-OCT-2001
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/note="Organ: pooled brain, lung, testis; Vector:"
pCMV-SPORT6; Site_1: Not!; Site_2: EcorV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11452 row: b column: 23
 1 (bases 1 to 50)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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 Length 50
 Pred. No. 2.7e+05;
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Matches 16, Conservative
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BI824288
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 Homo sapiens
EMBO Rep.
 11375929
 source
 source
 VERSION
KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 MEDLINE
PUBMED
COMMENT
 REFERENCE
AUTHORS
 JOURNAL
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 FEATURES
 BI824288
 FEATURES
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Location/Qualifiers
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 Homo sapiens (human)
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JOURNAL
 JOURNAL
COMMENT
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VERSION
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 REFERENCE
 AUTHORS
 ACCESSION
 VERSION
KEYWORDS
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 AUTHORS
 KEYWORDS
 FEATURES
 FEATURES
 COMMENT
 TITLE
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 GSS 13-DEC-2000
 ö
 02-APR-2002
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/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana TDNA insertion lines ach of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
 ö
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis. (Dases 1 to 30)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
dadrinab,C., Jeske,A., Karnes,M., Kin,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
 BH790466 102-55.x Arabidopsis thaliana TDNA insertion lines SALK 057108.32.55.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_057108.32.55.x, genomic
Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g14330.
 Gaps
 Gaps
 TA317F10Q 33 bp DNA linear GSS 13-DE
T. brucei sheared genomic DNA clone 317f10, reverse sequence,
 ô
 ö
 51.2%; Score 12.8; DB 8; Length 30; 70.8%; Pred. No. 3.2e+05; ive 0; Mismatches 7; Indels
 The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 640 459
Email: ecker@salk.edu
 Length 50;
 5; Indels
 organism="Arabidopsis thaliana"
 52.0%; Score 13; DB 4; 76.2%; Pred. No. 2.7e+05;
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 Arabidopsis thaliana (thale cress)
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Unpublished (2001)
Contact: Joseph R. Ecker
 BH790466.1 GI:19883564
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 Class: TDNA tagged.
 Conservative
 Conservative
 survey sequence.
BH790466
 Query Match
Best Local Similarity
Matches 16; Conserv
 Similarity
 17;
 Query Match
 Best Local
 TA317F100
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DEFINITION
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 DEFINITION
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 RESULT 12
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 JOURNAL
 VERSION
KEYWORDS
 BH790466
 FEATURES
 TITLE
 COMMENT
 ORIGIN
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Dilect Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTet 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 ö
 BE732614 13-SEP-2000 mRNA linear EST 15-SEP-2000 001571185F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3925725 5',
 Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 39)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM752 row: column: 22.
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 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
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50 bp mRNA linear EST 28-JAN-2004
AU105049 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT00293, mRNA sequence.
 Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 AU105060 50 Bar ST 28-JAN-2004 AU105060 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
2 uzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
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 KAT04574, mRNA sequence
 AU105060.1 GI:13554581
 51.2%;
87.5%;
 Contact: Yutaka Suzuki
 4 GAGCCTAGCAGATTCA 19
 Grecciaecacacica 25
 Homo sapiens (human)
 Homo sapiens (human)
 Best Local Similarity 87.5
Matches 14; Conservative
 ı. .50
 149-156 (1997)
 Homo sapiens
 AU105049
 11375929
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 source
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VERSION
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Site_2: EcoR1; cDNA made by oligo-dr priming.
Directionally cloned into EcoR1/XhoI sites using the
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for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
 AA715909
46 bp mRNA linear EST 22-JAN-1998
nv76g04.rl NCI_CGAP_Br4 Homo sapiens cDNA clone IMAGE:123576
similar to SW:NVJ4M_GORGO P03907 NADH-UBIQUINONE OXIDOREDUCTASE
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GSP clone distribution information can be
found through the I.M. G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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 Eukaryotzi, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. (base) 1 to 46)
NCI-CRAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
 / Issue trype="normal ductal tissue"
/lab host="DH10B"
/lone lib="NCI_CGAP_Br4"
/note="Organ: breast; Vector: pAMP10; mRNA made from normal breast ductal tissue, cDNA made by oligo-dT
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 ;
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 2 CTGAGCCTAGCAGATTCATGGCAC 25
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 Homo sapiens
 ACCESSION
VERSION
KEYWORDS
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COMMENT
 RESULT 15
AA715909
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Gaps

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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Ammania; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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 Contact: Yutaka Suzuki
Department of Wirology
Institute of Wirolal Science, University of Tokyo
Institute Anirokanedai, Minatoku, Tokyo 108-8639, Japan
 Score 12.8; DB 1; Length 50;
Pred. No. 3.4e+05;
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 2 CTGAGCCTAGCAGATTCATGGCAC 25
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 Location/Qualifiers
 AU105084.1 GI:13554605
EST.
 AU105091
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 KAT10642, mRNA sequence
 51.2%;
70.8%;
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 Homo sapiens (human)
Homo sapiens
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Best Local Similarity 70.8³
Matches 17, Conservative
 Best Local Similarity 70.83
Matches 17; Conservative
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 EST.
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 AUTHORS
 JOURNAL
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 Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Bali Suzuki, Maruki, Maruki, Maruki, Maruki, Marukama, M., Suyama, M., and
Sugamo, S. Construction and characterization of a full
Inength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 50 bp mRNA linear EST 28-JAN-2004 AU105083 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAT10532, mRNA sequence.
 Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[bases 1 to 50]

202uki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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KEYWORDS
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Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
 50 bp mRNA linear EST 28-JAN-2004 AU105091 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone ADSE01778, mRNA sequence.
 ö
 ö
 AU105084 50 bp mRNA linear EST 28-JAN-2004 AU105084 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Worishita,S., Okubo,K.,
Sakaki,Y., Nakamra,Y. Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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 15; Conservative
 nh1@sanger.ac.uk
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Best Local Similarity
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AUTHORS
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 임
 Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Bail: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 GSS 04-OCT-2000
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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 Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L. (basea; 1 to 28).

Dunn, D., Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 AZ480878 1005 10kb plasmid UUGC1M library Mus musculus genomic
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
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 Email: ddunn@genetics.utah.edu
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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EMBO Rep. 2 (5), 388-393 (2001)
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 Location/Qualifiers
 26 crcacgergreacrirearacae 3
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 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@qenet
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KEYWORDS
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 REFERENCE
 AUTHORS
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 TITLE
 TITLE
 COMMENT
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 ORIGIN
 SOURCE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymerase and 74 polymerase and 74 polymerase and 74 polymerase and 74 polymerase and 74 polymerlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreais. Vector DNA was prepared from a derivative of pWD42 (gil |473214 |qb| h1229072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
 Constructed at the Institute for Genomic Research (TICR),
Constructed at the Institute for Genomic Research (TICR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED927/4 GUTTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayedetigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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 GSS 13-DEC-2000
 chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
/lab host="B. Coli strain XLIO-Gold, T1-resistant, F-"
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/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
 Gaps
 אסט אין האסטיביי (45 pt) DNA linear GSS 13-DE T. brucei sheared genomic DNA clone 372a04, forward sequence, genomic survey sequence.
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Trypanosoma brucei
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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 Length 28;
 4; Indels
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Pred. No. 3.9e+05;
0; Mismatches 4;
 /organism="Trypanosoma brucei"
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Page 10

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Gaps

6

Indels

7;

Mismatches

5e+05;

Pred. No.

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 Unpublished (2000)
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 High gality sequence starts: 1 High gality sequence stops: 1 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: polyT not found Insert Length: 232 Std Error: 0.00
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hulkunn,M., Kucaba,T., Lacy,M., Le,M., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rikin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
 Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
 Gaps
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 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
 50.4%; Score 12.6; DB 9; Length 45; 78.9%; Pred. No. 4.18+05; ive 0; Mismatches 4; Indels
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 Homo sapiens (human)
 T65804.1 GI:674849
 Contact: Wilson RK
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Matches 15; Conserv
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8889549
 Query Match
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DEFINITION
 source
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ORGANISM
 JOURNAL
MEDLINE
PUBMED
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AUTHORS
 ACCESSION
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KEYWORDS
 FEATURES
 TITLE
 COMMENT
 ORIGIN
 ORIGIN
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49.6%; Score 12.4; DB 7; Length 36;

Query Match

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinae. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfa732114|gpl/AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
 5
 GSS 20-FEB-2001
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 38)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 AZB24424
2M0099D06F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
 49.6%; Score 12.4; DB 8; Length 38;
 0.00
 Tel: 801 585 5606

Sax: 801 585 717

Email: ddunn@genetics.utah.edu

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Class: plasmid ends
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 High quality sequence stop: 38.
Location/Qualifiers
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24
 36 crcceccrccanarrcacecca 14
 Mus musculus (house mouse)
Mus musculus
 CTGAGCCTAGCAGATTCATGGCA
 AZ824424.1 GI:12994332
 Query Match
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 EST 11-DEC-1995
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
I (bases I to 42)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Horaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 42 bp mRNA linear EST 11-DEC-19
yv91f07.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:250117 3' similar to gb:X54156_rnal CELLULAR TUMOR ANTIGEN
 Figures: INAGE Consortium, LINL

Source: INAGE Consortium, LINL

This clone is available royalty-free through LiNL; contact the

INAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1247 Std Error: 0.00
 Gaps
 Gaps
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0
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 Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
 Score 12.4; DB 7; Length 42;
Pred. No. 5.1e+05;
0; Mismatches 6; Indels
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 (HUMAN);, mRNA sequence.
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 Email: est@watson.wustl.edu
 49.6%; Scor.
72.7%; Pred
0; }
 Query Match
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Matches 16; Conservative (
 H97155.1 GI:1114198
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 Homo sapiens (human)
 16; Conservative
 Homo sapiens
 Similarity
 Wilson, R.
 Query Match
Best Local S
 source
 SOURCE
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 RESULT 26
H97155/c
 Matches
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JOURNAL
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 AUTHORS
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 Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3956610. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI Gor Plant Breeding Research in the context of the GAB1-Kat project (GAB1-Kat is part of the German Plant Genomics program designated 'GAB1. Information on line availability can be found at: Location/Qualifiers
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
 AL938370 39 bp DNA linear GSS 01-APR-2004
Arabidopsis thaliana T-DNA flanking sequence GK-234D12-014337,
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 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
 /ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
 for
 clone lib="Arabidopsis thaliana T-DNA insertion lines"
 Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
 Gaps
 Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A.
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
 ;
0
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 Indels
 4 (bases 1 to 39)
Rosso,M.G., Li,Y., Strizhov,N. and Weisshaar,B.
Direct Submission
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 /db_xref="taxon:3702"
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 Arabidopsis thaliana (thale cress)
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 10 dergadantecadargearge 31
 genomic survey sequence
 AL938370.1 GI:24370164
 Arabidopsis thaliana
 16; Conservative
 Weisshaar, B.
 Weisshaar, B.
Best Local Similarity
Matches 16; Conserv
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 2755829
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RESULT 27

GSS.

KEYWORDS

SOURCE

VERSION

ACCESSION

ORGANISM

REFERENCE AUTHORS

JOURNAL

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Xhof; The cDNA library was constructed from mRNA isolated
from stem tissue of 1 month old greenhouse grown plants
for the cultivar Raiden. Complementary DNA was
for the cultivar Raiden. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dI) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DHUBH host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy Shoemaker."
 1 (bases 1 to 50)
Shoemaker,R. Kaim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
 Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email:
 BG405996 50 bp mRNA linear EST 22-JUL-2004 sac40g01.y1 Gm-c1062 Glycine max cDNA clone GENOME SYSTEMS CLONE LD: Cm-c1062-2594 5', mRNA sequence.
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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 4444 Förest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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49.6%; Score 12.4; DB 4; Length 50;
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 Glycine max
 BG405996
 Glycine.
 ω
 25
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DEFINITION
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 TITLE
JOURNAL
COMMENT
 RESULT 28
 ACCESSION
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KEYWORDS
SOURCE
 REFERENCE
 AUTHORS
 BG405996
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 Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwapa (graph and propared from a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
WR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
 AZ491459 10Kb plasmid UUGCIM library Mus musculus genomic
 ô
 adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Gaps
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 Query Match 49.6%; Score 12.4; DB 8; Length 44; Best Local Similarity 92.9%; Pred. No. 5.2e+05; Matches 13; Conservative 0; Mismatches 1; Indels
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 AZ491459.1 GI:10663188
 /sex="Male"
 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
 AZ491459
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source

FEATURES

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Gaps

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RESULT 29 AI182198/c LOCUS

SOURCE

KEYWORDS

REFERENCE

AUTHORS

TITLE JOURNAL

COMMENT

ACCESSION VERSION

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50 bp mRNA linear EST 28-JAN-2004 AU102764 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CASO10112, mRNA sequence.
 Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
A-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Yv. Yoshitokomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
AU102762 AUGano Homo sapiens CDNA library Homo sapiens CDNA clone
 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primatee; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Otck,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S., Okubo,K., Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
 Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal Minatoku, Tokyo 108-8639, Japan
Email: yeuzukideims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
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 AU102764.1 GI:13552285
 Contact: Yutaka Suzuki
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 149-156 (1997)
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 REFERENCE
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KEYWORDS
SOURCE
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 AI182198 43 bp mRNA linear EST 08-OCT-1998 uc64f11.rl Soares mammary_gland_NDWMG Mus musculus cDNA clone IMAGE:1430445 5' Fimilar to TR:Q00574 Q00574 FILAMIN. ;, mRNA
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Marra,M., Hillier,L., Allen,M., E.M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
 ö
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Gaps
 Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 .
0
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Possible reversed clone: similarity on wrong strand
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High quality sequence stop: 1.
Location/Qualifiers
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 Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
 Waterston, R.
The WashU-HHMI Mouse EST Project
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 23
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14; Conservative
 sex="male"
 7 CCTAGCAGATTCATGGC
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 Mus musculus
 Query Match
Best Local Similarity
 AI182198
AI182198.1
 MGI:914513
 sequence.
 EST.
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source

FEATURES

31

Matches

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AU102762/c

RESULT 30

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Gaps

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11375929
 11375929
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 RESULT 34
AU102771/c
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 DEFINITION
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 Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2),
Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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 AU102765 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS01084, mRNA sequence.
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LOCUS AU102768 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU102768 Sugano Homo sapiens CDNA library Homo sapiens cDNA clone
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
L (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
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 Department of Virology
 Contact: Yutaka Suzuki
 48.8%;
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Matches 17; Conservative
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COMMENT
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50 bp mRNA linear EST 28-JAN-2004 AU102771 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CASJ050, mRNA sequence.
 Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitokomo.Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 Department of Virology Institute of Medical Science, University of Tokyo firstiute of Medical Science, University of Tokyo Marchandai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Bata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
 Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 50)

Suzuki,Y., TairaH., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale
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 Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 AU102775 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone CAS04123, mRNA sequence.
 EST 28-JAN-2004
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 Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla; Butheria, Primates; Catarrhini, Hominidae, Homo.

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

REBO Rep. 2 (5), 388-393 (2001)
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Matches 17; Conserv
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AUTHORS
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Contect: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: yanickanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,R., Suyama,A. and
Sugano,S. Construction and characterization of a full
Inenth-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
 ..
 50 bp mRNA linear EST 28-JAN-2004 AU102777 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CASO5434, mRNA sequence.
 Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Baril: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitokno-Vakkagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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SOURCE
 REFERENCE
 AUTHORS
 JOURNAL
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 Department of Vicology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1-ength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
 AU102782 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS07667, mRNA sequence.
AU102782
AU102782.1 GI:13552303
EST.
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 ö
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
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 Contact: Yutaka Suzuki
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirotkanedai, Minatoku, Tokyo 108-8619, Japan
Bani: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
 Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shizokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1ength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogali, T., Tanaka, T., Morishima-Sugano, J., Sese, J., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
Homo sapiens
Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bikaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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693, App 17, Appl 104928,

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104929, 26, Appl 56, Appl 56, Appl 56, Appl 56, Appl 56, Appl

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Sequence 4829, Ap Sequence 21353, A

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Run on:

Sequence:

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Sequence 10, Application US/07989160
Fatent No. 5429923
GENERAL INFORMATION:
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
 US-09-396-196G-54320

US-08-916-576B-33

US-08-916-576B-33

US-09-657-472-693

US-09-647-563-17

US-09-396-196G-104928

US-09-396-196G-104929

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US-09-396-196G-104929

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Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 25; Conservative 0; Mismatches 0;
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 COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
TELECHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
ITARE: mucleic acid
STRANDEDNESS: single
 ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
 GCTGAGCCTAGCAGATTCATGGCAC 25
 STATE: Massachusetts
COUNTRY: U.S.A.
 MOLECULE TYPE: CDNA
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 RESULT 1
US-07-989-160-10
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Listing first 45 summaries
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 Issued Patents NA:*
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Match Length
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 Length 38;
 FALCIL NO. 00939/4

APPLICANT: Onc. Koichiro

APPLICANT: Ontomo, Toshihiko

APPLICANT: Ontomo, Toshihiko

APPLICANT: Ontomo, Toshihiko

APPLICANT: Tsuchiya, Masayuki

APPLICANT: Yoshimara, Yasushi

APPLICANT: Yoshimara, Yasushi

APPLICANT: Koishihara, Yasushi

TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY

FILE REFERENCE: 35029-20007.00

CURRENT APPLICATION NUMBER: US/09/269,921

CURRENT APPLICATION NUMBER: PCT/JP97/03553

EARLIER FILING DATE: 1999-04-01

EARLIER FILING DATE: 1997-10-03

EARLIER FILING DATE: 1997-10-03

EARLIER FILING DATE: 1997-10-04

NUMBER OF SEQ ID NOS: 137

SOFTWARE: Patentin Ver. 2.0

EARLIER PATENTH: APPLICATION NUMBER: DE CATSE

LEARLIER FILING DATE: 1996-10-04
 Indels
 Query Match

56.8%; Score 14.2; DB 3;

Best Local Similarity 84.2%; Pred. No. 9.8e+02;

Matches 16; Conservative 0; Mismatches 3;
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-193
ATTORNEY AGENT INFORMATION:
NAME: WEGNERY, HAZOLD C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
 Sequence 17, Application US/08039198B; Patent No. 5858725; GENERAL INFORMATION: APPLICANT: CROWE, JAMES SCOTT APPLICANT: LEWIS, ALAN PETER
 RESULT 4
US-09-259-921-50
Sequence 50, Application US/09269921
Patent No. 6699974
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 16 GGTGTGCCAAGCAGATTCA 34
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 TYPE: DNA ORGANISM: Artificial Sequence
 TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 19-OCT-1994
 ; TOPOLOGY: linear
US-08-646-265A-37
 US-08-039-198B-17
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 Query Match 58.4%; Score 14.6; DB 4; Length 29; Best Local Similarity 81.0%; Pred. No. 5.7e+02; Matches 17; Conservative 0; Mismatches 4; Indels
 GENERAL NO. 0/23240

GENERAL WINTORMATION:
APPLICANT: Wang, Wei
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Albert
TITLE OF INVENTION: Antibodies that bind chemokine TECK
FILE REFERENCE: DX0589K1B US
CURRENT PEPLICATION NUMBER: US/10/039,659A
CURRENT PEPLICATION NUMBER: US 60/021,664
PRIOR PLILING DATE: 1997-07-03
PRIOR FILING DATE: 1996-07-05
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PRIOR PLICATION NUMBER: US 60/028,329
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PRIOR APPLICATION NUMBER: US 60/048,593
PRIOR PLING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 24
LENTH: 29
 Sequence 37, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A FILING DATE: 09-SEP-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION NUMBER: WO PCT/JD94/01763
 ; OTHER INFORMATION: exon 3-specific CRAM primer US-10-039-659A-24
 ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
1 GCTGAGCCTAGCAGATTCATGGCAC 25
 COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6723520
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 TYPE: DNA
ORGANISM: Artificial Sequence
 CITY: Washington STATE: D.C.
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 RESULT 3
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 Score 14.2; DB 2; Length 41; Pred. No. 1e+03;
 3; Indels
 Sequence 22, Application US/08465313
Patent No. 5997867
GENERAL INFORMATION:
APPLICANT: WALDMANN, HERMAN
APPLICANT: SIMS, MARTIN J.
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMMILTON, BROOK, SMITH & REYNOLDS, P.C.
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,313
FILING DATE: 05-JUN-1995
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/182,067
FILING DATE: 12-MRR.1994
PRIOR APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: GS 9115364.3
ATMAME: BROOK, DAVID E.
REGISTRATION NUMBER: 22,592
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 CLASSIFICATION A45

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01289
FILING DATE: 15-UUL-1992
PRIOR APPLICATION NUMBER: GB 9115364.3
FILING DATE: 15-UUL-1991
APPLICATION NUMBER: GB 9115364.3
FILING DATE: 16-UUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G:
REGISTRATION NUMBER: 30.377
REFERENCE/DOCKET NUMBER: 31.937
REFERENCE/DOCKET NUMBER: 31.937
RELECOMMUNICATION INFORMATION:
FILEDOMUNICATION INFORMATION:
TELEPAX: (202) 783-6040
TELEPAX: (202) 783-6040
TELEPAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
 1 GCTGAGCCTAGCAGATTCA 19
 22 GGTGTGCCAAGCAGATTCA 40
 Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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 STREET: TWO PAGE CITY: LEXINGTON STATE: MASSACHUSETTS
 ; ANTI-SENSE: NO
US-08-182-067-22
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US-08-465-313-22
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 PREPARATION OF CHIMAERIC ANTIBODIES RECOMBINANT PCR STRATEGY
 JS-GQUENCE 22, Application US/08182067

Patent No. 598579

GENERAL INFORMATION

APPLICANT: SIMS, MARTIN

APPLICANT: CROWE, SCOTT

TITLE OF INVENTION

MUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rothwell, Figg Ernst & Kurz

STREET: Suite 701-E, 555 Thirteenth St., N.W

CITY: Washington

STATE D. C.

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/182,067
TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODII
TITLE OF INVENTION: RECOMBINANT PCR STRATEGY
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STRATE: VIRGINIA
COUNTRY: U.S.A.
ZIPP 22201-4114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC COMPALIBLE
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 TYPE: nucleic acid
STRANDEDNESS: single
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US-08-039-198B-17
 US-08-182-067-22
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OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,620A
FILING APPLICATION ADATA:
APPLICATION NUMBER: US 08/235,705
FILING DATE: 29-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,480
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,601
FILING DATE: 12-CT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/424,233
FILING DATE: 12-CT-1989
FILING DATE: 12-CT-1989
FILING DATE: 12-FEB-1988
FILING DATE: 12-FEB-1988
PRIOR APPLICATION NUMBER: GB 88036228
FILING DATE: 12-FEB-1988
PRIOR APPLICATION NUMBER: GB 8804644
 Sequence 41, Application US/08407620A
Patent No. 6569430
GENERAL INFORMATION:
APPLICANT: CLARK, MICHAEL R.
APPLICANT: RIECHMANN, HERMAN
APPLICANT: RIECHMANN, LUTZ
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 FILING DATE: 25-FEB-1988
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEGNARD C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-325
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
 1 GCTGAGCCTAGCAGATTCA 19
 22 GGTGTGCCAAGCAGATTCA 40
 INDERINAL (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR EQ. ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
 CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
 STRANDEDNESS: single
 LENGTH: 49 base par
TYPE: nucleic acid
 TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
 S
 US-08-407-620A-41
 ; ANTI-SENSE:
US-09-378-967-22
 RESULT 9
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 Gaps
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 56.8%; Score 14.2; DB 2; Length 41; 84.2%; Pred. No. 1e+03; ive 0; Mismatches 3; Indels
 Sequence 22, Application US/09378967

| Patent No. 668969
| GENERAL INFORMATION |
| APPLICANT: SIMS, MARTIN J. |
| APPLICANT: SIMS, MARTIN J. |
| APPLICANT: CROME, J. SCOTT |
| TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18 |
| NUMBER OF SEQUENCES: 35 |
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. |
| STREET: TWO MILITIA DRIVE |
| CITY: LEXINGTON |
| STREET: WASACHUSETTS |
| COUNTRY: USA
 CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/378,967
FILING DATE: 23-40g-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/465,313
FILING DATE: 05-JUN-1995
PRIOR APPLICATION NUMBER: US 08/182,067
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/01289
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

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PRIOR APPLICATION DATA:
REPERENCE/DOCKET NUMBER: LYNX91-01A2
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 861-9540
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
 LYNX91-01A3
 APPLICATION NUMBER: GB 9115364.3
PILING DATE: 16-7UL-1991
ATTORNEY/AGENT INFORMATION:
NAME: WENDLER, HELEN E.
REGISTRATION NUMBER: 37,964
REPERENCE/DOCKET NUMBER: LYNX91-01A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D 861-6240
INFORMATION FOR SEQ 1D NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 22 GGTGTGCCAAGCAGATTCA 40
 1 GCTGAGCCTAGCAGATTCA 19
 Query Match 56.8 Best Local Similarity 84.2 Matches 16; Conservative
 TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

US-08-465-313-22
 nucleic acid
 02421
 US-09-378-967-22
 RESULT 8
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 55.2%; Score 13.8; DB 4; Length 25; 88.2%; Pred. No. 1.46+03; ive 0; Mismatches 2; Indels
 Length 25;
 Indels
 Sequence 4331, Application US/09396196G
Sequence 4331, Application US/09396196G
Patent NO. 6821724
GENERAL INFORMATION
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REPRENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PLING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43321
LENGTH: 25
 APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FESESEG for Windows Version 4.0
LENGTH: 25
 Ouery Match 55.2%; Score 13.8; DB 4; Best Local Similarity 88.2%; Pred. No. 1.4e+03; Matches 15; Conservative 0; Mismatches 2;
 RESULT 13
US-09-396-196G-43332
; Sequence 43332, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
 RESULT 14
US-09-396-196G-61733/c
; Sequence 61733, Application US/09396196G
; Patent No. 6821724
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 Query Match
Best Local Similarity 88.2°
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US-09-396-196G-43321
 ORGANISM: mus musculus
US-09-396-196G-43332
 RESULT 12
US-09-396-196G-43321
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 Query Match 56.8%; Score 14.2; DB 4; Length 49; Best Local Similarity 84.2%; Pred. No. 1e+03; Matches 16; Conservative 0; Mismatches 3; Indels
 55.2%; Score 13.8; DB 4; Length 25; 88.2%; Pred. No. 1.4e+03; Live 0; Mismatches 2; Indels
 56.0%; Score 14; DB 4; Length 25; 77.3%; Pred. No. 1.1e+03; tive 0; Mismatches 5; Indels
 RESULT 10
US-09-396-196G-24574/C
; Sequence 24574, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
APPLICANT: Michael Mittmann
; APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affwerrix, Inc.
TITLE OF INVENTY Affwerrix, Inc.
TITLE OF INVENTY APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE FRAESEQ for Windows Version 4.0
; SEQ ID NO 24574
LUSCORD APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION OF APPLICATION
 APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE FRAESEQ for Windows Version 4.0
SEQ ID NO 43320
 US-09-396-196G-43320
; Sequence 43320, Application US/09396196G
; Patent No. 682724
; GENERAL INPORMATION:
 1 GCTGAGCCTAGCAGATTCATGG 22
 25 GCAGAGACAGCAGACCCATGG 4
 1 GCTGAGCCTAGCAGATTCA 19
 12 GGTGTGCCAAGCAGATTCA 30
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
 Query Match
Best Local Similarity 77.3
Matches 17; Conservative
 Query Match 55.2
Best Local Similarity 88.2
Matches 15; Conservative
STRANDEDNESS: single
 TYPE: DNA
CORGANISM: Mus musculus
US-09-396-196G-24574
 TYPE: DNA
ORGANISM: mus musculus
 US-09-396-196G-43320
 ; MOLECULE TYP!
US-08-407-620A-41
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6 GCCTAGCAGATTCATGGCAC 25
 6 GCCTAGCAGATTCATGGCAC 25
 21 GCTTAGAAGAGTGATGGCAC 2
 25 GCCAGCATCTCCATGGCAC 6
 CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 104
LENGTH: 21
 Query Match
Best Local Similarity 80.04
Matches 16; Conservative
 sapiens
 TYPE: DNA
ORGANISM: primer
US-09-262-773-104
 ; ORGANISM: Homo E
US-09-866-108A-5529
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 Sequence 104, Application US/09262773
Sequence 104, Application US/09262773
General INCORATION:
General INCORATION:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Ballinger, Susanne
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myriad 3
CURRENT APPLICATION NUMBER: US/09/262,773
 55.2%; Score 13.8; DB 4; Length 25; 88.2%; Pred. No. 1.46+03; Live 0; Mismatches 2; Indels
 55.2%; Score 13.8; DB 4; Length 25; 88.2%; Pred. No. 1.4e+03; ive 0; Mismatches 2; Indels
 RESULT 15
US-09-396-196G-110219/C
Sequence 110219, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
FILLE REFERENCE: 3101.
FILLE REFERENCE: 3101.
CURRENT FILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NO 110219
LENTH: 25
 APPLICANT: Michael Mittmann
APPLICANT: Michael Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 61733
 3 TGAGCCTAGCAGATTCA 19
 7 CCTAGCAGATTCATGGC 23
 21 rgagccragaagarcca 5
 25 CCTCCCAGATTCATGGC 9
 Query Match
Best Local Similarity 88.2
Matches 15, Conservative
 Best Local Similarity 88.2
Matches 15, Conservative
 ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-61733
 : mus musculus
GENERAL INFORMATION:
 US-09-396-196G-110219
 RESULT 16
US-09-262-773-104/c
 TYPE: DNA ORGANISM:
 Query Match
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 APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: GRANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: ASONICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PEROR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PELICATION NUMBER: GB 24263.6

PRIOR PELING DATE: 2000-010-04

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

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PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663

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PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663
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54.4%; Score 13.6; DB 3; Length 21; 80.0%; Pred. No. 1.7e+03; ive 0; Mismatches 4; Indels
 Query Match 54.4%; Score 13.6; DB 4; Length 25; Best Local Similarity 80.0%; Pred. No. 1.8e+03; Matches 16; Conservative 0; Mismatches 4; Indels
 S-09-866-108A-5529/c
Sequence 5529, Application US/09866108A
Patent No. 6686188
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
 LING DATE:
 US-09-866-108A-5531
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 APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
TITLE OF INVENTION: MACK
TITLE OF INVENTION: MACK
TITLE OF INVENTION: MYORICA-T
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-27
PRIOR PLILOR DATE: 2000-09-27
PRIOR PLILOR DATE: 2000-09-27
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PLILOR DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00666
PRIOR PLILOR DATE: 2001-01-30
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PRIOR PLILOR DATE: 2001-01-30
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 APPLICANT: CHEN, Wensheng
PEPLICANT: SHAMNON, Mark
TITLE OF INVENTION: MYSOIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
 Gaps
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 ch 54.4%; Score 13.6; DB 4; Length 25; I Similarity 80.0%; Pred. No. 1.8e+03; 16; Conservative 0; Mismatches 4; Indels
 CURRENT APPLICATION NUMBER: US/09/866,108A CURRENT FILING DATE: 2001-05-25 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
5-09-866-108A-5530/c
Sequence 5530, Application US/09866108A
Patent No. 6686188
 US-09-866-108A-5531/c
; Sequence 5531, Application US/09866108A
; Patent No. 6686188
 6 GCCTAGCAGATTCATGGCAC 25
 24 GCCCAGCATCTCCATGGCAC 5
 GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
 GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
 RANK, David R. CHEN, Wensheng
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5530
 Query Match
Best Local Similarity
 APPLICANT:
 Matches
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PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PLICATION NUMBER: PCT/USO1/00667
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
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PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE:
 Patent No. 6686188

Patent No. 6686188

Patent No. 6686188

APPLICANT: GAN, Yizhong

APPLICANT: Ji, Yoongang

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: APANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE FILE REFERENCE: AEOMICA-7
 Gaps
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 Score 13.6; DB 4; Length 25;
Pred. No. 1.8e+03;
0; Mismatches 4; Indels
 CURRENT PEPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
 APPLICATION NUMBER: PCT/US01/00665
 APPLICATION NUMBER: PCT/US01/00668
 .09-866-108A-5532/c
Sequence 5532, Application US/09866108A
 6 GCCTAGCAGATTCATGGCAC 25
 GCCCAGCATCTCCATGGCAC 4
 54.4%;
 Query Match
Best Local Similarity 80.09
Matches 16; Conservative
 ORGANISM: Homo sapiens
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 PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-27
PRIOR PELING DATE: 2000-05-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
 Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: PENN, Sharron G.
APPLICANT: APPLICANT: ABANCEL, David K.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 5532
LENGTH: 25
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 54.4%; Score 13.6; DB 4; Length 25; 80.0%; Pred. No. 1.8e+03; 1ive 0; Mismatches 4; Indels
 ch 54.4%; Score 13.6; DB 4; Length 25; 1. Similarity 80.0%; Pred. No. 1.8e+03; 16; Conservative 0; Mismatches 4; Indels
 Sequence 5533, Application US/09866108A
 6 GCCTAGCAGATTCATGGCAC 25
 6 GCCTAGCAGATTCATGGCAC 25
 21 GCCCAGCATCTCCATGGCAC 2
 22 GCCCAGCATCTCCATGCCAC 3
 Query Match
Best Local Similarity 80.0°
Matches 16; Conservative
 ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-866-108A-5532
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5533
 Query Match
Best Local Similarity
Matches 16; Conserv
 US-09-866-108A-5533/c
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chen, Daniel

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT APPLICATION NUMBER: US/09/298,850

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER FILING DATE: 1999-04-21

EARLIER PILING DATE: 1999-11-23

EARLIER FILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-04-21

NUMBER: OF SEQ ID NOS: 11796

SEQ ID NO 3104

LENGTH: 47
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 Score 13.4; DB 4; Length 25;
Pred. No. 2.3e+03;
0; Mismatches 1; Indels
 Score 13.6; DB 4; Length 47;
Pred. No. 2.1e+03;
1; Mismatches 5; Indels
 ; OTHER INFORMATION: 99-2342-217 : polymorphic base C or T US-09-422-978-3104
 GENERAL INC. 0021/24

GENERAL INCORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REPERENCE: 3101.1
CURRENT APLICATION NUMBER: US/09/396,196G
CURRENT PILING DATE: 1999-09-15
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
ILBNGTH: 25
 US-09-396-196G-22130/c
; Sequence 22130, Application US/09396196G
; Patent No. 6821724
 US-09-422-978-3104; Sequence 3104, Application US/09422978; Patent No. 6537751
 4 GAGCCTAGCAGATTCATGGCAC 25
 GAGCCTTGGACTTTCATGACAY 24
 4 GAGCCTAGCAGATTCATGGC 23
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 24 GCGACCAGCACCTTCATGGC
 Query Match 54.4%;
Best Local Similarity 72.7%;
Matches 16; Conservative
 Query Match 53.6%;
Best Local Similarity 93.3%;
Matches 14; Conservative
 10 AGCAGATTCATGGCA 24
 CRGANISM: Mus musculus US-09-396-196G-22130
 ORGANISM: Homo Sapiens
 NAME/KEY: allele
 LOCATION: 24
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 Gaps
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 Query Match 54.4%; Score 13.6; DB 4; Length 25; Best Local Similarity 80.0%; Pred. No. 1.8e+03; Matches 16; Conservative 0; Mismatches 4; Indels
 54.4%; Score 13.6; DB 4; Length 25; 80.0%; Pred. No. 1.8e+03; ive 0; Mismatches 4; Indels
 54.4%; Score 13.6; DB 4; Length 25; 80.0%; Pred. No. 1.8e+03;
 4; Indels
 Sequence 104940, Application US/09396196G
Patent No. 6821724
GENERAL INPORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT APPLICATION NUMBER: 60/100,678
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-17
MINDER
 US-09-396-196G-65707/c

Sequence 65707, Application US/09396196G

Sequence 65707, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: APFLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1
 0; Mismatches
 CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65707
LENGTH: 25
 NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 104940
LENGTH: 25
 3 TGAGCCTAGCAGATTCATGG 22
 5 AGCCTAGCAGATTCATGGCA 24
 24 AGTCTAGCTCATTCACGGCA 5
 Query Match
Best Local Similarity 80.0
Matches 16; Conservative
 Conservative
 : LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24817
 ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65707
 CRGANISM: mus musculus US-09-396-196G-104940
 Local Similarity
nes 16; Conserv
 RESULT 25
US-09-396-196G-104940/c
SEQ ID NO 24817
 Query Match
 Matches
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TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G TITLE OF INVENTION: Protein-Coupled Receptors
FILE REPREMENT SERRENCE: AREA-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR PILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 105
LENGTH: 33
 Query Match 53.6%; Score 13.4; DB 4; Length 33; Best Local Similarity 73.9%; Pred. No. 2.4e+03; Matches 17; Conservative 0; Mismatches 6; Indels
 ALUKESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON STATE: DC
 KAESULT 31
US-08-916-576B-33/C

Sequence 33, Application US/08916576B
FALENT NO. 6171816
FALENT NO. 171816
FAPLICANT: YU, GUO-LIANG
APPLICANT: BILLOW PARRICK J.
APPLICANT: ENDRES, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSITT
STREET: 1100 NEW.
CITY.
 ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,576B

FILING DATE:
 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERRICE/DOCKET NUMBER: 36,688
TELECOMMUNICATION INFORMATION:
 1 GCTGAGCCTAGCAGATTCATGGC 23
 TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS:
 49 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 Liaw, Chen W.
 ORGANISM: Homo sapiens
US-09-826-509-105
 Lin, I-Lin
 ; TOPOLOGY: linear;
; MOLECULE TYPE: CDN;
US-08-916-576B-33
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 Score 13.4; DB 4; Length 25;
Pred. No. 2.3e+03;
0; Mismatches 1; Indels
 ch 53.6%; Score 13.4; DB 4; Length 25; 1 Similarity 73.9%; Pred. No. 2.3e+03; 17; Conservative 0; Mismatches 6; Indels
 KESULT 28
US-09-396-196G-22131/C
Sequence 22131, Application US/09396196G
Patent No. 6821724
JGENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
JAPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Mack
CURRENT: David Mack
JTLE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
RICHER TILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS 2231
LEAR OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTROL OF SECTION NOWER: CONTR
 US-09-396-196G-54320/c
; Sequence 54320, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: AFFINENT: Navid Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54320
 2 CTGAGCCTAGCAGATTCATGGCA 24
 24 CTGAGCAGAGCTGATGCAGGGAA 2
 Sequence 105, Application US/09826509
Patent No. 6806054
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
 53.6%;
93.3%;
 10 AGCAGATTCATGGCA 24
 16 AGCAGATTCATGGAA 2
 Query Match
Best Local Similarity 93.3
Matches 14; Conservative
22 AGCAGATTCATGGAA
 TYPE: DNA
CORGANISM: Mus musculus
US-09-396-196G-22131
 TYPE: DNA
CORGANISM: mus musculus
US-09-396-196G-54320
 Query Match
Best Local Similarity
 RESULT 30
US-09-826-509-105
 Matches
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Gaps

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TYPE: DNA
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 ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON
Query Match 53.6%; Score 13.4; DB 3; Length 49; Best Local Similarity 73.9%; Pred. No. 2.7e+03; Matches 17; Conservative 0; Mismatches 6; Indels
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/078,337
FILING DATE: 21-Peb-2002
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION: UNKNOWN>
PRIOR APPLICATION NUMBER: 08/916,576
FILING DATA:
APPLICATION NUMBER: 08/916,576
FILING DATA:
APPLICATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.050001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 53.6%; Score 13.4; DB 4; Length 49; 73.9%; Pred. No. 2.7e+03; tive 0; Mismatches 6; Indels
 ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
 TOPOLOGY: linear;
MOLECULE TYPE: cDNA;
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-078-337-33
 1 GCTGAGCCTAGCAGATTCATGGC 23
 33 GCTGAGTGTAGCATCATGATGGC 11
 1 GCTGAGCCTAGCAGATTCATGGC 23
 33 GCTGAGTGTAGCATCATGATGGC 11
 Sequence 693, Application US/09657472; Patent No. 6727063; GENERAL INFORMATION: APPLICANT: Lander, Eric S.; APPLICANT: Cargill, Michele
 COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 APPLICANT: YU, GUO-LIANG
DILLON, PATRICK J.
EBNER, REINHARD
 Sequence 33, Application US/10078337
Patent No. 6818412
GENERAL INFORMATION:
 (202) 371-2540
 LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
 17; Conservative
 Best Local Similarity
 RESULT 33
US-09-657-472-693/c
 RESULT 32
US-10-078-337-33/c
 Query Match
 Matches
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Sequence 17, Application US/09647563

Patent No. 6706475

GENERAL INFORMATION:
APPLICATION: Oligonucleotide Probes for Detecting Enterobacteriaceae and Quino TITLE OF INVENTION: Oligonucleotide Probes for Detecting Enterobacteriaceae and Quino; TITLE OF INVENTION: Resistant Enterbacteriaceae
FILE REFERENCE: 6395-57017
CURRENT APPLICATION NUMBER: US/09/647,563
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.0
SEQ ID NO 17
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APPLICANT: DOLON, SCACETY
APPLICANT: DOLON, GEORGE Q.
APPLICANT: MCCATCHY, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2025-1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
PRIOR PLING DATE: 2000-09-07
PRIOR PLING DATE: 1999-09-10
PRIOR PLING DATE: 2000-07-26
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PRIOR FILING DATE: 2000-07-26
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PRIOR FILING DATE: 2000-09-16
PRIOR FILING DATE: 2000-09-16
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 52.8%; Score 13.2; DB 4; Length 21; 75.0%; Pred. No. 2.8e+03;
 52.8%; Score 13.2; DB 4; Length 25; 83.3%; Pred. No. 2.9e+03; live 0; Mismatches 3; Indels
 Indels
 RESULT 35
US-09-396-104928/C
; Sequence 104928/Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: AFFINEERIX, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
 1; Mismatches
 CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
 5 AGCCTAGCAGATTCATGGCA 24
 21 AGCCTAGCACRTAGATGTCA 2
 6 GCCTAGCAGATTCATGGC 23
 25 GCCTAGTACGTTCATGGC 8
 Query Match
Best Local Similarity 75.Ut
The Section 15, Conservative
 TYPE: DNA; CRGANISM: Escherichia coli
US-09-647-563-17
 Matches 15; Conservative
 ; ORGANISM: Homo sapiens
US-09-657-472-693
 Query Match
Best Local Similarity
 RESULT 34
US-09-647-563-17/c
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Gaps

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Sequence 56. Application US/08484993B
; Sequence 56. Application US/08484993B
; Patent No. 5837497
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Podolski, Joseph S.
; TITLE OF INVENTION: Materials and Methods for Immunocontraception
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STREET: Illinois
; COUNTRY: United States of America
ZIP: 66066-4402
 Score 13.2; DB 3; Length 33;
Pred. No. 3.18+03;
0; Mismatches 3; Indels
 52.8%; Score 13.2; DB 2; Length 36; ilarity 83.3%; Pred. No. 3.1e+03; Conservative 0; Mismatches 3; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,993B
 CUREMI APPLICATION DATE
CURSENT FEBLICATION DATE:
FILING DATE: 09-NOV-1993
FILING DATE: 09-NOV-1993
FILING DATE: 09-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
FILING DATE: 29-JAN-1993
ATONENY, AGENT INPORMATION:
NAME: CLOUGH, DAVIG W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31745
TELECHONE: 312/474-6653
TELECHONE: 312/474-6653
 COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 US-08-484-158B-56; Sequence 56, Application US/08484158B; Patent No. 5976545
 12 AGCCTAGCAGGTTCGGGG 29
 5 AGCCTAGCAGATTCATGG 22
 crascasarcrarsscs 22
 52.8%;
 Query Match
Best Local Similarity 83.33
Matches 15; Conservative
 TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 36 base pairs
 nucleic acid
 Local Similarity
nes 15; Conserv
 STRANDEDNESS:
 ; MOLECULE TYPE;
US-08-484-993B-56
 US-08-484-993B-56
 US-09-136-605-26
 LENGTH:
 Query Match
 RESULT 39
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 Sequence 26, Application US/09136605A

Sequence 26, Application US/09136605A

Patent No. 6140052

GENERAL INFORMATION:

APPLICANT: He, Tong-Chuan

APPLICANT: Vogelstein, Bert

TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to

TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to

TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to

TITLE OF INVENTION: WHERE: US/09/136,605A

CURRENT APPLICATION NUMBER: US/09/136,605A

CURRENT FILING DATE: 1998-08-20

EARLIER APPLICATION NUMBER: 09/021,355

EARLIER PILING DATE: 1998-01-06

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSEQ for Windows Version 3.0
 52.8%; Score 13.2; DB 4; Length 25; 83.3%; Pred. No. 2.9e+03; Live 0; Mismatches 3; Indels
 52.8%; Score 13.2; DB 4; Length 25; 83.3%; Pred. No. 2.9e+03; ive 0; Mismatches 3; Indels
 RESULT 36
US-09-306-106G-104929/C

Sequence 104929, Application US/09396196G

Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SEQ ID NO 104929
LEASTHEE SESTES OF Windows Version 4.0
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 104928
LENGTH: 25
 6 GCCTAGCAGATTCATGGC 23
 6 GCCTAGCAGATTCATGGC 23
 25 GACCAGCAGCTTCATGGC
 24 daccadcadcrircardec
 Query Match
Best Local Similarity 83.33,
Conservative
Conservative
 Best Local Similarity 83.3
Matches 15; Conservative
 TYPE: DNA ORGANISM: mus musculus
 ; ORGANISM: mus musculus
US-09-396-196G-104929
 TYPE: DNA
ORGANISM: Homo sapiens
 US-09-396-196G-104928
 US-09-136-605-26
 SEQ ID NO 26
LENGTH: 33
 TYPE: DNA ORGANISM:
 Query Match
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Gaps

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STATE: Illinois
 TOPOLOGY: 1i
 US-08-484-596A-56
 COUNTRY:
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 Gaps
 APPLICANT: Harrists Ph.D., Jeffrey D.
APPLICANT: Har, Kuang T.
APPLICANT: Hau, Kuang T.
APPLICANT: How, Kuang T.
APPLICANT: Bodolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
 ö
 52.8%; Score 13.2; DB 2; Length 36; 83.3%; Pred. No. 3.1e+03;
 3; Indels
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: How, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Pharmaceutical Compositions for TITLE OF INVENTION: Immunocontraception
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS: 61
CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: Chicago
STARE: United States of America
ZIP: Chicago
STARE: Illinois
CONTURE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
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 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 83.3%; Pred.
 CURKENI AFFLICATION NUMBER: US/08/484,158B
PILING DATE: 07-JUNE-95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/149,223
PRIOR APPLICATION NUMBER: 08/012,990
PILING DATE: 29-JAN-93
PRIOR APPLICATION NUMBER: 08/012,990
PILING DATE: 29-JAN-93
PRIOR APPLICATION NUMBER: 07/973,341
FILING DATE: 05-NOV-92
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REFERENCE/DOCKET NUMBER: 36,107
 Sequence 56, Application US/08484596A Patent No. 5981228 GENERAL INFORMATION:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
 8 CTAGCAGATTCATGGCAC 25
 CTAGCAGATCTATGGCGC 22
 INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
 Best Local Similarity 83.3
Matches 15; Conservative
 single
 TOPOLOGY: linear MOLECULE TYPE: DNA
 STRANDEDNESS:
 US-08-484-158B-56
 RESULT 40
US-08-484-596A-56
 Query Match
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COUNTRY: United States of America

ZIP: G606-6401

COMPUTER READABLE FORM:
MEDIDA TREE: Floppy Compatible
COMPUTER: IMP Compatible
COMPUTER: IMP COMPATIBLE
COMPUTER: IMP COMPATIBLE
SOFTWARE: PARENTIN Release #1.0, Version #1.25

COMPATIBLE IMP COMPATIBLE
CLASSIFICATION DATA:
PRINCA PELICATION DATA:
PRINCA PAPLICATION DATA:
PRINCA PAPLICATION NUMBER: U5/9149,223
FILING DATE: U-NOV-1992
ATPORNEY ACADICATION NUMBER: 07/973,341
FILING DATE: U-NOV-1992
ATPORNEY ACADICATION NUMBER: 07/973,341
FILING DATE: U-NOV-1992
ATPORNEY ACADICATION NUMBER: 31745
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ATPORNEY ACADICATION NUMBER: 31745
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FILING DATE: U-NOV-1992
ATPORNEY ACADICATION NUMBER: 31745
FILING DATE: U-NOV-1992
ATPORNEY ACADICATION NUMBER: 31745
FILING DATE: U-NOV-1992
ATPORNEY ACADICATION NUMBER: 31745
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FILING DATE: U-NOV-1992
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FILING DATE: U-NOV-1992
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FILING DATE: U-NOV-1992
ATPORNEY ACADICATION NUMBER: 31745
FILING DATE: U-NOV-1992
ATPORNEY MACH SERVICE ACADICATION NUMBER: 31745
FILING DATE: U-NOV-1992
AUGUST TYPE: U-NO
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81247, A 384887,

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Sequence Sequence Sequence

644145, 738392,

Sequence Sequence Sequence

Sequence

1185, Ap 21199, A 853965, 369596,

10, Appl 697665,

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq

30872, A 435368,

Sequence Sequence Sequence

Sequence

482048

Sequence Sequence Sequence

24, Appl 24, Appl 394784, 906265, 643918,

Sequence Sequence Sequence

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Sequence 10, Application US/08469172
Sequence 10, Application US/08469172
Publication No. US20030054343A1
FUBLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: WATKINS, HUGH
APPLICANT: WATKINS, HUGH
TITLE OF INVENTION: A METHOD FOR DETECTING
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
US-11-060-756-203326
US-11-060-756-203327
US-10-719-956-623327
US-11-036-317-644145
US-10-719-956-815329
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US-11-036-317-482048
US-11-036-317-482048
US-10-759-860-24
 ALIGNMENTS
 ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,172
FILLIO DATE:
CLASSIFICATION:
 MEDIUM TYPE: Floopy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS GOTWARE: ASCII
 Massachusetts
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 U.S.A.
 CITY: BOSTON
STATE: Massac
 02109
 COUNTRY:
 116.2
116.2
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 Sequence 10, Appl
Sequence 10, Appl
Sequence 506713,
Sequence 179689,
Sequence 625525,
 November 18, 2005, 06:36:48; Search time 336.027 Seconds (without alignments) 615.265 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| cgn2 6/ptodata1/1/pubpna/USO9 FUBGOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
 US-10-788-779-10
US-11-036-317-506713
US-11-060-756-179689
US-10-719-956-625525
 Total number of hits satisfying chosen parameters:
 9794790 seqs, 4134909567 residues
 US-08-469-172-10
 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 SUMMARIES
 Published Applications NA: *
 - nucleic search, using sw model
 Listing first 45 summaries
 Gapop 10.0 , Gapext 1.0
 Post-processing: Minimum Match 0% Maximum Match 100%
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26
26
27
27
 US-10-788-779-10
25
 В
 Length
 IDENTITY NUC
 Copyright
 Minimum DB seq length: 0 Maximum DB seq length: 50
 Query
Match
 100.0
100.0
67.2
66.4
64.8
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25 25 16.8 16.6 16.2

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Score

Result Š.

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TYPE: DNA
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 Gaps
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 100.0%; Score 25; DB 8; Length 25; 100.0%; Pred. No. 0.014;
 0; Indels
 Sequence 10, Application US/10788779
Publication No. US20040152121A1
GENERAL INFORMATION:
APPLICANT: SEIDWAN, CHRISTINE
SEIDWAN, JOHN
WATKINS, HUGH
ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
DISEASE-ASSOCIATED MUTATIONS
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/788,779
FILING DATE: 27-Feb-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/469,172
FILING DATE: «Unknown»
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GML-111
TELECOMMUNICATION:
 ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
 0; Mismatches
 STATE: Massachusetts
CONTRX: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,160
FILING DATE: 11-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
TELECHONE: (617) 227-7400
TELECHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENOTH: 25 Dase pairs
 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 GCTGAGCCTAGCAGATTCATGGCAC 25
 TELEPHONE: (617) 227-7400
 SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 TELEPAX: (617) 227-5
INFORMATION FOR SEQ ID NO: 10:
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS
 Query Match
Best Local Similarity 100.0
 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
US-08-469-172-10
 RESULT 2
US-10-788-779-10
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Sequence 179689, Application US/11060756

Publication No. US20050221354A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William Martin

TITLE OF INVENTION: Target Genes

FILE REFERENCE: AM101083 (031896-042000)

CURRENT APPLICATION UNMERS: US/11/060,756

CURRENT FILING DATE: 2005-02-18

NUMBER OF SEQ ID NOS: 303284
 ö
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 RESULT 3
US-11-036-137-506713/C
US-11-036-137-506713/C
Sequence 506713, Application US/11036317
Sequence 506713, Application US/11036317
SENBEAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFRENCE: 3654.1
CURRENT APLICATION NUMBER: US/11/036,317
CURRENT PILING DATE: 2005-01-13
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 506713
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 67.2%; Score 16.8; DB 26; Length 25; 90.0%; Pred. No. 2.3e+02; ive 0; Mismatches 2; Indels C
 Length 25;
 0; Indels
 Indels
 Score 16.6; DB 26;
Pred. No. 2.9e+02;
0; Mismatches 4;
 Score 25; DB 20;
Pred. No. 0.014;
 0; Mismatches
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 1 ścicaścinaczadnicarcecac 25
 GCGGAGCCTAGCAGACTCAGGCC 25
 4 GAGCCTAGCAGATTCATGGC 23
 GAGCCTAGTAGATTGATGGC 3
 Query Match
Best Local Similarity 100.0%;
Matches 25; Conservative 0
 66.4%;
 SOFTWARE: Patentin version 3.2
SEQ ID NO 179689
LENGTH: 25
 Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
 Query Match
Best Local Similarity 82.6
Matches 19; Conservative
 ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-506713
 ORGANISM: probe US-11-060-756-179689
 US-11-060-756-179689
 ;
US-10-788-779-10
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Sequence 644165, Application US/11036317

Sequence 644165, Application US/11036317

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPERENCE: 3654.1

CURRENT PILING DATE: 2005-01-13

FRIOR APPLICATION NUMBER: US 60/536,639

FRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 641445
 Gaps
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 Length 25;
 Length 25;
 Length 25;
 TITLE OF INVENTION: Methods of Genetic Analysis of Rat FILL OF INVENTION: Methods of Genetic Analysis of Rat FILLS OF INVENTION: Methods of Genetic Analysis of Rat FILLS OF INVENTION WIMBER: US/10/719,956
CURRENT FILLING DATE: 2003-11-20
PRIOR APPLICATION WIMBER: 60/427,836
PRIOR FILLING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 696370
LENGTH: 25
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 Score 16.2; DB 26;
Pred. No. 4.6e+02;
0; Mismatches 3;
 Score 15.8; DB 24;
Pred. No. 7.4e+02;
0; Mismatches 2;
 Query Match 62.4%; Score 15.6; DB 26; Best Local Similarity 81.8%; Pred. No. 9.4e+02; Matches 18; Conservative 0; Mismatches 4;
 ; Sequence 696370, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
 1 GCTGAGCCTAGCAGATTCATGG 22
 ecrerecesecasarcares 3
 1 GCTGAGCCTAGCAGATTCATG 21
 4 GCGGAGCCTAGCAGACTCAGG 24
 2 CTGAGCCTAGCAGATTCAT 20
 23 crcadcccadcadarcar 5
 64.8%;
85.7%;
 63.2%;
89.5%;
) ORGANISM: Rattus norvegicus
US-10-719-956-696370
 Query Match
Best Local Similarity 89.5'
Matches 17; Conservative
 Query Match
Best Local Similarity 85.7
Matches 18; Conservative
 TYPE: DNA
CRGANISM: Mus musculus
US-11-036-317-644145
 US-10-719-956-696370/c
 US-11-036-317-644145/c
 ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-203327
 LENGTH: 25
 TYPE: DNA
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 Sequence 203326, Application US/11060756

Publication No. US20050221354A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION:
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SEQ ID NO 203326
LENGTH: 25
 Sequence 203327, Application US/11060756
Publication No. US200502213541
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE PERERENCE: AM101083 (031896-04200)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOCTWARE: Patentin version 3.2
SEQ ID NO 203327
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Sequence 625525

Sequence 625525

Sequence 625525

Publication No. US20040146910A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,836

PRIOR FILING DATE: 2002 11 20

NUMBER: OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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 Length 25;
 ch 64.8%; Score 16.2; DB 24; Length 1.1 Similarity 85.7%; Pred. No. 4.6e+02; 18; Conservative 0; Mismatches 3; Indels
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 1 GCTGAGCCTAGCAGATTCATG 21
 1 GCTGAGCCTAGCAGATTCATG 21
 4 GCGGAGCCTAGCAGACTCAGG 24
 ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-625525
 Query Match 64.8
Best Local Similarity 85.7
Matches 18; Conservative
 Best Local Similarity
Matches 18; Conserv
 RESULT 6
US-11-060-756-203326
 ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-203326
 US-11-060-756-203327
 Query Match
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Sequence 738392, Application US/11036317
Sequence 738392, Application US/11036317
Sequence 7018392, Application No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPRENT APLICATION NUMBER: US/11/036,317
CURRENT APLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFFWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 738392
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 Sequence 30711/c
; Sequence 30711, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: Wethods of Genetic Analysis of Mouse
; TITLE OF INVENTION: WIMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; RIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
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62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0
 Query Match 60.8%; Score 15.2; DB 22; Length 25; Best Local Similarity 85.0%; Pred. No. 1.5e+03; Matches 17; Conservative 0; Mismatches 3; Indels (
 APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 Sequence 841582, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
 1 GCTGAGCCTAGCAGATTCATGG 22
 ścrerczaczaczaczacze 25
 2 CTGAGCCTAGCAGATTCATG 21
 22 CTAAGGCTAGCAGAATCATG 3
 ; ORGANISM: Mus musculus US-11-036-317-738392
 ; ORGANISM: Mus musculus
US-10-719-900-30711
 US-10-719-900-841582/c
RESULT 10
US-11-036-317-738392
 TYPE: DNA
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Sequence 161796, Application US/10956157

Formalication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 161796

LENGTH: 25
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 Sequence 320514, Application US/10719956

publication No. US20040146910A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25

LENGTH: 25
 Length 25;
 Length 25;
 Length 25;
 Indels
 Indels
 Indels
 Score 15.2; DB 22;
Pred. No. 1.5e+03;
n. Mismatches 3;
 60.8%; Score 15.2; DB 24;
85.0%; Pred. No. 1.5e+03;
tive 0; Mismatches 3;
 60.8%; Score 15.2; DB 22; 85.0%; Pred. No. 1.5e+03;
 0; Mismatches
 0; Mismatches
 6 GCCTAGCAGATTCATGGCAC 25
 2 CTGAGCCTAGCAGATTCATG 21
 5 AGCCTAGCAGATTCATGGCA 24
 2 AGCCTGGCAGATGCCTGGCA 21
 25 CTAAGGCTAGCAGAATCATG 6
 60.8%;
85.0%;
 ; ORGANISM: Rattus norvegicus
US-10-719-956-320514
 Query Match
Best Local Similarity 85.0%
Matches 17; Conservative
 Query Match
Best Local Similarity 85.01
Matches 17; Conservative
 Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
 ; ORGANISM: Probe Sequence US-10-956-157-161796
 LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-841582
 RESULT 13
US-10-956-157-161796
SEQ ID NO 841582
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; SEQ ID NO 506712
 LENGTH: 25
 Query Match
 TYPE: DNA
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 APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
 Gaps
 Gaps
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 RESULT 16
US-10-719-956-625734/C

i Sequence 625734 Application US/10719956

i Publication No. US20040146910A1

i GENERAL INFORMATION:
 APPLICANT: Xue Mei Zhou

ITILE OF INVENTION: Methods of Genetic Analysis of Rat
 TITLE OF INVENTION: Wethods of Genetic Analysis of Rat
 CURRENT APPLICATION NUMBER: US/10/719,956

i CURRENT FILING DATE: 2003-11-20

FRIOR FILING DATE: 2003-11-20

i RHORE NO SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
 Sequence 460511, Application US/10719956

Sequence 460511, Application US/10719956

Publication No. US20040146910A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

ITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 357.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT PILING DATE: 2003-11-20

PRIOR RILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 699466

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
 Length 25;
 Query Match 60.8%; Score 15.2; DB 24; Length 25; Best Local Similarity 85.0%; Pred. No. 1.5e+03; Matches 17; Conservative 0; Mismatches 3; Indels
 NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 60.8%; Score 15.2; DB 24; Length
85.0%; Pred. No. 1.5e+03;
ive 0; Mismatches 3; Indels
 ; Sequence 506712, Application US/11036317; Publication No. US20050214823A1; GENERAL INFORMATION:
APPLICANT: Williams, Alan
 6 GCCTAGCAGATTCATGGCAC 25
 5 AGCCTAGCAGATTCATGGCA 24
 23 AGCTTCTCAGATTCATGGCA 4
 22 GCCTAGCAGAGCCTTGGCAC 3
 ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-460571
 TYPE: DNA ORGANISM: Rattus norvegicus
 17; Conservative
 Best Local Similarity
 RESULT 17
US-11-036-317-506712/c
 US-10-719-956-625734
 Query Match
 Matches
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Sequence 185070, Application US/11060756

Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wouths, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: UNDBRR: US/11/060,756
CURRENT APPLICATION NUMBRR: US/11/060,756
CURRENT FILING DATE: 2005-02-18
SOFTWARE: Patentin version 3.2
SEQ ID NO: 185070
LENGTH: 25
 Sequence 743982, Application US/11036317
; Sequence 743982, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TILE REFERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13
; CURRENT FILING DATE: 2006-01-13
; RIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SEOTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEOTWARE: LEAR APPLICATION FOR SEQUENCE LISTING GENERATOR V 1.1
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 Length 25;
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 Score 15.2; DB 26;
Pred. No. 1.5e+03;
0; Mismatches 3;
 60.8%; Score 15.2; DB 26;
85.0%; Pred. No. 1.5e+03;
 60.8%; Score 15.2; DB 26; ilarity 85.0%; Pred. No. 1.5e+03; Conservative 0; Mismatches 3;
 0; Mismatches
 3 TGAGCCTAGCAGATTCATGG 22
 4 GAGCCTAGCAGATTCATGGC 23
 6 rradccradcadarcrards 25
 4 GAGCCTAGCAGATTCATGGC 23
 22 GAGCCTAGTTGATGGC 3
 60.8%;
 Query Match
Best Local Similarity 85.01
Matches 17; Conservative
 Best Local Similarity 85.0
Matches 17; Conservative
TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-506712
 ; ORGANISM: Mus musculus
US-11-036-317-743982
 Query Match
Best Local Similarity
Matches 17; Conserv
 US-11-060-756-185070
 ; ORGANISM: probe
US-11-060-756-185070
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SEQ ID NO 616192
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 Sequence 81247, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INPORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFUTANE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81247
 Sequence 616192, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICAMT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; CURRENT PELICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2003-11
; PRIOR FILING DATE: 2003-11
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 60.0%; Score 15; DB 22; Length 25; 78.3%; Pred. No. 1.9e+03; Live 0; Mismatches 5; Indels
 PAPLICANT CONTINUED TO THE CONTINUED TO THE CONTINUED TO THE REFERENCE: 35.20 THILE REFERENCE: 35.20 THILE REFERENCE: 35.20 THILE REFERENCE: 35.20 THILE REFERENCE: 30.03-11-20 THILE REPELICATION NUMBER: 60/427, 808 PRIOR FILING DATE: 2002-11-20 NUMBER OF SEQ ID NOS: 982914 SOFTWARE MICROALING SEQUENCE LISTING Generator V 1.1 SEQ ID NO 34887
 Score 15; DB 22; Length 25;
Pred. No. 1.9e+03;
 Mismatches
 ; Sequence 384887, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
 2 CTGAGCCTAGCAGATTCATGGCA 24
 25 crcadcrredeadarrerredea 3
 60.0%; Scc.
100.0%; Pre
 6 GCCTAGCAGATTCAT 20
 7 GCCTAGCAGATTCAT 21
 Query Match 60.0
Best Local Similarity 100.
Matches 15; Conservative
 Best Local Similarity 78.3
Matches 18; Conservative
 ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-384887
 ORGANISM: Mus musculus
 US-10-719-900-81247/c
 US-10-719-900-384887
 US-10-719-900-616192
 US-10-719-900-81247
 Query Match
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 US-10-719-956-40306/C

Sequence 40306, Application US/10719956

Publication No. US2040146910A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REPERBUCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT PLING DATE: 2003-11-20

PRIOR PILING DATE: 2003-11-20

PRIOR PILING DATE: 2002 11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 40306

LENGTH: 256
 Sequence 513171, Application US/10719956
; Bublication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REPERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT APPLICATION NUMBER: 0503-11-20
; PRIOR APPLICATION WUMBER: 60/427,836
; PRIOR PILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
 Score 15; DB 24; Length 25; Pred. No. 1.9e+03; 0; Mismatches 5; Indels
 60.0%; Score 15; DB 24; Length 25; 78.3%; Pred. No. 1.9e+03; tive 0; Mismatches 5; Indels
 5; Indels
 . 1.9e+03;
 Score 15; DB 22;
Pred. No. 1.9e+03;
 0; Mismatches
 0; Mismatches
 2 GCCGAGCATAGCAGTTTTCTGGC 24
 1 GCTGAGCCTAGCAGATTCATGGC 23
 1 GCTGAGCCTAGCAGATTCATGGC 23
 3 TGAGCCTAGCAGATTCATGGCAC 25
 GCTGAGGCAGCCACATTCATGGC 3
 23 rerectreccaearrearceae 1
 Query Match 60.0%;
Best Local Similarity 78.3%;
Matches 18; Conservative
 Query Match 60.0%;
Best Local Similarity 78.3%;
Matches 18; Conservative (
 CRGANISM: Rattus norvegicus US-10-719-956-40306
 ; ORGANISM: Rattus norvegicus
US-10-719-956-513171
 Query Match
Best Local Similarity 78.3%
LENGTH: 25
TYPE: DNA
CRGANISM: Mus musculus
US-10-719-900-616192
 RESULT 24
US-10-719-956-513171/c
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 Length 25;
 Length 25;
 Length 25;
 CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 21199
LENGTH: 25
 FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT PILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 853965
 APPLICATE TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO THE REPERENCE: 3527.1
FILE REPERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 369596
 Indels
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 APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 Score 14.8; DB 22;
Pred. No. 2.4e+03;
0; Mismatches 2;
 Score 14.8; DB 22;
Pred. No. 2.4e+03;
0; Mismatches 2;
 Score 14.8; DB 24;
Pred. No. 2.4e+03;
0; Mismatches 2;
CURRENT APPLICATION NUMBER: US/10/719,900
 ; Sequence 853965, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
 ; Sequence 369596, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
 ;
0
 5 AGCCTAGCAGATTCATGG 22
 1 GCTGAGCCTAGCAGATTC 18
 21
 59.2%;
 59.2%;
 Query Match 59.2%;
Best Local Similarity 88.9%;
Matches 16; Conservative
 24 AGCCTACCACATTCATGG
 4 GCTGGGCCTAGTAGATTC
 ; ORGANISM: Rattus norvegicus
US-10-719-956-369596
 Query Match 59.2
Best Local Similarity 88.9
Matches 16; Conservative
 Query Match
Best Local Similarity 88.9
Matches 16, Conservative
 ; ORGANISM: Mus musculus
US-10-719-900-21199
 ; ORGANISM: Mus musculus
US-10-719-900-853965
 US-10-719-956-369596/c
 US-10-719-900-853965
 LENGTH: 25
 TYPE: DNA
 TYPE: DNA
 TYPE: DNA
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 APPLICANT: MOLISAGE..., C.J.
APPLICANT: PLY, KIRK
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Wordward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: METHODS AND COMPOSITIONS DISEASES
TITLE OF INVENTION: MUMBER: US/002.290
FILE REFERENCE: 506612000120
CURRENT PELICATION NUMBER: US 10/006,290
FRIOR FILING DATE: 2001-10-22
FRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOOTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1185
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 'MS-11-036-317-567135, Application US/11036317
'Sequence 567135, Application US/11036317
'PUBLication No. US20050214823A1
'GENERAL INFORMATION:
'APPLICANT: Williams, Alan
'APPLICANT: Blume, John
'TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 0; Gaps
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 ;
 Query Match 60.0%; Score 15; DB 26; Length 25; Best Local Similarity 78.3%; Pred. No. 1.9e+03; Matches 18; Conservative 0; Mismatches 5; Indels
 FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
 Length 50;
 1.9e+03;
 Score 15; DB 18; Length 50 Pred. No. 2.1e+03; 0; Mismatches 5; Indels
 Sequence 21199, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
ITILE OF INVERTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
 Sequence 1185, Application US/10131827
Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
 1 GCTGAGCCTAGCAGATTCATGGC 23
 3 TGAGCCTAGCAGATTCATGGCAC 25
 14 reacceacecacriacacacac
 25 dereadecreeradardearde 3
 Query Match
Best Local Similarity 78.3%;
Matches 18; Conservative
 TYPE: DNA ORGANISM: Mus musculus
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1185
 US-10-719-900-21199/c
 US-11-036-317-567135
 RESULT 27
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 Sequence 10, Application US/10623500
| Publication No. US20040133945A1
| GENERAL INFORMATION:
| APPLICANT: Bayer BioScience N.V.
| APPLICANT: Greet, Vanderkimpen
| APPLICANT: Greet, Vanderkimpen
| APPLICANT: Greet, Vanderkimpen
| TITLE OF INVENTION: Corn root preferential promoters and uses thereof
| TITLE OF INVENTION: Corn root preferential
| FILE REFERENCE: 021565-119
| CURRENT APPLICATION NUMBER: US/10/623,500
| CURRENT PILING DATE: 2003-07-22
| PRIOR FILING DATE: 2002-07-31
| NUMBER OF SEQ ID NOS: 32
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 10
| INDICATION NO 10
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 58.4%; Score 14.6; DB 20; Length 25; 81.0%; Pred. No. 3.1e+03; ive 0; Mismatches 4; Indels (
 58.4%; Score 14.6; DB 22; Length 25; larity 81.0%; Pred. No. 3.1e+03; Conservative 0; Mismatches 4; Indels
 NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 697665
LENGTH: 25
 Sequence 697665, Application US/10719900
PUblication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
ITILE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REPERENCY: 328.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
 OTHER INFORMATION: oligonucleotide primer GVK30
 Sequence 16200, Application US/10956157; Publication No. US20050118625A1
 4 GAGCCTAGCAGATTCATGGCA 24
 3 TGAGCCTAGCAGATTCATGGC 23
 2 reaccrearcacarrearese 22
 23 GAGCATAGTCGATCCATGGCA 3
7 CCTAGCAGATTCATGGCA 24
 20 CCTAGGAGATTCATGACA 3
 Best Local Similarity 81.0
Matches 17; Conservative
 TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-697665
 TYPE: DNA
ORGANISM: Artificial
 Best Local Similarity
Matches 17; Conserv
 US-10-956-157-16200/c
 RESULT 31
US-10-719-900-697665
 US-10-623-500-10/c
 US-10-623-500-10
 Query Match
 Query Match
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APPLICANT: Wyeth
APPLICANT: Woults, William
APPLICANT: Woults, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-110-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 16200
LENGTH: 25
 APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 16201
 Sequence 16202, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: HUMAN OSTECARTHAITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE PARENTI VERSION 3.2
SOFTWARE PARENTI VERSION 3.2
LENGTH: 25
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 58.4%; Score 14.6; DB 22; Length 25; 81.0%; Pred. No. 3.1e+03;
 Indels
 Indels
 Query Match 58.4%; Score 14.6; DB 22; Best Local Similarity 81.0%; Pred. No. 3.1e+03; Matches 17; Conservative 0; Mismatches 4;
 0; Mismatches
 Sequence 16201, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
 5 AGCCTAGCAGATTCATGGCAC 25
 5 AGCCTAGCAGATTCATGGCAC 25
 23 AGCCTCTCAGATTCATTGAAC 3
 24 AGCCTCTCAGATTCATTGAAC
 Best Local Similarity 81.03
Matches 17; Conservative
 TYPE: DNA
ORGANISM: Probe Sequence
US-10-956-157-16201
 TYPE: DNA
CRGANISM: Probe Sequence
US-10-956-157-16200
 TYPE: DNA
CRGANISM: Probe Sequence
US-10-956-157-16202
 US-10-956-157-16201/c
 RESULT 34
US-10-956-157-16202/c
 Query Match
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Sequence 43586, Application US/11036317

Sequence 43586, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3664.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT PILING DATE: 2005-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOUTHWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 435368
 GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INFORMATION:
WEthod of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 30872
LENGTH: 25
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 Length 25;
 58.4%; Score 14.6; DB 26; Length 25; 81.0%; Pred. No. 3.1e+03; cive 0; Mismatches 4; Indels
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 625526
LENGTH: 25
 Indels
 58.4%; Score 14.6; DB 24;
81.0%; Pred. No. 3.1e+03;
live 0; Mismatches 4;
 Sequence 30872, Application US/11036317; Publication No. US20050214823A1
 2 GCTGAGCCCAGGTGATGCATG 22
 1 GCTGAGCCTAGCAGATTCATG 21
 1 GCTGAGCCTAGCAGATTCATG 21
 4 ścickáccickáckáritczie 24
 ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-625526
 17; Conservative
 Best Local Similarity 81.0
Matches 17; Conservative
 ; ORGANISM: Mus musculus
US-11-036-317-30872
 TYPE: DNA ORGANISM: Mus musculus
 Query Match
Best Local Similarity
 RESULT 39
US-11-036-317-435368
 RESULT 38
US-11-036-317-30872
 TYPE: DNA
 Query Match
 Matches
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 Sequence 16203, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
PUBLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: WYETHON: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTECARTRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-04300 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 16203
LENGTH: 25
 Sequence 16206, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION OF 1200 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARKE: PATENTIN VERSION 3.2

SEQ ID NO 16206
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 / Match 58.4%; Score 14.6; DB 22; Length 25; Local Similarity 81.0%; Pred. No. 3.1e+03; nes 17; Conservative 0; Mismatches 4; Indels
 Length 25;
 58.4%; Score 14.6; DB 22; Length 25; 81.0%; Pred. No. 3.1e+03; ive 0; Mismatches 4; Indels
 Query Match 58.4%; Score 14.6; DB 22; Best Local Similarity 81.0%; Pred. No. 3.1e+03; Matches 17; Conservative 0; Mismatches 4;
 Sequence 625526, Application US/10719956; Publication No. US20040146910A1; GENERAL INFORMATION:
 5 AGCCTAGCAGATICATGGCAC 25
 5 AGCCTAGCAGATTCATGGCAC 25
 5 AGCCTAGCAGATTCATGGCAC 25
 21 AGCCTCTCAGATTCATTGAAC 1
 22 AGCCTCTCAGATTCATTGAAC 2
 25 AGCCTCTCAGATTCATTGAAC 5
 Query Match
Best Local Similarity 81.0
Matches 17; Conservative
 ; TYPE: DNA; ORGANISM: Probe Sequence US-10-956-157-16203
 ; ORGANISM: Probe Sequence
US-10-956-157-16206
 US-10-956-157-16203/c
 RESULT 37
US~10-719-956-625526
 Query Match
 TYPE: DNA
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 RESULT 40

US-11-036-317-482048/c

Sequence 482048, Application US/11036317

Publication No. US20050214823A1

GENERAL INVENDATION:

APPLICANT: Williams, Alan

TILLS OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.11

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2004-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 482048
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 Query Match 58.4%; Score 14.6; DB 26; Length 25; Best Local Similarity 81.0%; Pred. No. 3.1e+03; Matches 17; Conservative 0; Mismatches 4; Indels C
 Query Match 58.4%; Score 14.6; DB 26; Length 25; Best Local Similarity 81.0%; Pred. No. 3.1e+03; Matches 17; Conservative 0; Mismatches 4; Indels (
 5 AGCCTAGCAGATTCATGGCAC 25
 1 GCTGAGCCTAGCAGATTCATG 21
 4 GCTGAGCCTGGGAGTTTCCTG 24
 TYPE: DNA
CRGANISM: Mus musculus
US-11-036-317-482048
US-11-036-317-435368
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Search completed: November 18, 2005, 15:41:10 Job time : 336.027 secs

24 AGCCTAGCCGTTCATGTCAC 4

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